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OM protein - protein search, using sw model

Run on: November 28, 2003, 08:03:09 ; Search time 17 Seconds  
(without alignments)  
246.399 Million cell updates/sec

Title: US-10-059-395-142  
Perfect score: 99  
Sequence: 1 MKIPVLPAVLLSLVLHSA.....LNWDAFPKLGKLSATPDQ 99

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*

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6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	100.0	99	4	US-09-996-243-201 Sequence 201, App
2	9	9.1	344	4	US-09-252-991A-22286 Sequence 22286, A
3	8	8.1	61	2	US-08-359-222-2 Sequence 2, Appli
4	8	8.1	61	3	US-09-094-563-2 Sequence 2, Appli
5	8	8.1	146	4	US-09-107-532A-5900 Sequence 5900, Ap
6	7	7.1	72	4	US-09-205-258-333 Sequence 333, App
7	7	7.1	80	2	US-08-747-121-7 Sequence 7, Appli
8	7	7.1	133	4	US-09-152-060-75 Sequence 75, Appl
9	7	7.1	254	4	US-09-107-532A-4795 Sequence 4795, A
10	7	7.1	257	4	US-09-252-991A-26002 Sequence 26002, A
11	7	7.1	312	2	US-08-518-862C-2 Sequence 2, Appli
12	7	7.1	373	4	US-09-066-281B-19 Sequence 19, Appl
13	7	7.1	407	3	US-08-948-997-3 Sequence 3, Appli
14	7	7.1	410	3	US-09-348-817A-3 Sequence 3, Appli
15	7	7.1	410	4	US-09-722-292-3 Sequence 3, Appli
16	7	7.1	457	2	US-08-847-900-3 Sequence 3, Appli
17	7	7.1	648	4	US-09-198-452A-594 Sequence 594, App
18	7	7.1	814	3	US-09-813-819-4 Sequence 4, Appli
19	7	7.1	814	4	US-09-920-048-4 Sequence 4, Appli
20	7	7.1	855	3	US-09-813-819-2 Sequence 2, Appli
21	7	7.1	855	4	US-09-920-048-2 Sequence 2, Appli
22	6	6.1	9	2	US-08-747-121-15 Sequence 15, Appl
23	6	6.1	18	1	US-08-295-085-3 Sequence 3, Appli
24	6	6.1	18	1	US-08-295-085-4 Sequence 4, Appli
25	6	6.1	18	1	US-08-295-085-5 Sequence 5, Appli
26	6	6.1	18	5	PCT-US95-10741-3 Sequence 3, Appli
27	6	6.1	18	5	PCT-US95-10741-4 Sequence 4, Appli

28	6	6.1	18	5	PCT-US95-10741-5	Sequence 5, Appli
29	6	6.1	26	4	US-09-504-633-2	Sequence 2, Appli
30	6	6.1	29	4	US-09-227-357-176	Sequence 176, App
31	6	6.1	33	4	US-09-205-258-295	Sequence 295, App
32	6	6.1	45	4	US-08-469-260A-483	Sequence 483, App
33	6	6.1	45	4	US-08-488-446-483	Sequence 483, App
34	6	6.1	45	4	US-08-467-344A-483	Sequence 483, App
35	6	6.1	50	3	US-09-346-860-14	Sequence 14, Appl
36	6	6.1	50	4	US-09-735-685-14	Sequence 14, Appl
37	6	6.1	63	4	US-09-504-633-4	Sequence 4, Appli
38	6	6.1	73	4	US-09-345-236B-88	Sequence 88, Appl
39	6	6.1	97	4	US-08-973-544-4	Sequence 4, Appli
40	6	6.1	98	1	US-08-375-346A-2	Sequence 2, Appli
41	6	6.1	98	2	US-08-467-123B-2	Sequence 2, Appli
42	6	6.1	98	3	US-08-943-336A-2	Sequence 2, Appli
43	6	6.1	98	4	US-09-635-899-2	Sequence 2, Appli
44	6	6.1	98	5	PCT-US95-01780-2	Sequence 2, Appli
45	6	6.1	104	4	US-08-973-544-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-09-996-243-201  
Sequence 201 / Application US/09996243

09/990443

Patent No. 6479825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavir, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996,243  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28



Sat Nov 29 17:52:31 2003

us-10-059-395-142.011.ra1

**Page 2**

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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
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PRIOR FILING DATE: 1998-06-17
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3	PRIOR FILING DATE: 1998-06-17
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5	PRIOR FILING DATE: 1998-06-18
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65	PRIOR FILING DATE: 1998-07-02
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69	PRIOR FILING DATE: 1998-07-02
70	PRIOR APPLICATION NUMBER: 60/0916266
71	PRIOR FILING DATE: 1998-07-02
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73	PRIOR FILING DATE: 1998-07-02

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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 99; DB 4; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.8e-93;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKIPVLPVAVLVLVLSLVLHSAQATIGGPEESTIENYASRPEAFNTPLNIDKLSAFKA 60

QY 61 DEFILNWHALFESIKRKLPLNWDAPPKLGLRSATPDAQ 99  
Db 61 DEFILNWHALFESIKRKLPLNWDAPPKLGLRSATPDAQ 99

## RESULT 2

US-09-252-991A-22286  
; Sequence 22286, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 22286  
; LENGTH: 344  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-22286

Query Match 9.1%; Score 9; DB 4; Length 344;  
Best Local Similarity 100.0%; Pred. No. 0.27;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 GLRSATPDA 98  
Db 210 GLRSATPDA 218

RESULT 3  
US-08-359-222-2  
; Sequence 2, Application US/08359222  
; Patent No. 5824648

; GENERAL INFORMATION:  
; APPLICANT: YANG, Mabel M.  
; APPLICANT: CHEN, George  
; TITLE OF INVENTION: RNASE-CV (CORIOLUS VERSICOLOR)  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jerome J. No. 5824648ris  
; STREET: 1919 18th Street, N.W., Suite 750  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/359,222  
FILING DATE: 19-DEC-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5824648ris, Jerome J.  
REGISTRATION NUMBER: 24,696  
REFERENCE/DOCKET NUMBER: 599.31757PX1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-737-4410  
TELEFAX: 202-737-3315  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Bos taurus ribonuclease  
TISSUE TYPE: Pancreas  
US-08-359-222-2

Query Match 8.1%; Score 8; DB 2; Length 61;  
Best Local Similarity 100.0%; Pred. No. 0.55;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLISLVL 17  
Db 8 VLISLVL 15

RESULT 4  
US-09-094-563-2  
; Sequence 2, Application US/09094563  
; Patent No. 6087335

; GENERAL INFORMATION:  
; APPLICANT: YANG, Mabel M.  
; APPLICANT: CHEN, George  
; TITLE OF INVENTION: RNASE-CV (CORIOLUS VERSICOLOR)  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jerome J. No. 6087335ris  
; STREET: 1919 Pennsylvania Avenue, N.W., Suite 200  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/094,563  
FILING DATE: 15-JUN-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6087335ris, Jerome J.  
REGISTRATION NUMBER: 24,696  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-737-4410  
TELEFAX: 202-737-3315  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO

ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Bos taurus ribonuclease  
TISSUE TYPE: Pancreas  
US-09-094-563-2

Query Match 8.1%; Score 8; DB 3; Length 61;  
Best Local Similarity 100.0%; Pred. No. 0.55;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLISLVL 17  
Db 8 VLISLVL 15

RESULT 5  
US-09-107-532A-5900  
Sequence 5900, Application US/09107532A  
Patent No. 6583275

## GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354

## COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997

## ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007

## TELECOMMUNICATION INFORMATION:

TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 5900:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 146 amino acids  
TYPE: amino acid

## MOLECULE TYPE: linear

## HYPOTHETICAL: YES

## ORIGINAL SOURCE:

## ORGANISM: Enterococcus faecium

## FEATURE:

NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...146  
SEQUENCE DESCRIPTION: SEQ ID NO: 5900:  
US-09-107-532A-5900

Query Match 8.1%; Score 8; DB 4; Length 146;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLISLVL 17  
Db 42 VLISLVL 49

## RESULT 6

US-09-205-258-333  
Sequence 333, Application US/09205258  
Patent No. 6525174

## GENERAL INFORMATION:

APPLICANT: Young et al.

TITLE OF INVENTION: 207 Human Secreted Proteins

FILE REFERENCE: P2007P1

CURRENT APPLICATION NUMBER: US/09/205,258

EARLIER APPLICATION NUMBER: 1998-12-04

EARLIER APPLICATION NUMBER: PCT/US98/11422

EARLIER FILING DATE: 1998-06-04

EARLIER APPLICATION NUMBER: 60/048,885

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049,375

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,881

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,880

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,896

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049,020

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,876

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,895

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,884

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,894

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,971

EARLIER FILING DATE: 1997-06-06

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EARLIER APPLICATION NUMBER: 60/048,882

EARLIER FILING DATE: 1997-06-06

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EARLIER FILING DATE: 1997-06-06

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EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,900

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,901

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,892

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,915

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049,019

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,970

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,972

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,916

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049,373

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,875

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049,374

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,917

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,949

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,974

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,883

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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 333
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (72)
; OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-333

Query Match
Best Local Similarity 7.1%; Score 7; DB 4; Length 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LLSLVL 17
Db 10 LLSLVL 16

RESULT 7
US-08-747-121-7
; Sequence 7, Application US/08747121
; Patent No. 5874290
; GENERAL INFORMATION:
; APPLICANT: Murphy, Gerald
; APPLICANT: Boynton, Alton
; APPLICANT: Sehgal, Anil
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID
; TITLE OF INVENTION: SEQUENCES OF A D2-2 GENE ASSOCIATED WITH
; TITLE OF INVENTION: BRAIN TUMORS AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,121
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Baldwin, Geraldine F
; REGISTRATION NUMBER: 31,232
; REFERENCE/DOCKET NUMBER: 8511-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)7909090
; TELEFAX: (212)8698864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-747-121-7

Query Match
Best Local Similarity 7.1%; Score 7; DB 2; Length 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LLSLVL 17
Db 11 LLSLVL 17

RESULT 8
US-09-152-060-75
; Sequence 75, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; EARLIER FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-75

Query Match
Best Local Similarity 7.1%; Score 7; DB 4; Length 133;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LLSLVL 17
Db 11 LLSLVL 17
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Db 6 LSLVL 12

RESULT 9  
US-09-107-532A-4795  
; Sequence 4795, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 4795:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 254 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (B) LOCATION 1...254  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4795:  
US-09-107-532A-4795

Query Match 7.1%; Score 7; DB 4; Length 254;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 KRKL PFL 80  
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Db 33 KRKL PFL 39

RESULT 10  
US-09-252-991A-26002  
; Sequence 26002, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 26002  
; LENGTH: 257  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-26002

Query Match 7.1%; Score 7; DB 4; Length 257;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 LKGLRSA 94  
| | | | |  
Db 247 LKGLRSA 253

RESULT 11  
US-08-518-862C-2  
; Sequence 2, Application US/08518862C  
; Patent No. 5843757  
; GENERAL INFORMATION:  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth W.  
; APPLICANT: Nicolaides, Nicholas C.  
; TITLE OF INVENTION: Human JTV1 Gene Overlaps PMS2 Gene  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Witcoff, Ltd.  
; STREET: 1001 G Street, N.W.  
; CITY: Washington, D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/518,862C  
; FILING DATE: 24-AUG-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kagan, Sarah A.  
; REGISTRATION NUMBER: 32,141  
; REFERENCE/DOCKET NUMBER: 01107.49697  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-508-9100  
; TELEFAX: 202-508-9299  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 312 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-518-862C-2

Query Match 7.1%; Score 7; DB 2; Length 312;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LSLVLH 18  
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Db 133 LSLVLH 139

RESULT 12  
US-09-066-281B-19  
; Sequence 19, Application US/09066281B

Patent No. 6475783  
; GENERAL INFORMATION:  
; APPLICANT: LUCAS, Sophie; DE SMET, Charles; BOON-FALLEUR, Thierry  
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING  
; FOR TUMOR REJECTION ANTIGEN PRECURSOR MAGE-C1 AND MAGE-C2  
; TITLE OF INVENTION: AND USES THEREOF  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski L.L.P.  
; STREET: 666 Fifth Avenue  
; CITY: New York City  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/066,281B  
; FILING DATE: April 24, 1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/845,528  
; FILING DATE: April 25, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mary Anne Schofield  
; REGISTRATION NUMBER: 36,669  
; REFERENCE/DOCKET NUMBER: LUD-5455.2 US - JEL/WAS  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 318-3100  
; TELEFAX: (212) 752-5958  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 373  
; TYPE: amino acid  
; STRANDEDNESS: single-stranded  
; TOPOLOGY: linear  
; US-09-066-281B-19  
Query Match 7.1%; Score 7; DB 4; Length 373;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 25 LGPPEE 31  
Db 63 LGPPEE 69  
RESULT 13  
US-08-948-997-3  
; Sequence 3, Application US/08948997  
; Patent No. 6008020  
; GENERAL INFORMATION:  
; APPLICANT: HASTINGS, GREGG  
; APPLICANT: COLEMAN, TIM  
; APPLICANT: LAWRENCE, DANIEL  
; TITLE OF INVENTION: BRAIN-ASSOCIATED INHIBITOR OF  
; TISSUE-TYPE PLASMINOGEN ACTIVATOR  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
; STREET: 9410 KEY WEST AVENUE  
; CITY: ROCKVILLE  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/948,997  
; FILING DATE: Oct-10-97  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: A. ANDERS BROOKES  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF336  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 407 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-948-997-3  
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Best Local Similarity 100.0%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 LLSLVL 17  
Db 6 LLSLVL 12  
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US-09-348-817A-3  
; Sequence 3, Application US/09348817A  
; Patent No. 6191260  
; GENERAL INFORMATION:  
; APPLICANT: Hastings et al.  
; TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen  
; FILE REFERENCE: PF336D1  
; CURRENT APPLICATION NUMBER: US/09/348,817A  
; CURRENT FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: 08/948,997  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: 60/028,117  
; PRIOR FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
; US-09-348-817A-3  
Query Match 7.1%; Score 7; DB 3; Length 410;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 LLSLVL 17  
Db 6 LLSLVL 12  
RESULT 15  
US-09-722-292-3  
; Sequence 3, Application US/09722292  
; Patent No. 6541452  
; GENERAL INFORMATION:  
; APPLICANT: Hastings et al.  
; TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen  
; FILE REFERENCE: PF336D1  
; CURRENT APPLICATION NUMBER: US/09/722,292  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 09/348,817

; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: 60/028,117  
; PRIOR FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-09-722-292-3

Query Match 7.1%; Score 7; DB 4; Length 410;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 LLSLVL 17  
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Db 6 LLSLVL 12

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Job time : 19 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2003, 07:56:46 ; Search time 35 Seconds

(without alignments)  
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Title: US-10-059-395-142

Perfect score: 99

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	99	100.0	99 20 AAW67828	Human secreted pro
2	99	100.0	99 21 AAY66681	Membrane-bound pro
3	99	100.0	99 22 AAB20117	Human immunostimul
4	99	100.0	99 22 AAB65204	Human PRO826 (UNQ4
5	99	100.0	99 22 AAB50916	Human PRO826 prote
6	99	100.0	99 22 AAB53094	Human angiotensin
7	99	100.0	99 23 ABB69586	Human polypeptide
8	99	100.0	99 23 ABB95488	Human angiotensin
9	99	100.0	99 23 ABB34040	Human Pro peptide

10	99	100.0	99 23 ABB84882	Human PRO826 prote
11	99	100.0	99 23 AAU83664	Human PRO protein,
12	99	100.0	99 23 AAU81964	Human PRO826. Hom
13	99	100.0	99 24 ABUS9097	Novel human secret
14	99	100.0	99 24 ABUS9244	Human secreted/tra
15	99	100.0	99 24 ABUS9393	Novel human secret
16	99	100.0	99 24 ABUS9393	Novel human secret
17	99	100.0	99 24 ABUS8019	Human secreted/tra
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19	99	100.0	99 24 ABUS8950	Human secreted/tra
20	99	100.0	99 24 ABUS8950	Human secreted/tra
21	56	56.6	96 23 ABP69669	Human PRO polypept
22	44	44.4	85 23 ABP69587	Human polypeptide
23	8	8.1	61 21 AAB14344	Human polypeptide
24	8	8.1	102 22 ABB48744	Human liver peptid
25	8	8.1	102 22 ABB28730	Peptide #1381 enco
26	8	8.1	102 22 ABB33909	Peptide #1415 enco
27	8	8.1	102 22 ABB19350	Protein #1349 enco
28	8	8.1	102 22 AAM54676	Human bone marrow
29	8	8.1	102 22 AAM67078	Human bone marrow
30	8	8.1	102 22 AAM14940	Peptide #1374 enco
31	8	8.1	102 22 AAM27370	Peptide #1407 enco
32	8	8.1	102 22 AAM02668	Peptide #1350 enco
33	8	8.1	102 23 ABB36737	Human peptide enco
34	8	8.1	133 22 ABB05986	Novel human diagno
35	8	8.1	1163 22 ABB60191	Drosophila melanog
36	7	7.1	55 20 AAY12863	Human 5' EST secre
37	7	7.1	55 21 AAG00453	Human secreted pro
38	7	7.1	72 20 AAM88618	Secreted protein e
39	7	7.1	72 20 ABB50385	Human secreted pro
40	7	7.1	80 19 AAM49763	Human secreted pro
41	7	7.1	81 23 ABB33411	Human D2-2 protein
42	7	7.1	96 11 AAR06605	Human ORF2384 prot
43	7	7.1	96 19 AAB53651	Calpastatin-like p
44	7	7.1	102 21 AAB24999	Amino acid sequenc
45	7	7.1	108 21 AAB24998	Plant SDF encoded

#### ALIGNMENTS

RESULT 1	AAW67828	standard; Protein; 99 AA.
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XX	AAW67828;	
AC		
XX		
DT	25-MAR-1999	(first entry)
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DB	Human secreted protein encoded by gene 22 clone HFEAF41.	
XX		
KW	Human; secreted protein; fusion protein; gene therapy; protein therapy;	
KW	diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;	
KW	developmental abnormality; foetal deficiency; blood; allergy; renal;	
KW	immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;	
KW	inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;	
KW	cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;	
KW	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;	
KW	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.	
OS	Homo sapiens.	
XX		
PN	WO9842738-A1.	
XX		
PD	01-OCT-1998.	
XX		
PF	19-MAR-1998;	98WO-US05311.
XX		
PR	30-MAY-1997;	97US-0050937.
PR	21-MAR-1997;	97US-0041276.
PR	21-MAR-1997;	97US-0041277.
PR	21-MAR-1997;	97US-0041281.
PR	21-MAR-1997;	97US-0042344.

PR 30-MAY-1997; 97US-0048069.  
PR 30-MAY-1997; 97US-0048094.  
PR 30-MAY-1997; 97US-0048095.  
PR 30-MAY-1997; 97US-0048096.  
PR 30-MAY-1997; 97US-0048099.  
PR 30-MAY-1997; 97US-0048131.  
PR 30-MAY-1997; 97US-0048135.  
PR 30-MAY-1997; 97US-0048154.  
PR 30-MAY-1997; 97US-0048160.  
PR 30-MAY-1997; 97US-0048186.  
PR 30-MAY-1997; 97US-0048187.  
PR 30-MAY-1997; 97US-0048188.  
PR 30-MAY-1997; 97US-0048350.  
PR 30-MAY-1997; 97US-0048351.  
PR 30-MAY-1997; 97US-0048352.  
PR 30-MAY-1997; 97US-0048355.  
PR 05-AUG-1997; 97US-0054804.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA;  
PI Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS;  
PI Rosen CA, Ruben SM, Shi Y, Young P;  
XX  
DR WPI; 1999-070066/06.  
DR N-PSDB; AAX00632.  
XX  
PT New isolated human genes and the secreted polypeptides they encode -  
PT useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders  
XX  
PS Claim 11; Page 285; 385pp; English.  
XX  
CC This sequence represents a secreted human protein encoded by the gene  
CC clone detailed in the descriptor line. The gene can be used to generate  
CC fusion proteins by linking to the gene to a human immunoglobulin Fc  
CC portion (e.g. AAX00602) for increasing the stability of the fused  
CC protein as compared to the human protein only.  
CC The invention relates to 87 novel genes and their fragments (nucleic  
CC acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004)  
CC which are useful for preventing, treating or ameliorating medical  
CC conditions e.g. by protein or gene therapy. Also, pathological  
CC conditions can be diagnosed by determining the amount of the new  
CC polypeptides in a sample or by determining the presence of mutations in  
CC the new polynucleotides. Specific uses are described for each of the 87  
CC polynucleotides, based on which tissues they are most highly expressed in  
CC (see AAX00611 for described uses).  
XX  
SQ Sequence 99 AA;  
Query Match 100.0%; Score 99; DB 20; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.7e-89;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKIPVLPAVLLSLVLSAOGATLGGPEBESTIENYASRPEAFNTPLNIDKLSAFKA 60  
Db 1 MKIPVLPAVLLSLVLSAOGATLGGPEBESTIENYASRPEAFNTPLNIDKLSAFKA 60  
QY 61 DEFLNWHALFESIKRKLPLFNWDAFPKLKGLRSATPDAQ 99  
Db 61 DEFLNWHALFESIKRKLPLFNWDAFPKLKGLRSATPDAQ 99  
RESULT 2  
ID AAY66681 standard; protein; 99 AA.  
XX AAY66681;  
AC AAY66681;  
XX  
DT 05-APR-2000 (first entry)  
XX  
DE Membrane-bound protein PRO826.  
XX

KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping.  
XX Homo sapiens.  
OS  
XX  
PN WO9963088-A2.  
XX  
PD 09-DEC-1999.  
XX  
PF 02-JUN-1999; 99WO-US12252.  
XX  
PR 02-JUN-1998; 98US-0087607.  
PR 02-JUN-1998; 98US-0087609.  
PR 02-JUN-1998; 98US-0087759.  
PR 03-JUN-1998; 98US-0087827.  
PR 04-JUN-1998; 98US-0088021.  
PR 04-JUN-1998; 98US-0088025.  
PR 04-JUN-1998; 98US-0088028.  
PR 04-JUN-1998; 98US-0088029.  
PR 04-JUN-1998; 98US-0088030.  
PR 04-JUN-1998; 98US-0088033.  
PR 04-JUN-1998; 98US-0088326.  
PR 05-JUN-1998; 98US-0088167.  
PR 05-JUN-1998; 98US-0088202.  
PR 05-JUN-1998; 98US-0088212.  
PR 05-JUN-1998; 98US-0088217.  
PR 05-JUN-1998; 98US-0088655.  
PR 09-JUN-1998; 98US-0088722.  
PR 10-JUN-1998; 98US-0088727.  
PR 10-JUN-1998; 98US-0088730.  
PR 10-JUN-1998; 98US-0088734.  
PR 10-JUN-1998; 98US-0088738.  
PR 10-JUN-1998; 98US-0088740.  
PR 10-JUN-1998; 98US-0088741.  
PR 10-JUN-1998; 98US-0088742.  
PR 10-JUN-1998; 98US-0088810.  
PR 10-JUN-1998; 98US-0088811.  
PR 10-JUN-1998; 98US-0088824.  
PR 10-JUN-1998; 98US-0088825.  
PR 10-JUN-1998; 98US-0088826.  
PR 11-JUN-1998; 98US-0088858.  
PR 11-JUN-1998; 98US-0088861.  
PR 11-JUN-1998; 98US-0088863.  
PR 12-JUN-1998; 98US-0089090.  
PR 12-JUN-1998; 98US-0089105.  
PR 16-JUN-1998; 98US-0089440.  
PR 16-JUN-1998; 98US-0089512.  
PR 16-JUN-1998; 98US-0089514.  
PR 17-JUN-1998; 98US-0089532.  
PR 17-JUN-1998; 98US-0089538.  
PR 17-JUN-1998; 98US-0089598.  
PR 17-JUN-1998; 98US-0089599.  
PR 17-JUN-1998; 98US-0089600.  
PR 17-JUN-1998; 98US-0089653.  
PR 18-JUN-1998; 98US-0089801.  
PR 18-JUN-1998; 98US-0089907.  
PR 18-JUN-1998; 98US-0089908.  
PR 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089948.  
PR 19-JUN-1998; 98US-0089952.  
PR 22-JUN-1998; 98US-0090246.  
PR 22-JUN-1998; 98US-0090252.  
PR 22-JUN-1998; 98US-0090254.  
PR 23-JUN-1998; 98US-0090349.  
PR 23-JUN-1998; 98US-0090355.  
PR 24-JUN-1998; 98US-0090429.  
PR 24-JUN-1998; 98US-0090431.  
PR 24-JUN-1998; 98US-0090435.  
PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090445.  
PR 24-JUN-1998; 98US-0090461.  
PR 24-JUN-1998; 98US-0090472.  
PR 24-JUN-1998; 98US-0090535.

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PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.

PR 12-JAN-1999; 99US-0115565.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK,
PI Wood WI, Yuan J;
XX
XX WPI; 2000-072883/06.
DR N-PSDB; AAZ65018.
XX
XX Membrane-bound proteins and related nucleotide sequences -
PT
XX
XX Claim 12; Fig 129; 822pp; English.
PS
XX
XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
XX Sequence 99 AA;

Query Match 100.0%; Score 99; DB 21; Length 99;
Best local Similarity 100.0%; Pred. No. 3.7e-89;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVLPAVVLISLVLHSAAGATLGGPREESTIENTYASRPEAFNTPLNIDKLSAFKA 60
DB 1 MKIPVLPAVVLISLVLHSAAGATLGGPREESTIENTYASRPEAFNTPLNIDKLSAFKA 60
QY 61 DEFLNWHALFESIKRKLPFLNWDAPFKLKGIRSATPDAQ 99
DB 61 DEFLNWHALFESIKRKLPFLNWDAPFKLKGIRSATPDAQ 99

RESULT 3
AAB20117
ID AAB20117 standard; Protein; 99 AA.
XX
XX AAB20117;
AC
XX
XX 30-APR-2001 (first entry)
DT
XX
XX Human immunostimulant PRO826.
DE
XX
XX PRO826; UNQ467; human; immune disease; autoimmune disease;
KW antirheumatic; antiarthritic; antiinflammatory; antianaemic;
KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;
KW hepatotropic; virucide; dermatological; antipsoriatic;
KW antiasthmatic; antiallergic; immunostimulant.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1..22
FT /label= Signal_peptide
FT Protein 23..99
FT /label= Mature_protein
FT Modified-site 22..28
FT /note= "N-myristoylation site"
FT Modified-site 90..96
FT /note= "N-myristoylation site"
FT Region 16 48
FT /note= "homology to peroxidase"
```

```
XX PN WO200105972-A1.
XX PD 25-JAN-2001.
XX PF 15-MAR-2000; 2000WO-US06884.
XX PR 20-JUL-1999; 99US-0144758.
XX PA (GETH ) GENENTECH INC.
XX PI Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;
PI Hillan KJ, Mark MR, Maxsters SA, Pitti RM, Tumas D, Watanabe CK;
PI Wood WI;
XX WPI; 2001-103149/11.
DR N-PSDB; AAF30059.
XX PT New PRO polypeptides, nucleic acids and (ant)agonists, useful for
PT diagnosing and treating immune-related disorders, such as multiple
PT sclerosis, rheumatoid arthritis and diabetes -
XX PS Claim 20; Fig 20; 127pp; English.
XX CC The present sequence is that of novel human immunomodulator PRO826
CC (UNQ467), as deduced from cDNA (see AAF30059) isolated from a
CC database screening. PRO826 has a mol.wt. of 11 kDa and a pI of
CC 7.47. The invention provides polynucleotides (see AAF30050-62)
CC encoding novel human PRO proteins (see AAB20108-20) including PRO826.
CC Claimed compositions comprising these proteins or their agonists
CC are useful for increasing infiltration of inflammatory cells into
CC a tissue of a mammal, stimulating or enhancing an immune
CC response, or increasing the proliferation of T-lymphocytes in a
CC mammal in response to an antigen. Claimed compositions comprising
CC a PRO polypeptide or its antagonist have the opposite effect. A
CC claimed method for treating an immune related disorder, such as a T
CC cell disorder, involves administering a PRO polypeptide, an agonist
CC antibody or an antagonist antibody. The disorder is selected from
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, spondyloarthritis, systemic sclerosis,
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated
CC renal disease, demyelinated diseases (such as multiple sclerosis),
CC autoimmune chronic active hepatitis, primary biliary cirrhosis,
CC granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel
CC disease (ulcerative colitis and Crohn's disease), gluten-sensitive
CC enteropathy, Whipple's disease, (auto)immune-mediated skin diseases
CC (such as bullous skin disease, erythema multiforme and psoriasis),
CC allergic diseases (such as asthma, allergic rhinitis, atopic
CC dermatitis, food hypersensitivity and urticaria), immunologic
CC diseases of the lung and transplantation associated diseases (such
CC as graft rejection and graft-versus-host disease) (all claimed).
CC Claimed methods of diagnosing these disorders comprise detecting
CC the level of expression of the PRO gene. Also claimed are a method
CC of identifying a compound capable of inhibiting the expression or
CC activity of the PRO polypeptide, vectors, host cells, antibodies,
CC and a method of stimulating the proliferation of T lymphocytes
CC using PRO826.
XX SQ Sequence 99 AA;
XX Query Match 100.0%; Score 99; DB 22; Length 99;
XX Best Local Similarity 100.0%; Pred. No. 3.7e-89;
XX Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MKIPVLPAVLLSLVLSHAQATLGGPEESTTENYASRBEAFNTPLINDIKLSAFKA 60
Db 1 MKIPVLPAVLLSLVLSHAQATLGGPEESTTENYASRBEAFNTPLINDIKLSAFKA 60
QY 61 DEFLNHALFESIKRKLPLINWDAPFKLGLRSATPDAQ 99
Db 61 DEFLNHALFESIKRKLPLINWDAPFKLGLRSATPDAQ 99
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RESULT 4
AAB65204
ID AAB65204 standard; Protein; 99 AA.
XX AC AAB65204;
XX DT 02-APR-2001 (first entry)
XX DE Human PRO826 (UNQ467) protein sequence SEQ ID NO:201.
XX KW Human; secreted and transmembrane protein; PRO; cytosolic;
XX KM cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
XX XM diagnostic assay.
XX OS Homo sapiens.
XX PN WO200073454-A1.
XX PD 07-DEC-2000.
XX PF 30-MAR-2000; 2000WO-US08439.
XX PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
XX PA (GETH ) GENENTECH INC.
XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin JF, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX WPI; 2001-032160/04.
DR N-PSDB; AAF44164.
XX PT PRO polynucleotides used to produce polypeptides used to target
PT bioactive molecules such as toxins, radiolabels or antibodies, to
PT specific cells, to cause targeted cell death -
XX PS Claim 12; Fig 129; 935pp; English.
XX CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA
CC and DNA. They may also be used to produce transgenic animals which are
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CC used to develop and screen therapeutically useful reagents. The PRO  
 CC nucleotide and protein sequence can be used for tissue typing and in  
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.

XX  
 SQ Sequence 99 AA;

Query Match 100.0%; Score 99; DB 22; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-89;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKIPVLPAVLLSLVLSAOGATLGGPEESTIENYASRPEAFNTPLNIDKLSAFKA 60  
 DB 1 MKIPVLPAVLLSLVLSAOGATLGGPEESTIENYASRPEAFNTPLNIDKLSAFKA 60

OY 61 DEFLNMHALFESIKRKLPLNWDAPFKLGKLSATPDAQ 99  
 DB 61 DEFLNMHALFESIKRKLPLNWDAPFKLGKLSATPDAQ 99

RESULT 5  
 AAB50916  
 ID AAB50916 standard; Protein; 99 AA.

XX  
 AC AAB50916;

DT 21-MAR-2001 (first entry)

DE Human PRO826 protein.

XX  
 KW Human; PRO; antiinflammatory; dermatological; antiarthritic;  
 KW anti-rheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;  
 KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;  
 KW antiallergic; antiasthmatic; immune related disorder;  
 KW hepatobiliary disease; autoimmune disease; allergy.

XX  
 OS Homo sapiens.

PN WO200073452-A2.

PD 07-DEC-2000.

PF 02-JUN-2000; 2000WO-US15264.

XX 02-JUN-1999; 99WO-US12252.

PR 20-JUL-1999; 99US-0144732.

PR 20-JUL-1999; 99US-0144758.

PR 28-JUL-1999; 99US-0146222.

PR 01-SEP-1999; 99WO-US20111.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99WO-US28313.

PR 01-DEC-1999; 99WO-US28634.

PR 09-DEC-1999; 99US-0170262.

PR 20-DEC-1999; 99WO-US30911.

PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PR 15-MAR-2000; 2000WO-US06884.

PR 20-MAR-2000; 2000WO-US07377.

PR 21-MAR-2000; 2000WO-US07532.

PR 30-MAR-2000; 2000WO-US08439.

PR 17-MAY-2000; 2000WO-US13705.

XX 22-MAY-2000; 2000WO-US14042.

PA (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;

PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;

PI Wood WI;

XX WPI; 2001-025253/03.

DR N-PSDB; AAC91475.

XX

PT Thirty three nucleic acids encoding PRO polypeptides which are useful

PT in the diagnosis and treatment of immune related disorders, e.g.

PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,

PT thyroiditis and diabetes mellitus -

XX Claim 58; Fig 30; 218pp; English.

CC The present sequence is one of thirty three novel PRO polypeptides.

CC The PRO polypeptides, anti-PRO antibodies, agonists and

CC antagonists are useful for treating and diagnosing immune related

CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,

CC osteoarthritis, juvenile chronic inflammatory myopathies, Sjogren's

CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic

CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,

CC immune-mediated renal disease, demyelinating diseases of the central

CC and peripheral nervous systems (such as multiple sclerosis, idiopathic

CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic

CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases

CC (such as infectious, autoimmune chronic active hepatitis, primary

CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),

CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's

CC disease, autoimmune or immune-mediated skin diseases (such as bullous

CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),

CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,

CC food hypersensitivity and urticaria), immunological diseases of the

CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis

CC and hypersensitivity pneumonitis), transplantation associated diseases

XX including graft rejection and graft-versus-host diseases.

SQ Sequence 99 AA;

Query Match 100.0%; Score 99; DB 22; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-89;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKIPVLPAVLLSLVLSAOGATLGGPEESTIENYASRPEAFNTPLNIDKLSAFKA 60

DB 1 MKIPVLPAVLLSLVLSAOGATLGGPEESTIENYASRPEAFNTPLNIDKLSAFKA 60

OY 61 DEFLNMHALFESIKRKLPLNWDAPFKLGKLSATPDAQ 99

DB 61 DEFLNMHALFESIKRKLPLNWDAPFKLGKLSATPDAQ 99

RESULT 6

AAB53094  
 ID AAB53094 standard; Protein; 99 AA.

XX AAB53094;

DT 28-FEB-2001 (first entry)

DE Human angiogenesis-associated protein PRO826, SEQ ID NO:158.

KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;

KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;

KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;

KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;

KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;

KW Alzheimer's disease; Huntington's disease; stroke; drug screening;

XX gene therapy; transgenic animal.

OS Homo sapiens.



XX WO200053753-A2.  
PN  
XX  
PD 14-SEP-2000.  
XX  
PF 05-JAN-2000; 2000WO-US00219.  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
XX  
DR WPI; 2001-090793/10.  
DR N-PSDB; AAC97491.  
XX  
PT New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
XX  
PS Claim 69; Fig 62; 293pp; English.  
XX  
CC The invention relates to novel human angiogenesis-associated proteins  
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
CC PRO proteins. The invention also relates to vectors and host cells  
CC comprising a PRO nucleic acid, the recombinant production of a PRO  
CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
CC compounds which inhibit the expression of a PRO gene. The invention  
CC additionally encompasses methods of identifying modulators of PRO  
CC expression or activity; diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
CC mutations in a PRO gene, or the expression level of a PRO gene within a  
CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
CC administration of a PRO protein, or an agonist or antagonist thereof.  
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
CC agonists and PRO antagonists may be used as therapeutic agents to treat  
CC cardiovascular, endothelial or angiogenic disorders, such as  
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
CC endometriosis, ulcers, cancer, Alzheimer's disease, Huntington's  
CC disease, or stroke. PRO nucleic acids are additionally useful in the  
CC recombinant production of PRO proteins, as hybridisation probes to  
CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
CC animals useful for the development and screening of potential  
CC therapeutic agents. The present sequence represents a PRO protein of the  
CC invention.  
XX  
SQ Sequence 99 AA;

Query Match 100.0%; Score 99; DB 22; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.7e-89;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MKIPVLPVLLSLVLSAQAATLGGPEESTIENYASRPEAFNTPFLNIDKLSAFKA 60  
Db 1 MKIPVLPVLLSLVLSAQAATLGGPEESTIENYASRPEAFNTPFLNIDKLSAFKA 60  
OY 61 DEFLNWHALFESIKRKLPLFLNWDAPFKLKGLRSATPDAQ 99  
Db 61 DEFLNWHALFESIKRKLPLFLNWDAPFKLKGLRSATPDAQ 99  
RESULT 7  
ABP69586  
ID ABP69586 standard; Protein; 99 AA.  
XX  
AC ABP69586;  
XX  
DT 20-JAN-2003 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 1633.  
XX  
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;  
KW cell-proliferative disorder; neurodegenerative disease; bacterial;  
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;  
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;  
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;  
KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;  
KW antiarthritic.  
XX  
OS Homo sapiens.  
XX  
PN WO200270539-A2.  
XX  
PD 12-SEP-2002.  
XX  
PF 05-MAR-2002; 2002WO-US05095.  
XX  
PR 05-MAR-2001; 2001US-0799451.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;  
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
PI Wehrman T, Wang J, Wang D, Drmanac RT;  
XX  
DR WPI; 2002-759812/82.  
DR N-PSDB; ABZ11803.  
XX  
PT New polynucleotides comprising sequences assembled from expressed  
PT sequence tags (ESTs), useful for treating cell-proliferative,  
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or  
PT platelet or coagulation disorders -  
XX  
PS Claim 9; SEQ ID NO 1633; 1012pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated polynucleotide (I) comprising a  
CC nucleotide sequence selected from any of 948 sequences  
CC (ABZ1119-ABZ12066) or their mature protein coding portion, active domain  
CC coding protein or complementary sequences. The polynucleotides are useful  
CC for identifying expressed genes or for physical mapping of human genome.  
CC The encoded polypeptides (ABP68902-ABP69849) are useful as molecular  
CC weight markers, as a food supplement, for generating antibodies, in  
CC medical imaging, screening and diagnostic assays and for treating  
CC cell-proliferative disorders (cancer), neurodegenerative diseases  
CC (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple  
CC sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid  
CC disorders, platelet or coagulation disorders, wound, burns, incision,  
CC ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal,  
CC parasitic), arthritis, etc.  
CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 99 AA;

Query Match 100.0%; Score 99; DB 23; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.7e-89;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVLPVAVLTLVLVLSAQAQATLGPEESTIENYASRPEAFNTPLNIDKLSAFKA 60  
DB 1 MKIPVLPVAVLTLVLVLSAQAQATLGPEESTIENYASRPEAFNTPLNIDKLSAFKA 60

QY 61 DEFLNWHALFESIKRKLPLNWDAPFKLGKLSATPDAQ 99  
DB 61 DEFLNWHALFESIKRKLPLNWDAPFKLGKLSATPDAQ 99

RESULT 8

ABB95488  
ID ABB95488 standard; Protein; 99 AA.

XX ABB95488;

XX 19-JUL-2002 (first entry)

DE Human angiogenesis related protein PRO826 SEQ ID NO: 132.

KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
KW cardiact; cytosstatic; antiangiogenic; hypotensive; vulnerary;  
KW antiarteriosclerotic.

XX Homo sapiens.

XX WO200208284-A2.

XX 31-JAN-2002.

PF 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.

PR 25-JUL-2000; 2000US-220624P.

PR 25-JUL-2000; 2000US-220664P.

PR 28-JUL-2000; 2000WO-US20710.

PR 02-AUG-2000; 2000US-222695P.

PR 17-AUG-2000; 2000US-0643657.

PR 23-AUG-2000; 2000WO-US23522.

PR 24-AUG-2000; 2000WO-US23328.

PR 07-SEP-2000; 2000US-230978P.

PR 15-SEP-2000; 2000US-000000P.

PR 18-SEP-2000; 2000US-0664610.

PR 18-SEP-2000; 2000US-0665350.

PR 24-OCT-2000; 2000US-242922P.

PR 08-NOV-2000; 2000US-0709238.

PR 08-NOV-2000; 2000WO-US30952.

PR 10-NOV-2000; 2000WO-US30873.

PR 01-DEC-2000; 2000WO-US32678.

PR 20-DEC-2000; 2000US-0747259.

PR 20-DEC-2000; 2000WO-US34956.

PR 22-JAN-2001; 2001US-0767609.

PR 28-FEB-2001; 2001US-0796498.

PR 28-FEB-2001; 2001WO-US06520.

PR 01-MAR-2001; 2001WO-US06666.

PR 09-MAR-2001; 2001US-0802706.

PR 14-MAR-2001; 2001US-0808689.

PR 22-MAR-2001; 2001US-0816744.

PR 05-APR-2001; 2001US-0828366.

PR 10-MAY-2001; 2001US-0854280.

PR 10-MAY-2001; 2001US-0854280.

PR 25-MAY-2001; 2001US-0866028.

PR 25-MAY-2001; 2001US-0866034.

PR 25-MAY-2001; 2001WO-US17092.

PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 28-JUN-2001; 2001WO-US00000.

XX (GETH ) GENENTECH INC.

PA (BAKE/) BAKER K P.

PA (FERR/) FERRARA N.

PA (GERB/) GERBER H.

PA (GERR/) GERRITSEN M E.

PA (GODD/) GODDARD A.

PA (GODO/) GODOWSKI P J.

PA (GURN/) GURNEY A L.

PA (HILL/) HILLAN K J.

PA (MARS/) MARSTERS S A.

PA (PANJ/) PAN J.

PA (PAON/) PAONI N F.

PA (STEE/) STEPHAN J F.

PA (WATA/) WATANABE C K.

PA (WILL/) WILLIAMS P M.

PA (WOOD/) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,

PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI, 2002-171999/22.

DR N-PSDB; ABL95626.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial

PT infarction), endothelial or angiogenic disorders in a mammal -

XX Claim 11; Fig 132; 567pp; English.

XX The present invention provides the protein and coding sequences of human

CC PRO proteins. These are useful for treating or diagnosing a

CC cardiovascular, endothelial or angiogenic disorder, including cardiac

CC hypertrophy, trauma, cancer, age-related macular degeneration,

CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,

CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour

CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound

CC healing. The present sequence is a PRO protein of the invention.

XX Sequence 99 AA;

Query Match 100.0%; Score 99; DB 23; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.7e-89;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVLPVAVLTLVLVLSAQAQATLGPEESTIENYASRPEAFNTPLNIDKLSAFKA 60  
DB 1 MKIPVLPVAVLTLVLVLSAQAQATLGPEESTIENYASRPEAFNTPLNIDKLSAFKA 60

QY 61 DEFLNWHALFESIKRKLPLNWDAPFKLGKLSATPDAQ 99  
DB 61 DEFLNWHALFESIKRKLPLNWDAPFKLGKLSATPDAQ 99

RESULT 9

ABG34040  
ID ABG34040 standard; Protein; 99 AA.

XX ABG34040;

DT 15-JUL-2002 (first entry)

XX Human Pro peptide #11.

KW Human; PRO; secreted protein; transmembrane protein;

KW genetic disorder; tumour; cancer.



OS Homo sapiens.  
XX  
PN WO200224888-A2.  
XX  
PD 28-MAR-2002.  
XX  
PF 29-AUG-2001; 2001WO-US27099.  
XX  
PR 01-SEP-2000; 2000US-229896P.  
PR 05-SEP-2000; 2000US-230621P.  
PR 22-SEP-2000; 2000US-235147P.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 12-JAN-2001; 2001US-261878P.  
PR 16-JAN-2001; 2001US-261910P.  
PR 16-JAN-2001; 2001US-261939P.  
PR 16-JAN-2001; 2001US-262150P.  
PR 25-JAN-2001; 2001US-264395P.  
PR 02-FEB-2001; 2001US-266421P.  
PR 09-FEB-2001; 2001US-267623P.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 09-MAR-2001; 2001US-274399P.  
PR 03-APR-2001; 2001US-280982P.  
PR 04-APR-2001; 2001US-282129P.  
PR 04-APR-2001; 2001US-282199P.  
PR 09-MAY-2001; 2001US-290589P.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;  
XX  
XX WPI; 2002-362426/39.  
DR N-PSDB; ABK69971.  
XX  
XX  
PT New PRO polypeptides and polynucleotides encoding the polypeptides,  
PT useful in gene therapy, chromosome identification, tissue typing, or  
PT for genetic analysis of individuals with genetic disorders -  
XX  
XX  
PS Claim 11; Figure 22; 218pp; English.  
XX  
XX This invention relates to the cDNA and protein sequences of novel  
CC secreted and transmembrane polypeptides PRO polypeptides. The  
CC invention also comprises a method for producing the proteins of the  
CC invention by recombinant means and antibodies specific for the protein  
CC of the invention. The antibody may be used for detecting the PRO  
CC proteins of the invention and may be used to modify their activity.  
CC polynucleotides may be used as hybridisation probes for a cDNA library  
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, to  
CC construct hybridisation probes for mapping the gene which encodes that  
CC PRO and for genetic analysis of individuals with genetic disorders, in  
CC assays to identify other proteins or molecules involved in binding  
CC reaction, to generate transgenic animals or knock-out animals which in  
CC turn are useful in the development and screening of therapeutically  
CC useful reagents, for chromosome identification, and tissue typing. The  
CC PRO polypeptides are useful in gene therapy, and as molecular weight  
CC markers for protein electrophoresis purposes. The sequences may  
CC also be used to detect overexpression on PRO polypeptides in cancerous  
CC tumours and for screening for differentially expressed genes using  
CC microarray technology. The present sequence represents a human PRO  
CC protein of the invention.  
XX  
XX  
SQ Sequence 99 AA;

Query Match 100.0%; Score 99; DB 23; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.7e-89;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVPAVVLISLLVLSAOGATLGGPREESTIENTYASRPEAFNTPLNIDKLSAFKA 60  
Db 1 MKIPVPAVVLISLLVLSAOGATLGGPREESTIENTYASRPEAFNTPLNIDKLSAFKA 60  
QY 61 DEFLNWHALFESIKRKLPLFNWDAPFKLKGSRATPDAQ 99  
Db 61 DEFLNWHALFESIKRKLPLFNWDAPFKLKGSRATPDAQ 99  
RESULT 10  
AB84882  
ID ABB84882 standard; Protein; 99 AA.  
XX  
AC ABB84882;  
XX  
DT 16-MAY-2002 (first entry)  
XX  
DE Human PRO826 protein sequence SEQ ID NO:132.  
XX  
KW Human; angiogenesis; cardiant; cytosatic; antiangiogenic; hypotensive;  
KW vulnerable; arteriosclerotic; PRO agonist; PRO antagonist; trauma;  
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
KW age-related macular degeneration; arterial restenosis; angina;  
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
KW wound healing; chromosome mapping; gene mapping.  
XX  
OS Homo sapiens.  
XX  
XX WO200200690-A2.  
XX  
XX 03-JAN-2002.  
XX  
PD 20-JUN-2001; 2001WO-US19692.  
XX  
PF 23-JUN-2000; 2000US-213637P.  
PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 02-AUG-2000; 2000US-222695P.  
PR 17-AUG-2000; 2000US-0643657.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 07-SEP-2000; 2000US-230978P.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-0709238.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
XX  
PA (GETH ) GENENTECH INC.

```
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2002-090516/12.
DR N-PSDB; ABL88137.
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX Claim 11; Fig 132; 565pp; English.
PS ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cycostatic,
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC degeneration, atherosclerosis, hypertension, arterial restenosis,
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC carcinoma) and wound healing. The PRO polynucleotides have applications
CC in molecular biology, including use as hybridisation probes, and in
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC probes used in the exemplification of the present invention.
XX
SQ Sequence 99 AA;
Query Match 100.0%; Score 99; DB 23; Length 99;
Best Local Similarity 100.0%; Pred. No. 3.7e-89;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKIPVLPVAVLLSLVLHSAOGATLGGPEESTIENTYASRPEAFNTPLNIDKLSAFKA 60
Db 1 MKIPVLPVAVLLSLVLHSAOGATLGGPEESTIENTYASRPEAFNTPLNIDKLSAFKA 60
QY 61 DEFLNWHALFESIKRKLPLNWDAPFKLKGLRSATPDAQ 99
Db 61 DEFLNWHALFESIKRKLPLNWDAPFKLKGLRSATPDAQ 99
RESULT 11
ID ABL83664 standard; Protein; 99 AA.
XX
AC ABL83664;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human PRO protein, Seq ID No 146.
XX
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha.
XX
OS Homo sapiens.
XX
PN WO200208288-A2.
XX
PD 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US21066.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220585P.
PR 25-JUL-2000; 2000US-220605P.
PR 25-JUL-2000; 2000US-220607P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220638P.
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PR 25-JUL-2000; 2000US-220664P.
PR 25-JUL-2000; 2000US-220666P.
PR 26-JUL-2000; 2000US-220893P.
PR 28-JUL-2000; 2000WO-US20710.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 15-SEP-2000; 2000US-000000P.
PR 10-NOV-2000; 2000WO-US30873.
PR 28-NOV-2000; 2000US-253646P.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001WO-US17092.
XX
PA (GENTH ) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldt JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2002-172001/22.
DR N-PSDB; ABK33608.
XX
PS Claim 11; Figure 146; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC protein sequences of the invention.
XX
SQ Sequence 99 AA;
Query Match 100.0%; Score 99; DB 23; Length 99;
Best Local Similarity 100.0%; Pred. No. 3.7e-89;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKIPVLPVAVLLSLVLHSAOGATLGGPEESTIENTYASRPEAFNTPLNIDKLSAFKA 60
Db 1 MKIPVLPVAVLLSLVLHSAOGATLGGPEESTIENTYASRPEAFNTPLNIDKLSAFKA 60
QY 61 DEFLNWHALFESIKRKLPLNWDAPFKLKGLRSATPDAQ 99
Db 61 DEFLNWHALFESIKRKLPLNWDAPFKLKGLRSATPDAQ 99
RESULT 12
ID ABL1964 standard; Protein; 99 AA.
XX
AC ABL1964;
XX
DT 09-APR-2002 (first entry)
XX
DE Human PRO826.
XX
```

KW Human; PRO; antiinflammatory; ophthalmological; vasotropic;  
KW retinal cell injury; ocular disease; retinitis pigmentosa;  
KW macular degeneration; retinal detachment; retinal tear; retinopathy;  
KW retinal degenerative disease; macular hole; degenerative myopia;  
KW acute retinal necrosis syndrome; traumatic chorioretinopathy;  
KW Purtscher's retinopathy; oedema; ischaemic condition;  
KW retinal vision occlusion; collagen vascular disease;  
KW thrombocytopaenic purpura; uveitis; retinal vasculitis; Bales disease;  
KW systemic lupus erythematosus; environmental trauma.  
XX  
OS Homo sapiens.  
XX  
PN WO200109327-A2.  
XX  
PD 08-FEB-2001.  
XX  
PF 28-JUL-2000; 2000WO-US20710.  
XX  
PR 28-JUL-1999; 99US-146222P.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;  
PI Kijavich IJ, Lafleur M, Mark MR, Marsters SA, Pitti RM;  
PI Watanabe CK, Wood WI;  
XX  
DR WPI; 2002-130120/17.  
DR N-PSDB; ABK28600.  
XX  
PT Promoting survival of retinal cells, or delaying or preventing retinal  
PT cell injury or death, by contacting retinal cells with PRO175, 220,  
PT 216, 243, 306, 346, 322, 536, 943, 840, 828, 1068 or PRO1132  
PT polypeptide -  
XX  
PS Claim 44; Fig 25; 152pp; English.  
XX  
XX The invention relates to promoting the survival of retinal cells, or  
CC delaying or preventing retinal cell injury or death, by contacting the  
CC retinal cells with the polypeptide such as PRO175, PRO220, PRO216,  
CC PRO243, PRO306, PRO346, PRO322, PRO536, PRO943, PRO840, PRO828, PRO826,  
CC PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids  
CC encoding the PRO proteins, a vector comprising the nucleic acids  
CC cell comprising the vector, and anti-PRO antibody. The PRO proteins are  
CC useful for promoting survival of retinal cells (retinal neurons such as  
CC retinal ganglion cells, displaced retinal ganglion cells, amacrine  
CC cells, displaced amacrine cells, horizontal neurons or bipolar neurons,  
CC rod photoreceptors, or supportive cells such as Muller cells or pigment  
CC epithelial cells), or delaying or preventing retinal cell injury or  
CC death caused by ocular disease (which is or is associated with  
CC retinitis pigmentosa, macular degeneration, retinal detachment, retinal  
CC tear, retinopathy, retinal degenerative disease, macular hole,  
CC degenerative myopia, acute retinal necrosis syndrome, traumatic  
CC chorioretinopathy or contusion, Purtscher's retinopathy, oedema, an  
CC ischaemic condition, central or branch retinal vision occlusion,  
CC collagen vascular disease, thrombocytopaenic purpura, uveitis, retinal  
CC vasculitis, occlusion associated with Bales disease or systemic lupus  
CC erythematosus), retinal injury or environmental trauma. The retinal  
CC cell injury or death is delayed or prevented by substantially not

CC causing angiogenesis or mitogenesis. The present sequence represents  
CC a PRO protein.  
XX  
SQ Sequence 99 AA;  
Query Match 100.0%; Score 99; DB 23; Length 99;  
Best local Similarity 100.0%; Pred. No. 3.7e-89;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MKIPVLPVAVLLSLVLHSAQGATLGGPEESTIENYASRPEAFNTPLNIDKLSAFKA 60  
OY 61 DEFLNWHALFESIKRKLPLFNWDAPFKLGKRSATPDAQ 99  
DB 61 DEFLNWHALFESIKRKLPLFNWDAPFKLGKRSATPDAQ 99  
RESULT 13  
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ID ABU59097 standard; Protein; 99 AA.  
XX  
AC ABU59097;  
XX  
DT 28-APR-2003 (first entry)  
XX  
DE Novel human secreted or transmembrane protein PRO826.  
XX  
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosum; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis.  
XX  
OS Homo sapiens.  
XX  
PN US2002132252-A1.  
XX  
PD 19-SEP-2002.  
XX  
PF 14-NOV-2001; 2001US-0990442.  
XX  
PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
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PR 15-SEP-1999; 99WO-US21547.  
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PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 06-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US00356.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
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PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.

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PR	22-MAY-2000	2000WO-US14047.
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PR	24-AUG-2000	2000WO-US23328.
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PR	01-JUN-2001	2001WO-US17800.
PR	20-JUN-2001	2001WO-US19692.
PR	29-JUN-2001	2001WO-US21066.
PR	09-JUL-2001	2001WO-US21735.
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PR	13-NOV-1997	97US-065311P.
PR	24-NOV-1997	97US-066770P.
PR	25-FEB-1998	98US-075945P.
PR	20-MAR-1998	98US-078910P.
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PR	02-JUN-1998	98US-087607P.
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PR	02-JUN-1998	98US-087759P.
PR	03-JUN-1998	98US-087827P.
PR	04-JUN-1998	98US-088021P.
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PR	18-JUN-1998	98US-089680P.
PR	18-JUN-1998	98US-089907P.
PR	18-JUN-1998	98US-089908P.
PR	28-AUG-2001	2001US-0941992.

PI	Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI	Zhang Z;
XX	
XX	
DR	WPI; 2003-247083/24.
DR	N-PSDB; ABX80254.
XX	
PT	Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT	and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT	are therapeutically useful for enhancing immune response and in cancer
PT	treatments -
XX	
XX	
PS	Claim 12, Fig 129; 648pp; English.

PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;

OS Homo sapiens.  
XX  
PN US2003027162-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 15-NOV-2001; 2001US-0997428.  
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PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
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PR 24-AUG-2000; 2000WO-US23328.  
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PR 29-JUN-2001; 2001WO-US21066.  
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Query Match 100.0%; Score 99; DB 24; Length 99;  
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RESULT 15  
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AC ABUS9393;  
XX  
DT 22-APR-2003 (first entry)  
XX  
DE Novel human secreted or transmembrane protein PRO819.  
XX  
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;

KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis.  
XX Homo sapiens.  
XX US2003027985-A1.  
XX 06-FEB-2003.  
XX 14-NOV-2001; 2001US-0990562.  
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PR 15-SEP-1999; 99WO-US21090.  
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PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
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PR 24-FEB-2000; 2000WO-US04914.  
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PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
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PR 02-JUN-2000; 2000WO-US15264.  
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PR 01-DEC-2000; 2000WO-US32678.  
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PR 13-NOV-1997; 97US-065311P.  
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PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
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PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089599P.  
PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 19-JUN-1998; 98US-089947P.  
PR 19-JUN-1998; 98US-089948P.  
PR 19-JUN-1998; 98US-089952P.  
PR 22-JUN-1998; 98US-090246P.  
PR 22-JUN-1998; 98US-090252P.  
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PR 23-JUN-1998; 98US-090349P.  
PR 23-JUN-1998; 98US-090355P.  
PR 24-JUN-1998; 98US-090429P.  
PR 24-JUN-1998; 98US-090431P.  
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PR 24-JUN-1998; 98US-090444P.  
PR 24-JUN-1998; 98US-090445P.  
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PR 24-JUN-1998; 98US-090557P.  
PR 25-JUN-1998; 98US-090676P.  
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PR 26-JUN-1998; 98US-090863P.  
PR 01-JUL-1998; 98US-091360P.  
PR 01-JUL-1998; 98US-091544P.  
PR 02-JUL-1998; 98US-091478P.  
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PR 02-JUL-1998; 98US-091646P.  
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PR 09-JUL-1998; 98US-092182P.  
PR 10-JUL-1998; 98US-092472P.  
PR 20-JUL-1998; 98US-093339P.  
PR 30-JUL-1998; 98US-094651P.  
PR 04-AUG-1998; 98US-095282P.  
PR 04-AUG-1998; 98US-095285P.

PR 04-AUG-1998; 98US-095301P.  
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PR 04-AUG-1998; 98US-095321P.  
PR 04-AUG-1998; 98US-095325P.  
PR 10-AUG-1998; 98US-095916P.  
PR 10-AUG-1998; 98US-095929P.  
PR 10-AUG-1998; 98US-096012P.  
PR 11-AUG-1998; 98US-096143P.  
PR 11-AUG-1998; 98US-096146P.  
PR 12-AUG-1998; 98US-096329P.  
PR 17-AUG-1998; 98US-096757P.  
PR 17-AUG-1998; 98US-096766P.  
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PR 18-AUG-1998; 98US-096950P.  
PR 18-AUG-1998; 98US-096959P.  
PR 18-AUG-1998; 98US-096960P.  
PR 18-AUG-1998; 98US-097022P.  
PR 19-AUG-1998; 98US-097141P.  
PR 20-AUG-1998; 98US-097218P.  
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PR 26-AUG-1998; 98US-097955P.  
PR 26-AUG-1998; 98US-097971P.  
PR 26-AUG-1998; 98US-097974P.  
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Query Match 100.0%; Score 99; DB 24; Length 99;  
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Search completed: November 28, 2003, 08:03:44  
Job time : 38 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 08:05:08 ; Search time 2856 Seconds

(without alignments)  
1418.086 Million cell updates/sec

Title: US-10-059-395-142

Perfect score: 510

Sequence: 1 MKIPVLPAVVLISLVLSA.....LNWDAFPKLGKLSATPDAQ 99

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Fgapop 6.0 ,	Fgapext 7.0
Delop 6.0 ,	Delext 7.0

Searched: 2888711 segs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	510	100.0	414	6	AX055438	AX055438 Sequence
2	510	100.0	415	6	AR252517	AR252517 Sequence
3	510	100.0	415	6	AX077031	AX077031 Sequence
4	510	100.0	415	6	AX358892	AX358892 Sequence
5	510	100.0	415	6	AX362385	AX362385 Sequence
6	510	100.0	415	6	AX403313	AX403313 Sequence
7	510	100.0	415	6	AX454546	AX454546 Sequence
8	510	100.0	415	6	AX491024	AX491024 Sequence
9	510	100.0	415	6	AX574494	AX574494 Sequence
10	510	100.0	456	6	BD082389	BD082389 87 human
11	510	100.0	490	6	AX080817	AX080817 Sequence
12	503	98.6	529	9	HS293408	AJ293408 Homo sapi
13	497	97.5	435	6	AX080816	AX080816 Sequence
14	481	94.3	432	6	AX080815	AX080815 Sequence
15	481	94.3	432	6	AX080818	AX080818 Sequence
16	322.5	63.2	449	10	AB011028	AB011028 Rattus no
17	308	60.4	278	6	AX041085	AX041085 Sequence
18	267.5	52.5	288	6	AR248775	AR248775 Sequence
19	140	27.5	44679	9	CH19F21246	AD001502 Homo sapi
20	106	20.8	154673	2	AC079472	AC079472 Mus muscu
21	84	16.5	223443	2	AC112801	AC112801 Rattus no
22	84	16.5	252427	2	AC111287	AC111287 Rattus no
23	82.5	16.2	590	6	BD025234	BD025234 Sequence
24	82	16.1	104892	2	AC093775	AC093775 Homo sapi
25	82	16.1	244944	2	AC120613	AC120613 Rattus no
26	82	16.1	263584	2	AC099301	AC099301 Rattus no
27	80	15.7	75415	10	AL591425	AL591425 Mouse DNA
28	80	15.7	181557	10	AC069014	AC069014 Mus muscu
29	80	15.7	218866	2	BX323890	BX323890 Mus muscu
30	79.5	15.6	240273	2	AC109533	AC109533 Rattus no
31	79	15.5	235178	2	AC098921	AC098921 Rattus no
32	78.5	15.4	700	6	AX135555	AX135555 Sequence
33	78.5	15.4	1000	9	BC011886	BC011886 Homo sapi
34	78.5	15.4	1579	9	AK096215	AK096215 Homo sapi
35	78.5	15.4	1982	9	BC035311	BC035311 Homo sapi
36	78.5	15.4	112626	9	AC035144	AC035144 Homo sapi
37	78	15.3	11533	1	AE009124	AE009124 Agrobacte
38	78	15.3	12074	1	AB008089	AB008089 Agrobacte
39	78	15.3	156508	3	AC007581	AC007581 Drosophill
40	78	15.3	171151	3	AC007574	AC007574 Drosophill
41	78	15.3	310958	3	AE003464	AE003464 Drosophill
42	77.5	15.2	62750	2	AC017209	AC017209 Drosophill
43	77.5	15.2	72887	2	AC017882	AC017882 Drosophill
44	77.5	15.2	160931	3	AC093498	AC093498 Drosophill
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#### ALIGNMENTS

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Percent Similarity:	100.00%	Conservative:	0		
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Qy	1 MetLysIleProValIeuProAlaValIeuLeuSerIeuLeuValIeuHisSerAla	20			
Db	13 ATGAAGATCCCGGCTCTTCTGCGGTGCTCTCTCTCTGCTCCACTCTGCC	72			
Qy	21 GInGlyAlaThrLeuGlyGlyProGluGluGluSerIleGluAsnTyraIaSerArg	40			
Db	73 CAGGAGCCACCCTGGGTGCTCTGAGGAAGAAGACCAATTGAGATTATGCGTCACGA	132			
Qy	41 ProGluAlaPheAsnThrProPheLeuAsnIleAspIysLeuArgSerAlaPheIysAla	60			
Db	133 CCCGAGGCTTTAACACCCCGTTCTCTGAACATCGACAAATTGCGATCTGCGTTAAGGCT	192			
Qy	61 AspGluPheLeuAsnTrpHisAlaIeuPheGluSerIleIysArgIysLeuProPheLeu	80			
Db	193 GATGAGTTCCTGAACCTGGCAGCCCTCTTGAGTCATCAAAAGAACTTCTTCTC	252			
Qy	81 AsnTrpAspAlaPheProIysLeuIysGlyLeuArgSerAlaThrProAspAlaGln	99			
Db	253 AACTGGATGCTTCTCTTAAGCTGAAGAGACTGAGGAGCGCACTCTGATGCCAG	309			
RESULT 3					
LOCUS	AX077031	415 bp	DNA	linear	PAT 22-FEB-2001
DEFINITION	Sequence 19 from Patent WO0105972.				
ACCESSION	AX077031				
VERSION	AX077031.1	GI:13121661			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 Ashkenazi,A.J., Baker,K.P., Fong,S., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Mark,M.R., Masters,S.A., Pitti,R.M., Tumas,D., Watanabe,C.K. and Wood,W.I. Compositions and methods for the treatment of immune related diseases Patent: WO 0105972-A 19 25-JAN-2001;				
AUTHORS	Genentech, Inc. (US)				
TITLE	Location/Qualifiers				
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BASE COUNT	99 a	126 c	92 g	98 t	
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[illegible]

Db	253 AACTGGATGCTTTCCTAAGCTGAAGAAGACTGAGAGCGCAACTCCTGATGCCAG	309
RESULT 5		
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LOCUS	AX362385	415 bp DNA linear PAT 15-FEB-2002
DEFINITION	Sequence 145 from Patent WO0208288.	
ACCESSION	AX362385	
VERSION	AX362385.1 GI:18694650	
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P., Watanabe,C.K. and Wood,W.I. Secreted and transmembrane polypeptides and nucleic acids encoding the same Patent: WO 0208288-A 145 31-JAN-2002; Genentech, Inc. (US) Location/Qualifiers 1..415 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"	
AUTHORS		
TITLE		
JOURNAL		
FEATURES		
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ORIGIN		
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Db	73 CAGGAGCCACCCTGGGTGTCTCTGAGGAAGAAAGAACATTGAGAAATTAATGCGTCACGA 132	
OY	41 ProGLuaIaPheAsnThrProPheLeuAsnIleaSpLySeuArGSerAlaphelySAla 60	
Db	133 CCCGAGCCCTTAAACACCCCGTCTCTGAACAATTCGATCTGCCGTTAAAGGCT 192	
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Db	193 GATGAGTTCCTGAACCTGGCACGCCCTCTTGAGTCTATCAAAAAGAACTTCCTTCCTC 252	
OY	81 AsnTrPaSPalaPheProLySleuLySGlyLeuArGSerAlathrProASPalagln 99	
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LOCUS	AX403313	415 bp DNA linear PAT 14-JUN-2002
DEFINITION	Sequence 200 from Patent WO0073454.	
ACCESSION	AX403313	
VERSION	AX403313.1 GI:21436871	
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D., Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,	



QY 1 MetLysIleProValIleuProAlaValIleuLeuSerIleuLeuValIleuHisSerAla 20  
Db 13 ATGAAGATCCCGGTCTTCTGCGCGTGTGCTCTCTCTCTGCTGTGCTCTCTCTGCT 72

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QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspIysLeuArgSerAlaPheIysAla 60  
Db 133 CCCGAGGCTTTAACACCCCGTTCCTGACATCGACAAATTGCGATCTGCGTTAAGGCT 192

QY 61 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleIysArgLysLeuProPheLeu 80  
Db 253 AACTGGATGCCTTCTTAAGCTGAAGAGACTGAGAGCGCAACTCTGATGCCAG 309

RESULT 9  
AX574494 415 bp DNA linear PAT 07-JAN-2003  
LOCUS Sequence 21 from Patent WO0224888.  
ACCESSION AX574494  
VERSION AX574494.1 GI:27551800  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Baker, K.P., Baton, D.L., Filvaroff, E., Goddard, A., Grimaldi, J.C., Guirney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K., Wood, W.I., Zhang, Z. and Fong, S.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same  
JOURNAL Patent: WO 0224888-A 21 28-MAR-2002;  
GENENTECH, INC. (US)  
FEATURES  
source 1. .415  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 3.73e-57 Length: 415  
Score: 510.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142 (1-99) x AX574494 (1-415)

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QY 21 GlnGlyAlaThrLeuGlyGlyProGluGluSerThrIleGluAsnTyraIleSerArg 40  
Db 73 CAGGAGCCACCCCTGGTGGTCTCTGAGGAAGAACCATTTGAGATTATGCGTCACGA 132

QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspIysLeuArgSerAlaPheIysAla 60  
Db 133 CCCGAGGCTTTAACACCCCGTTCCTGACATCGACAAATTGCGATCTGCGTTAAGGCT 192

QY 61 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleIysArgLysLeuProPheLeu 80  
Db 193 GATGAGTTCCTGAAGCTGCGACGCCCTCTTGAAGTATCAAAAAGAACTTCTTCTCCTC 252

QY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
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RESULT 10  
BD082389 456 bp DNA linear PAT 27-AUG-2002  
LOCUS BD082389  
DEFINITION 87 human secreted proteins.  
ACCESSION BD082389  
VERSION BD082389.1 GI:22627999  
KEYWORDS JP 2001522239-A/31.  
SOURCE Mastadenovirus  
ORGANISM Mastadenovirus  
REFERENCE Viruses; dsDNA viruses, no RNA stage; Adenoviridae.  
1 (bases 1 to 456)  
AUTHORS Young, P., Greene, J.M., Ferrie, A.M., Ruben, S.M., Rosen, C.A., Duan, R.D., Hu, J.S., Florence, K.A., Olsen, H.S., Ebner, R., Brewer, L.A., Moore, P.A., Shi, Y., Lafleur, D.W. and Ni, J.  
TITLE 87 human secreted proteins  
JOURNAL Patent: JP 2001522239-A 31 13-NOV-2001;  
HUMAN GENOME SCIENCES INC SECRETARY OF THE DEPARTMENT OF HEALTH  
HUMAN SERVICES  
PN JP 2001522239-A/31  
PD 13-NOV-2001  
PF 19-MAR-1998 JP 1998542119  
PR 21-MAR-1997 US 60/041281, 21-MAR-1997 US 60/041276 PR  
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30-MAY-1997 US 60/048350, 05-AUG-1997 US 60/054804 PR  
19-AUG-1997 US 60/056370, 02-OCT-1997 US 60/060862 PI  
YOUNG, JOHN M GREENE, ANN M FERRIE, STEVEN M RUBEN, CRAIG A PI  
ROSEN, C  
PI ROXANNE D DUAN, JING SHAN HU, KIMBERLY A FLORENCE, HENRIK S  
OLSEN, H  
PI REINHARD EBNER, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W  
PI LAFLEUR, D  
PI JIAN NI  
PC C07K14/00  
CC Strandedness: Double;  
CC Topology: Linear;  
FH Key Location/Qualifiers.

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source 1. .456  
/organism="Mastadenovirus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10509"  
BASE COUNT 117 a 136 c 104 g 98 t 1 others  
ORIGIN

Alignment Scores:  
Pred. No.: 4.16e-57 Length: 456  
Score: 510.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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US-10-059-395-142 (1-99) x BD082389 (1-456)

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Db 21 ATGAAGATCCCGGTCTTCTGCGCGTGTGCTCTCTCTCTGCTGTGCTCTCTGCT 80

QY 21 GlnGlyAlaThrLeuGlyGlyProGluGluSerThrIleGluAsnTyraIleSerArg 40



Db	81	CAGGAGCACCCCTGGGTGGTCTCGAGGAAGAACCATTGAGATTATGCGTCACGA	140
QY	41	ProGluAlaPheAsnThrProPheLeuAsnIleAspIysLeuArgSerAlaPheIysAla	60
Db	141	CCCGAGGCCCTTTAACACACCCCGCTCTGACATCGACAAATTGCCATCTGCGTTAAGGCT	200
QY	61	AspGluPheLeuAsnTyrHisAlaLeuPheGluSerIleIysArgIysLeuProPheLeu	80
Db	201	GATGAGTTCCTGAACCTGGCACGCCCTCTTTGAGTCTATCAAAAGAACTTCCTTCCCTC	260
QY	81	AsnTyrAspAlaPheProIysLeuLysGlyLeuArgSerAlaThrProAspAlaGln	99.
Db	261	AACTGGATGCTCTTCTTAAGCTGAAGAGACTGAGAGCGCACTCTGATGCCCAG	317

RESULT	11		
AX080817			
LOCUS	AX080817	490 bp	DNA
DEFINITION	Sequence 63 from Patent WO0109327.		linear
ACCESSION	AX080817		PAT 27-FEB-2001
VERSION	AX080817.1	GI:13169786	
KEYWORDS			
SOURCE			
ORGANISM			
	synthetic construct		
	synthetic construct		
	artificial sequences.		

REFERENCE  
AUTHORS  
1  
Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,

**TITLE** Method of preventing the injury or death of retinal cells and treating ocular diseases  
**JOURNAL** Patent: WO 0109327-A 63 08-FEB-2001;  
Genentech, Inc. (US)

FEATURES	Location/Qualifiers
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/organism="synthetic construct"
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DNA57694."

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Query Match:	100.00%
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Length:	490
Matches:	99
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Mismatches:	0
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US-10-059-395-142 (1-99) X AX080817 (1-490)

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Db	80	ATGAAGATCCCGGTCCTTCGCGCGTGGTGTCTCTCCCTCGGTGTCTCACTGTGCC	139
QY	21	GInglYAlaThrLeuGlYglYProGlUGlUGlSerThrIleGlUAsnTYrAlaSerArg	40
Db	140	CAGGAGCCACCCCTGGGTGTCTGTAGAGAGAAGACACCATTTAGAAATTATGGCTACAGA	199
QY	41	ProGlUAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla	60
Db	200	CCCGAGGCGCTTAAACACCCCGTTCCTGAACATCGACAATTGGCATCTGCGTTAAGGCT	259
QY	61	AspGlUphLeuAsnTrpHisAlaLeuPheGlUSeRIleLysArgLysLeuProPheLeu	80
Db	260	GATGAGTTCCTGAACCTGGCACGCCCTCTTGACTCTATCAAAAGGAACTTCCTTCCCTC	319
QY	81	AsnTrpAspAlaPheProLysLeuLysGlYLeuArgSerAlaThrProAspAlaGln	99
Db	320	AACGTGGATGCGCTTTCCTTAAGCTGAAGGACTGAGGAGCGCACTCCTGTATGCCACG	376

RESULT	12
HSA293408	
LOCUS	
DEFINITION	HSA293408 529 bp mRNA linear PRI 06-JAN-2003
	Homo sapiens mRNA differentially expressed in malignant melanoma,
	clone NN 15.
ACCESSION	AJ293408
VERSION	AJ293408.1 GI:27526545
KEYWORDS	differential expression; malignant; melanoma.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	1	Deichmann, M., Thome, M., Wacker, J. and Naeher, H.
AUTHORS		Genes differentially expressed in malignant melanoma
TITLE		Unpublished
JOURNAL	2 (bases 1 to 529)	
REFERENCE		Deichmann, M.
AUTHORS		Direct Submission
TITLE		Submitted (28-JUN-2000) Deichmann M., Dermatology, University Of
JOURNAL		Heidelberg, Vossstrasse 2, 69115 Heidelberg, GERMANY

FEATURES	Location/Qualifiers
Source	1. .529

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/organism="Homo sapiens"
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/clone="NN 15"
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/note="differentially expressed in malignant melanoma"								
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Score:	503.00
Percent Similarity:	98.99%
Best Local Similarity:	98.99%
Query Match:	98.63%
DB:	9
Length:	529
Matches:	98
Conservative:	0
Mismatches:	1
Indels:	0
Gaps:	0

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Qy		1 MetLysIleProValLeuProAlaValValLeuSerLeuLeuValLeuHisSeraLa 20
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Qy	21 GInGIYAlathrLeuGIYGIYProGLUGLUserThrIleGIUAsnTYraLSerArg 40	
Db	111 CAGGAGCCACCGCTGGGTGGTCTCTGAGAAAGAAGCAACATTGAGAATTATGCGTCACA 170	
Qy	41 ProGLUAlaphesAntTrpHisAlaleuPheGLUserylElysaRgylsleuProPhelu 60	
Db	171 CCCGAGGCCTTTAACACCCCCGTTCTCTGAACATCGACAATGCGATCTGCGTTAAGGCT 230	
Qy	61 AspGLUPhelLeuAsnTrpHisAlaleuPheGLUserylElysaRgylsleuProPhelu 80	
Db	231 GATGAGTTCCTGAACTGGCACGCCCTCTTGAGTCTATCAAAGGAAACTTCCTTCTC 290	
Qy	81 AsnTrpAspAlaphesProLYsleuLYsGLYLLeuArGSeralATHrProAspAlaGln 99	
Db	291 AACTGGATGCCCTTCTTAAGCTGAAGGAGCTGAGGAGCGCAACTCCTGATGCCCCAG 347	
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DEFINITION	Sequence 62 from Patent WO0109327.	
ACCESSION	AX080816	
VERSION	AX080816.1 GI:13169785	
KEYWORDS	.	
SOURCE	synthetic construct	
ORGANISM	synthetic construct	
REFERENCE	artificial sequences.	
REFERENCE	1	

AUTHORS Ashkenazi,A.J., Baker,K.P., Goddard,A., Godowski,P.J., Gurney,A.L., Kljavin,I.J., Lafleur,M., Mark,M.R., Marsters,S.A., Pitti,R.M., Watanabe,C.K. and Wood,W.I.  
TITLE Method of preventing the injury or death of retinal cells and treating ocular diseases  
JOURNAL Patent: WO 0109327-A 62 08-FEB-2001;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..435  
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/mol\_type="genomic DNA"  
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QY 21 GlnGlyAlaThrIleuGlyGlyProGluGluSerThrIleGluAsnIleAlaSerArg 40  
DB 75 CAGGAGCCACCCCTGGTGGTCTGAGGAAGAAGCAACATTGAGATTATGCTCAGCA 134  
QY 41 -ProGluAlaPheAsnThrProPheIleuAsnIleAspIleuArgSerAlaPheIleuAl 60  
DB 135 CCCCAGGCGCTTAACACCCCGTTCCTGACATCGACAATTGCGATCGCTTAAGGC 194  
QY 60 AAspGluPheIleuAsnThrHisAlaIleuPheGluSerIleIleuArgIleuProPheIle 80  
DB 195 TGATGAGTCTCGAAGTGGACGCGCTCTTGTAGTCTATCAAAAGAACTTCCTTCCCT 254  
QY 80 uAsnTrpAspAlaPheProIleuIleuGlyIleuArgSerAlaThrProAspAlaGln 99  
DB 255 CAACGTGGATGCTTCTTAAGCTGAAGAGACTGAGAGCGCAACTCTGATGCCAG 312  
RESULT 14  
AX080815 432 bp DNA linear PAT 27-FEB-2001  
LOCUS Sequence 61 from Patent WO0109327.  
ACCESSION AX080815  
VERSION AX080815.1 GI:13169784  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Ashkenazi,A.J., Baker,K.P., Goddard,A., Godowski,P.J., Gurney,A.L., Kljavin,I.J., Lafleur,M., Mark,M.R., Marsters,S.A., Pitti,R.M., Watanabe,C.K. and Wood,W.I.  
TITLE Method of preventing the injury or death of retinal cells and treating ocular diseases  
JOURNAL Patent: WO 0109327-A 61 08-FEB-2001;  
Genentech, Inc. (US)  
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source 1..432  
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DB 73 CAGGAGCCACCCCTGGGTGT-CCTGAGGAAGAAGCAACATTGAGATTATGCGTCACGA 131  
QY 41 ProGluAlaPheAsnThrProPheIleuAsnIleAspIleuArgSerAlaPheIleuAla 60  
DB 132 CCCCAGGCGCTTAAACACCCCGTTCCTGACATCGACAATTGCGATCGCTTAAGGCT 191  
QY 61 AAspGluPheIleuAsnThrHisAlaIleuPheGluSerIleIleuArgIleuProPheIleu 80  
DB 192 GATGAGTCTCGAAGTGGACGCGCTTGTAGTCTATCAAAAGAACTTCCTTCCCTC 251  
QY 81 AsnTrpAspAlaPheProIleuIleuGlyIleuArgSerAlaThrProAspAlaGln 99  
DB 252 AACTGGATGCTTCTTAAGCTGAAGAGACTGAGAGCGCAACTCTGATGCCCAA 308  
RESULT 15  
AX080818 432 bp DNA linear PAT 27-FEB-2001  
LOCUS Sequence 64 from Patent WO0109327.  
ACCESSION AX080818  
VERSION AX080818.1 GI:13169787  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Ashkenazi,A.J., Baker,K.P., Goddard,A., Godowski,P.J., Gurney,A.L., Kljavin,I.J., Lafleur,M., Mark,M.R., Marsters,S.A., Pitti,R.M., Watanabe,C.K. and Wood,W.I.  
TITLE Method of preventing the injury or death of retinal cells and treating ocular diseases  
JOURNAL Patent: WO 0109327-A 64 08-FEB-2001;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
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QY 21 GlnGlyAlaThrLeuGlyGlyProGlnGlnGluSerThrIleGluAsnTyrAlaSerArg 40  
Db 73 CAGGAGCCACCCTGGGTGT-CCTGAGAGAAAGCAACCATTGAGATTATGGCTCACGA 131  
QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
Db 132 CCGGAGGCTTTAAACACCCCGTTCCTGACATCGACAATTCGATCTGCGTTTAAGGCT 191  
QY 61 AspGluPheLeuAsnThrPheAlaLeuPheGlnSerIleLysArgLysLeuProPheLeu 80  
Db 192 GATGAGTTCCTGAACCTGGACGCCCTCTTTGAGTCTATCAAAAGAAACTTCTTCCCTC 251  
QY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

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and is derived by analysis of the total score distribution.

SUMMARIES

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2	267.5	52.5	288	4	US-09-313-294A-4134 Sequence 4134, Ap
3	78.5	15.4	686	3	US-09-328-111-364 Sequence 364, App
4	67.5	13.2	1830121	4	US-09-557-884-1 Sequence 1, Appli
5	67.5	13.2	1830121	4	US-09-643-990A-1 Sequence 1, Appli
6	66.5	13.0	1230025	4	US-09-198-452A-1 Sequence 1, Appli
7	65.5	12.8	234	4	US-09-107-532A-2008 Sequence 2008, Ap
8	65	12.7	1830121	4	US-09-557-884-1 Sequence 1, Appli
9	65	12.7	1830121	4	US-09-643-990A-1 Sequence 1, Appli
10	63	12.4	11461	3	US-08-669-161A-29 Sequence 29, Appl
11	62.5	12.3	2523	4	US-09-620-312D-290 Sequence 290, App
12	62.5	12.3	4084	3	US-08-866-340-1 Sequence 1, Appli

C	13	62.5	12.3	4460	3	US-09-103-875-4	Sequence 4, Appli
	14	62.5	12.3	7216	2	US-08-750-703-3	Sequence 3, Appli
	15	62	12.2	936	4	US-09-252-991A-1763	Sequence 1763, Ap
	16	62	12.2	1845	4	US-09-328-352-1350	Sequence 1350, Ap
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	23	61	12.0	771	4	US-09-252-991A-13016	Sequence 13016, A
	24	60.5	11.9	655	4	US-09-288-143-20	Sequence 20, Appl
	25	60.5	11.9	1893	4	US-09-252-991A-3131	Sequence 3131, Ap
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	35	59.5	11.7	46899	1	US-08-471-119A-1	Sequence 1, Appli
	36	59	11.6	862	4	US-09-149-476-91	Sequence 91, Appl
	37	59	11.6	3520	4	US-09-220-132-84	Sequence 84, Appl
	38	59	11.6	3684	4	US-09-252-991A-65	Sequence 65, Appl
	39	59	11.6	7527	4	US-09-252-991A-71	Sequence 71, Appl
	40	59	11.6	40123	4	US-08-311-731A-137	Sequence 137, App
	41	59	11.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	42	58.5	11.5	1095	3	US-08-882-501-31	Sequence 31, Appl
	43	58.5	11.5	1113	4	US-09-107-532A-2266	Sequence 2266, Ap
	44	58.5	11.5	1430	4	US-09-489-847-39	Sequence 39, Appl
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ALIGNMENTS

RESULT 1  
US-09-996-243-200  
; Sequence 200, Application US/09996243  
; Patent No. 6478825  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Geritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC13  
; CURRENT APPLICATION NUMBER: US/09/996,243  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250	PRIOR FILING DATE: 1997-10-17	PRIOR APPLICATION NUMBER: 60/065186	PRIOR FILING DATE: 1997-11-12	PRIOR APPLICATION NUMBER: 60/065311	PRIOR FILING DATE: 1997-11-13	PRIOR APPLICATION NUMBER: 60/066770	PRIOR FILING DATE: 1997-11-24	PRIOR APPLICATION NUMBER: 60/075945	PRIOR FILING DATE: 1998-02-25	PRIOR APPLICATION NUMBER: 60/078910	PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/083322	PRIOR FILING DATE: 1998-04-28	PRIOR APPLICATION NUMBER: 60/084600	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/087106	PRIOR FILING DATE: 1998-05-28	PRIOR APPLICATION NUMBER: 60/087607	PRIOR FILING DATE: 1998-06-02	PRIOR APPLICATION NUMBER: 60/087609	PRIOR FILING DATE: 1998-06-02	PRIOR APPLICATION NUMBER: 60/087759	PRIOR FILING DATE: 1998-06-02	PRIOR APPLICATION NUMBER: 60/087827	PRIOR FILING DATE: 1998-06-03	PRIOR APPLICATION NUMBER: 60/088021	PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088025	PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088026	PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088028	PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088029	PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088030	PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088033	PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088326	PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088167	PRIOR FILING DATE: 1998-06-05	PRIOR APPLICATION NUMBER: 60/088202	PRIOR FILING DATE: 1998-06-05	PRIOR APPLICATION NUMBER: 60/088212	PRIOR FILING DATE: 1998-06-05	PRIOR APPLICATION NUMBER: 60/088217	PRIOR FILING DATE: 1998-06-05	PRIOR APPLICATION NUMBER: 60/088655	PRIOR FILING DATE: 1998-06-09	PRIOR APPLICATION NUMBER: 60/088734	PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/088738	PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/088742	PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/088810	PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/088824	PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/088826	PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/088858	PRIOR FILING DATE: 1998-06-11	PRIOR APPLICATION NUMBER: 60/088861	PRIOR FILING DATE: 1998-06-11	PRIOR APPLICATION NUMBER: 60/088876	PRIOR FILING DATE: 1998-06-11	PRIOR APPLICATION NUMBER: 60/089105	PRIOR FILING DATE: 1998-06-12	PRIOR APPLICATION NUMBER: 60/089440
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1	PRIOR FILING DATE: 1998-06-16
2	PRIOR APPLICATION NUMBER: 60/089512
3	PRIOR FILING DATE: 1998-06-16
4	PRIOR APPLICATION NUMBER: 60/089514
5	PRIOR FILING DATE: 1998-06-16
6	PRIOR APPLICATION NUMBER: 60/089532
7	PRIOR FILING DATE: 1998-06-17
8	PRIOR APPLICATION NUMBER: 60/089538
9	PRIOR FILING DATE: 1998-06-17
10	PRIOR APPLICATION NUMBER: 60/089598
11	PRIOR FILING DATE: 1998-06-17
12	PRIOR APPLICATION NUMBER: 60/089599
13	PRIOR FILING DATE: 1998-06-17
14	PRIOR APPLICATION NUMBER: 60/089600
15	PRIOR FILING DATE: 1998-06-17
16	PRIOR APPLICATION NUMBER: 60/089653
17	PRIOR FILING DATE: 1998-06-17
18	PRIOR APPLICATION NUMBER: 60/089801
19	PRIOR FILING DATE: 1998-06-18
20	PRIOR APPLICATION NUMBER: 60/089907
21	PRIOR FILING DATE: 1998-06-18
22	PRIOR APPLICATION NUMBER: 60/089908
23	PRIOR FILING DATE: 1998-06-18
24	PRIOR APPLICATION NUMBER: 60/089947
25	PRIOR FILING DATE: 1998-06-19
26	PRIOR APPLICATION NUMBER: 60/089948
27	PRIOR FILING DATE: 1998-06-19
28	PRIOR APPLICATION NUMBER: 60/089952
29	PRIOR FILING DATE: 1998-06-19
30	PRIOR APPLICATION NUMBER: 60/090246
31	PRIOR FILING DATE: 1998-06-22
32	PRIOR APPLICATION NUMBER: 60/090252
33	PRIOR FILING DATE: 1998-06-22
34	PRIOR APPLICATION NUMBER: 60/090254
35	PRIOR FILING DATE: 1998-06-22
36	PRIOR APPLICATION NUMBER: 60/090349
37	PRIOR FILING DATE: 1998-06-23
38	PRIOR APPLICATION NUMBER: 60/090355
39	PRIOR FILING DATE: 1998-06-23
40	PRIOR APPLICATION NUMBER: 60/090429
41	PRIOR FILING DATE: 1998-06-24
42	PRIOR APPLICATION NUMBER: 60/090431
43	PRIOR FILING DATE: 1998-06-24
44	PRIOR APPLICATION NUMBER: 60/090435
45	PRIOR FILING DATE: 1998-06-24
46	PRIOR APPLICATION NUMBER: 60/090444
47	PRIOR FILING DATE: 1998-06-24
48	PRIOR APPLICATION NUMBER: 60/090445
49	PRIOR FILING DATE: 1998-06-24
50	PRIOR APPLICATION NUMBER: 60/090472
51	PRIOR FILING DATE: 1998-06-24
52	PRIOR APPLICATION NUMBER: 60/090535
53	PRIOR FILING DATE: 1998-06-24
54	PRIOR APPLICATION NUMBER: 60/090540
55	PRIOR FILING DATE: 1998-06-24
56	PRIOR APPLICATION NUMBER: 60/090542
57	PRIOR FILING DATE: 1998-06-24
58	PRIOR APPLICATION NUMBER: 60/090557
59	PRIOR FILING DATE: 1998-06-24
60	PRIOR APPLICATION NUMBER: 60/090676
61	PRIOR FILING DATE: 1998-06-25
62	PRIOR APPLICATION NUMBER: 60/090678
63	PRIOR FILING DATE: 1998-06-25
64	PRIOR APPLICATION NUMBER: 60/090690
65	PRIOR FILING DATE: 1998-06-25
66	PRIOR APPLICATION NUMBER: 60/090694
67	PRIOR FILING DATE: 1998-06-25
68	PRIOR APPLICATION NUMBER: 60/090695
69	PRIOR FILING DATE: 1998-06-25
70	PRIOR APPLICATION NUMBER: 60/090696
71	PRIOR FILING DATE: 1998-06-25
72	PRIOR APPLICATION NUMBER: 60/090862
73	PRIOR FILING DATE: 1998-06-26









OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (600001)..(615000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (615001)..(630000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (630001)..(645000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (645001)..(660000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (660001)..(675000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (675001)..(690000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (690001)..(705000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (705001)..(720000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (720001)..(735000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (735001)..(750000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (750001)..(765000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (765001)..(780000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (780001)..(795000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (795001)..(810000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (810001)..(825000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (825001)..(840000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (840001)..(855000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (855001)..(870000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (870001)..(885000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (885001)..(900000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (900001)..(915000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature

## Alignment Scores:

Pred. No.:	1.78e+05	Length:	1230025
Score:	66.50	Matches:	19
Percent Similarity:	46.15%	Conservative:	11
Best Local Similarity:	29.23%	Mismatches:	28
Query Match:	13.04%	Indels:	7
DB:	4	Gaps:	1

US-10-059-395-142 (1-99) x US-09-198-452A-1 (1-1230025)  
QY 11 LeuLeuSerLeuLeuValLeuHisSerAlaGlnGlyAlaThrLeuGlyGlyProGluGlu 30  
Db 1034560 TTAATAATCTTGTCATCTATGACTACATAATGTTGTTCTCGATGATATCTTAAT 1034619  
QY 31 GluSerThrIleGluAsnTyraIaSerArgProGluAlaPheAsnThrProPheLeuAsn 50  
Db 1034620 GAAATTAGTGTGAGATACAAAAACGTTTGAAGCCTATGCTGGAGATATATGAA 1034679  
QY 51 IleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnTyraIaLeuPhe 70  
Db 1034680 ATTGAT-----GGGTATGATTTTACCATATTCATGACATTC 1034718  
QY 71 GluSerIleIysArg 75  
Db 1034719 TCGAGCATCAACGG 1034733

## RESULT 7

US-09-107-532A-2008  
; Sequence 2008, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arinello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 2008:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 234 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...234  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2008:  
US-09-107-532A-2008

## Alignment Scores:

Pred. No.: 0.547 Length: 234  
Score: 65.50 Matches: 24  
Percent Similarity: 40.66% Conservative: 13  
Best Local Similarity: 26.37% Mismatches: 33  
Query Match: 12.84% Indels: 21  
DB: 4 Gaps: 4

US-10-059-395-142 (1-99) x US-09-107-532A-2008 (1-234)

QY 4 ProValLeuProAlaValValLeuLeuSerLeuLeuValLeuHisSerAlaGlnGlyAla 23  
|||::|||  
Db 16 CCGATCCTTCCA-----AGCCATGGCAGC 39  
QY 24 ThrLeuGlyGlyProGluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAla 43  
|||::|||  
Db 40 ACGATTCAGACCCCTGCTATCCAGCAATTAGTAGAAATGTAC-----CCTAGAGTT 90  
QY 44 PheAsnThrProPheLeu-----AsnIleAspLysLeuArgSerAlaPheLysAlaAsp 61  
|||::|||  
Db 91 CTGTACACCCCGCATGTAGTTCAATACAGATGACATTATCAAAATATGATTTCGACA 150  
QY 62 GluPheLeuAsnTyrHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeuAsn 81  
|||::|||  
Db 151 AGTTTCGAGAACTTCGTGAATAATAGAACTGAAAAACGAAA-----AAT 198  
QY 82 TrpAspAlaPheProLysLeuLysGlyLeuArg 92  
|||::|||  
Db 199 GAGGTATCTCTCTTAAGCCCGTCAATTAGA 231

## RESULT 8

US-09-557-884-1/c  
Sequence 1, Application US/09557884  
Patent No. 6506581

## GENERAL INFORMATION:

APPLICANT: Fleischmann et al.  
TITLE OF INVENTION: The Nucleotide sequence of  
the Haemophilus influenzae Rd Genome, Fragments  
Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD

COUNTRY: USA  
ZIP: 20850

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS V6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/557,884

FILING DATE: 25-Apr-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/476,102

FILING DATE: JUN-5-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Michelle S. Marks

REGISTRATION NUMBER: 41,971

REFERENCE/DOCKET NUMBER: PB186P3

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1830121 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-557-884-1

Alignment Scores:  
Pred. No.: 4.62e+05 Length: 1830121  
Score: 65.00 Matches: 22  
Percent Similarity: 45.33% Conservative: 12  
Best Local Similarity: 29.33% Mismatches: 35  
Query Match: 12.75% Indels: 6  
DB: 4 Gaps: 2

US-10-059-395-142 (1-99) x US-09-557-884-1 (1-1830121)

QY 26 GlyGlyProGluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsn 45  
|||::|||  
Db 1767958 GGGGACGAGCGCGTTCTATTAATGTTGCTAATGCTCTTGCTAAACAGGATATGAT 1767899  
QY 46 ThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsn 65  
|||::|||  
Db 1767898 GTTCTTTTATTAAGCATTTGGCGTAACAGCCTTTTCCAGTTGATGAAAAATTAAAT 1767839  
QY 66 TrpHisAlaLeuPheGluSerIleLysArgLysLeuProPhe---LeuAsnTrpAspAla 84  
|||::|||  
Db 1767838 ATTTACGCAATG-----AATAAATTGCCCTATTCTTGAATAAAGATTAT 1767794  
QY 85 PheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
|||::|||  
Db 1767793 TTTCTATCACTAAAAATTAAAGAGATTAGTTAAAGAAATTACAG 1767749

## RESULT 9

US-09-643-990A-1/c  
Sequence 1, Application US/09643990A  
Patent No. 6528289

## GENERAL INFORMATION:

APPLICANT: Robert D. Fleischmann  
Mark D. Adams  
Owen White  
Hamilton O. Smith  
J. Craig Venter

TITLE OF INVENTION: The Nucleotide sequence of  
the Haemophilus influenzae Rd Genome, Fragments  
Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD

COUNTRY: USA  
ZIP: 20850

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS V6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/643,990A

FILING DATE: 23-Aug-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/487,429

FILING DATE: 1995-06-07

APPLICATION NUMBER: 08/426,787

FILING DATE: 1995-04-21

ATTORNEY/AGENT INFORMATION:  
NAME: Kenley K. Hoover

REGISTRATION NUMBER: 40,302

REFERENCE/DOCKET NUMBER: PB186P1C1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-610-5790

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1830121 base pairs

TYPE: nucleic acid



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; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_fl_genes version 1.0
; SEQ ID NO 290
; LENGTH: 2523
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (81)..(2138)
US-09-620-312D-290

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Alignment Scores:	
Pred. No.:	58
Score:	62.50
Percent Similarity:	34.78%
Best Local Similarity:	26.96%
Query Match:	12.25%
DB:	4
Length:	2523
Matches:	31
Conservative:	9
Mismatches:	38
Gaps:	37
Indels:	5

US-10-059-395-142 (1-99) X US-09-620-312D-290 (1-2523)

QY 11 LeuLeuSerLeuLeuValLeuHisSerAlaGlnGlyAlaThrLeuGlyGlyProGluGlu 30  
||| ||| ||| ||| :|||  
Db 1086 TTATCTGCTTATTGCTTTAGTCTGTCTTGACACTGTGTTACTTAGACCCAAAGA 1145

31 GluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPheLeuAsn 50

DB 1146 AAGAACGATGTAGAATATTAGTGAACCAAGAGCTACTGAGACAGAATTTGTTAAT 1203

QY 51 -----IIeasplysleuarg----- 55

Db 1206 CCTCTGAGATATATGCAATGTGTGTGCCACAAAATTTATGAACTGAGGAAAATACTT 1265

Gy 56 -----SerAlaphelysAla-----AspGluPheIeu 64

Db 1266 GAAAAGGTGAGGCGTCATCAGATTACCTCTGAGAGAAAAGATCCTGAGGAATTCCTTG 1323

Qy 65 AsnTrpHisAlaLeupheGlnSerIleLysArgLysLeuProhLeuAsnTrpAspAla 84

Db 1326 AAT-----ATTCTGTTTCATCATATTTTAAGGGTAGAACCTTGTCTAAA

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Db      1371 -----ATGAGATCAGCAGGTCAAAAGGTACAA 1397
RESULT 12
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; Sequence 1, Application US/0886340
; Patent No. 6020318
;
; GENERAL INFORMATION:
;
; APPLICANT: Szyf, Moshe
; APPLICANT: Bigey, Pascal
; APPLICANT: Ramchandani, Shyam
; TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC
; TITLE OF INVENTION: SEQUENCES AND ANTISENSE OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
;

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; APPLICATION NUMBER: US/08/866,340
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Keown, Wayne A.
; REGISTRATION NUMBER: 33,923
; REFERENCE/DOCKET NUMBER: 106.101.187
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4084 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
US-08-866-340-1

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Alignment Scores:	
Pred. No.:	121
Score:	62.50
Percent Similarity:	56.60%
Best Local Similarity:	33.96%
Query Match:	12.25%
DB:	3
Length:	4084
Matches:	18
Conservative:	12
Mismatches:	12
Indels:	11
Gaps:	3

US-10-059-395-142 (1-99) x US-08-866-340-1 (1-4084)

[illegible]

Qy 64 LeuAsnTrp---HisAlaLeuPheGluSer-----IleYsArg 75  
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Db 2694 CTTTATTGAGCCACAAGTGTGTCACTCAGATTTCGTAATAAGAAAATTTTAAAGAGC 2635

Qy	76	LysLeuProPheLeuAsnTrpAspAlaPheProLysLeu	88
		:::	
Db	2634	AGATTACCTTTCTGTAAAGCTGTCCTTTCCAAATCTT	2596

RESULT 13  
US-09-103-875-4/c  
; Sequence 4, Application US/09103875A

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; GENERAL INFORMATION:
; APPLICANT: Szyf, Moshe
; APPLICANT: Bigey, Pascal
; APPLICANT: Ramchandani, Shyam
; TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC SEQUENCES AND ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES
; FILE REFERENCE: 106101.194
; CURRENT APPLICATION NUMBER: US/09/103, 875A
; CURRENT FILING DATE: 1998-06-24
; EARLIER APPLICATION NUMBER: 60/069, 865
; EARLIER FILING DATE: 1997-12-17
; EARLIER APPLICATION NUMBER: 08/866, 340
; EARLIER FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 138

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Alignment Scores:	139	Length:	4460
Pred. No.:		Matches:	18
Score:	62.50	Conservative:	12
Percent Similarity:	56.60%	Mismatches:	12
Best Local Similarity:	33.96%		



Query Match: 12.25% Indels: 11  
DB: 3 Gaps: 3  
US-10-059-395-142 (1-99) x US-09-103-875-4 (1-4460)  
QY 44 PheAsnThrProPheLeuAsnIleAspLysLeuArgSeraIaPheLysAlaAspGluPhe 63  
DB 2743 TTGAAACTCATG-----GAAAAATGCAAAATCCAATTAAAGAAAAACAATT 2693  
QY 64 LeuAsnTrp--HisAlaLeuPheGluSer-----IleLysArg 75  
DB 2692 CTTTATGAGCCACAAAGTGTCTCAGATTTGGTAATAAGAAAAATTTAAGGAGG 2633  
QY 76 LysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 88  
DB 2632 AGATTACCTTTCTGTAAAGCTGTCTCTTCCAATCTT 2594  
RESULT 14  
US-08-750-703-3  
; Sequence 3, Application US/08750703  
; Patent No. 5891633  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Frank J.; Idle, Jeffrey R.  
; TITLE OF INVENTION: DEFECTS IN DRUG  
; TITLE OF INVENTION: METABOLISM  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morgan & Finnegan  
; STREET: 345 Park Ave.  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10154-0053  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/750,703  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/07605  
; FILING DATE: 16-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dorothy R. Auth  
; REGISTRATION NUMBER: 36,434  
; REFERENCE/DOCKET NUMBER: 2026-4196PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 758-4800  
; TELEFAX: (212) 751-6849  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7216 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: genomic DNA  
; FEATURE:  
; NAME/KEY: CYP2A6v2  
; LOCATION:  
; OTHER INFORMATION:  
; US-08-750-703-3  
Alignment Scores:  
Pred. No.: 290 Length: 7216  
Score: 62.50 Matches: 30  
Percent Similarity: 37.07% Conservative: 13  
Best Local Similarity: 25.86% Mismatches: 32  
Query Match: 12.25% Indels: 41  
DB: 2 Gaps: 5

US-10-059-395-142 (1-99) x US-08-750-703-3 (1-7216)  
QY 5 ValLeuProAlaValLeuLeuSerLeuValLeuHisSeraIaGlnGlyAlaThr 24  
DB 2974 ATGCTCCCTACCAAGTCTTCTGAATATTAAACACCGGAACCTGGGTACCTAAC 3033  
QY 25 -----LeuGlyGlyProGluGluGluSerThrIleGlu 35  
DB 3034 TTCCCTGTAACCTTAGAGATTAGTTCCTATCCGGCCCTCTGA-----ATACCT 3084  
QY 36 AsnTyraIaSerArgProGluAlaPheAsnThr----- 46  
DB 3085 AACCAAC--CGAGAGACAGATGCTTAACTCAGTTCCTCCTTGCTATGAACAATCC 3141  
QY 47 -----ProPheLeuAsnIleAspLysLeuArg 55  
DB 3142 CATCCCATCAGCTCTGCCCCGTGACAGCTGTCTCCCTCCATCTCTCTGCAA 3201  
QY 56 SeraIaPheLysAlaAspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleLysArg 75  
DB 3202 CCCAGCTC-----TATGAGATGTTCTCTCGGTGATGAAA 3237  
QY 76 LysLeuProPheLeuAsnTrpAspAlaPheProLysLeuLysGlyLeu 91  
DB 3238 CACCTGCCAGACCGCAGCAACAGCCCTTCAAGTGTGCAAGGGCTG 3285  
RESULT 15  
US-09-252-991A-1763  
; Sequence 1763, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 1763  
; LENGTH: 936  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
; US-09-252-991A-1763  
Alignment Scores:  
Pred. No.: 15.1 Length: 936  
Score: 62.00 Matches: 25  
Percent Similarity: 51.14% Conservative: 20  
Best Local Similarity: 28.41% Mismatches: 23  
Query Match: 12.16% Indels: 20  
DB: 4 Gaps: 5  
US-10-059-395-142 (1-99) x US-09-252-991A-1763 (1-936)  
QY 18 HisSeraIaGlnGlyAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAsnTy 37  
DB 652 AACGCGTGGTGGCGCCAGCTTCTTGGCGGGCGAGAGCGTCCACTGACGACCTG 711  
QY 38 AlaSerArgProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSeraIa 57  
DB 712 GCCAGCCGC-----TTTTCG-----GTCAACCTGTTGAAGCTGCAGCAGCG 753  
QY 58 PheLysAlaAspGlu-----PheLeuAsnTrpHisAla 68  
DB 754 CCGCAGAACGACGAGAGATCGCCAGGCGCTGCGCAGCGATCAAGTGCACACTAC 813  
QY 69 LeuPheGluSerIleLys-----ArgLysLeuProPheLeu---AsnTrpAsp 83  
DB 814 ATCGAGAAGTCCCTGCGCAACTACAACCAAGACAGCGTGCCTTCTGTGCAACAAGAT 873

Qy 84 AlapheProLysLeuLysGlyLeu 91  
|||  
:: |||||  
Db 874 GCAGACCGGATCATCGATGGCTG 897

Search completed: November 28, 2003, 09:42:29  
Job time : 958 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 07:55:16 ; Search time 26 Seconds  
(without alignments)  
366.181 Million cell updates/sec

Title: US-10-059-395-142  
Perfect score: 510  
Sequence: 1 MKIPVLPAVVLSTLVLSA.....LNWDAFPKLGKLSATPDAG 99

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*  
1: pirl:\*  
2: pirl2:\*  
3: pirl3:\*  
4: pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	14.9	234	2 D81342	tRNA (guanine-N1-)
2	74	14.5	807	2 S29242	sucrose synthase (
3	73	14.3	390	2 G97561	para-aminobenzoate
4	72.5	14.2	741	2 G84888	probable transke
5	70	13.7	500	2 T36090	probable integral
6	69	13.5	521	2 S55318	cytochrome P450 1A
7	69	13.5	521	2 S34184	cytochrome P450 1A
8	69	13.5	522	2 A28789	cytochrome P450 1A
9	68.5	13.4	871	2 B97035	DNA polymerase I,
10	68	13.3	292	2 AB3564	D-ribose-binding p
11	68	13.3	522	2 S51557	cytochrome P450, 3
12	68	13.3	1225	1 B64234	hypothetical prote
13	67.5	13.2	459	2 A75097	hypothetical prote
14	67	13.1	208	2 AF0278	probable ribose-bi
15	67	13.1	263	1 S23009	insulin-like growt
16	66.5	13.0	366	2 S46727	hypothetical prote
17	66.5	13.0	376	2 A83905	hypothetical prote
18	66	12.9	360	2 AB3534	spermidine/putresc
19	66	12.9	443	2 AF1901	hypothetical prote
20	66	12.9	1044	2 T43800	protein kinase sub
21	66	12.9	1298	2 T47523	DNA-binding protei
22	65.5	12.8	321	2 C89823	hypothetical prote
23	65.5	12.8	506	2 S63181	hypothetical prote
24	65.5	12.8	518	2 E87754	protein C43B1.10
25	65.5	12.8	2434	2 S44861	DNA topoisomerase
26	65	12.7	301	2 H95308	probable ABC trans
27	65	12.7	353	2 F64175	hypothetical prote
28	65	12.7	368	2 A71727	hypothetical prote
29	65	12.7	670	2 S77463	transketolase (EC

30	65	12.7	735	2 D86465	probable integral
31	65	12.7	736	2 D90574	hypothetical prote
32	64.5	12.6	519	2 S54300	transketolase (EC
33	64.5	12.6	583	2 JT0395	DNA-binding protei
34	64.5	12.6	1350	2 T13254	nitric-oxide synth
35	64.5	12.6	1400	2 T31555	hypothetical prote
36	64	12.5	253	1 PMRTYM	phosphoglycerate m
37	64	12.5	480	2 T18905	hypothetical prote
38	64	12.5	569	2 B99587	hypothetical prote
39	64	12.5	732	2 T40861	hypothetical zinc
40	63.5	12.5	129	2 A98038	hypothetical prote
41	63.5	12.5	397	2 AD0040	aromatic-amino-aci
42	63.5	12.5	663	2 A97066	transketolase, TKT
43	63.5	12.5	1777	2 AC2088	serine/threonine k
44	63	12.4	659	2 B81082	transketolase NMB1
45	63	12.4	856	2 AD0042	enhancing factor (

ALIGNMENTS

RESULT 1

D81342  
tRNA (guanine-N1-)-methyltransferase (EC 2.1.1.31) Cj0713 [imported] - Campylobacter jej  
C;Species: Campylobacter jejuni  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 03-Jun-2002  
C;Accession: D81342  
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chilling  
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrell  
Nature 403, 665-668, 2000  
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp  
A;Reference number: A81250; MUID:20150912; PMID:10688204  
A;Accession: D81342  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-234 <PAR>  
A;Cross-references: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB72987.1; PID:g696817  
A;Experimental source: serotype O2, strain NCTC 11168  
C;Genetics:  
A;Gene: trmD; Cj0713  
C;Superfamily: tRNA (guanine-N1) methyltransferase  
C;Keywords: methyltransferase; S-adenosylmethionine

Query Match 14.9%; Score 76; DB 2; Length 234;

Best Local Similarity 33.0%; Pred. NO. 1;

Matches 29; Conservative 10; Mismatches 39; Indels 10; Gaps 5;

QY 6 LPAVVLSTLVLSAQCATLGGPE--EESTIENYASRPBAPNTPLNIDKLSAFKADDF 63

Db 142 LPALVMCD-ALPARNVG-VLGNMESLEESGFENNLLLEAPAFSKPFIFEKKNKFFYPSEF 199

QY 64 LNW-HALFESIKR-----KLPLNWDAP 85

Db 200 LKGNHARIASLKTTLASCKTKFRPDLF 227

RESULT 2

S29242

sucrose synthase (EC 2.4.1.13) Ssl - barley

N;Alternate names: sucrose-UDP glucosyltransferase; UDPglucose-fructose glucosyltransfer

C;Species: Hordeum vulgare (barley)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 18-Jun-1999

C;Accession: S29242; S21494

R;de la Hoz, P.S.; Vicente-Carabajosa, J.; Mena, M.; Carbonero, P.

FEBS Lett. 310, 46-50, 1992

A;Title: Homologous sucrose synthase genes in barley (Hordeum vulgare) are located in ch

A;Reference number: S29242; MUID:92405741; PMID:1388123

A;Accession: S29242

A;Molecule type: mRNA

A;Residues: 1-807 <HOZ>

A;Cross-references: EMBL:X65871; NID:g19105; PIDN:CAA46701.1; PID:g19106

C;Genetics:

A;Map position: 7H

C/Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology  
C/Keywords: glycosyltransferase; hexosyltransferase  
F/276-749/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

Query Match 14.5%; Score 74; DB 2; Length 807;  
Best Local Similarity 27.7%; Pred. No. 7.4;  
Matches 26; Conservative 12; Mismatches 32; Indels 24; Gaps 3;

QY 30 ESTIENYASRP-----EAFNTPLNIDKLSAFKADFLNMH--ALFESIKRKLFP 79  
Db 116 KEQLVDEHASRKFLVLEDFEPFNASFPSPMSKSYGKVQFLNRHLSKLFQDKESLYPL 175

QY 80 LNM-----DAFPKLKGLRSATPDAQ 99  
Db 176 LNFPLKANYKGTMTILNDRIGSLRGLQSAARAE 209

#### RESULT 3

G97561

para-aminobenzoate synthase, component I VC1303 [imported] - Agrobacterium tumefaciens  
C/Species: Agrobacterium tumefaciens

C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002

C/Accession: G97561

R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Mollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001

A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A/Reference number: A97359; MUID:21608551; PMID:11743194

A/Accession: G97561

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-390 <KUR>

A/Cross-references: GB:AE007869; PIDN:AAK87448.1; PID:G15156766; GSPDB:GN00169

C/Genetics:

A/Gene: AGR\_C\_3082

A/Map position: circular chromosome

Query Match 14.3%; Score 73; DB 2; Length 390;  
Best Local Similarity 33.7%; Pred. No. 4.1;  
Matches 30; Conservative 11; Mismatches 34; Indels 14; Gaps 5;

QY 22 GATLGPPEESTIENYASRPEAFNTPLNIDKLSAFK-ADEFINMHA--LFE----- 71  
Db 20 GTVTAFTPEPEEII--VADEPEAFTALQRMETLRAGKYLAGYMSYEAGFLFEPKLAFA 77

QY 72 SIKRKLPLNMDAF--PKLKGLRSATPDA 98  
Db 78 AEPRNVPLNFGVFSGPQDEGRFARFPA 106

#### RESULT 4

G84888

probable transketolase precursor [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001

C/Accession: G84888

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Mofat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Talion, L.; eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: G84888

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-741 <STO>

A/Cross-references: GB:AE002093; NID:G2583125; PIDN:AAB82634.1; GSPDB:GN00139

C/Genetics:

A/Gene: At2g45290

A/Map position: 2

C/Superfamily: transketolase; thiamin pyrophosphate-binding domain homology

Query Match 14.2%; Score 72.5; DB 2; Length 741;

Best Local Similarity 25.7%; Pred. No. 9.8;  
Matches 27; Conservative 15; Mismatches 26; Indels 37; Gaps 5;

QY 18 HSAQATLGPPEESTIENYASRPEAFNTPLNIDKLS-----AFKADEFINMH 67  
Db 337 YSVHGAALGEKEVEATRNLTGMPEPEFHV-----EDVKSHWSRHTPEGAALAEAD-----WN 388

QY 68 ALFESIKRKLFP-----LNMDAFPKLKGLRSATPDA 98  
Db 389 AKFAAYEKYPBEAAELKSIISGELPVGE-----KALPTYTPDS 428

#### RESULT 5

T36090

probable integral membrane efflux protein - Streptomyces coelicolor  
C/Species: Streptomyces coelicolor

C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999

C/Accession: T36090

R/Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrall, B.G.; Rajandream, M.A submitted to the EMBL Data Library, April 1999

A/Reference number: Z21596

A/Accession: T36090

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-500 <SAU>

A/Cross-references: EMBL:AL049661; PIDN:CAB41206.1; GSPDB:GN00070; SCOEDB:SCE134.08

A/Experimental source: strain A3(2)

C/Genetics:

A/Gene: SCOEDB:SCE134.08

Query Match 13.7%; Score 70; DB 2; Length 500;  
Best Local Similarity 24.8%; Pred. No. 12;  
Matches 30; Conservative 16; Mismatches 45; Indels 30; Gaps 3;

QY 6 LPAVVLISLVLSAQATLGPPEESTIENYASRPEA-----FNTPLNIDKLS 56  
Db 257 LACMLMRSRELHAVERAPRGKGLREGRLRYVAGRPDLVPIVLVGFGTALNFPVHL 316

QY 57 AFKADEF--LNMHALF-----ESIKRKLPLNMDAFPKLKGLRSAT 95  
Db 317 AFADVDVFDAGAGAYSLFNTLVAGSLTGALLAARHEATRRRLPFLAALAFGLQAVAAVA 376

QY 96 P 96  
Db 377 P 377

#### RESULT 6

S55318

cytochrome P450 1A, hepatic - Stenotomus chrysops  
N/Contains: oxidoreductase (EC 1.-.-.-)

C/Species: Stenotomus chrysops

C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 28-Jul-2000

C/Accession: S55318

R/Morrisson, H.G.; Oleksak, M.F.; Cornell, N.W.; Sogin, M.L.; Stegeman, J.J. Biochem. J. 308, 97-104, 1995

A/Title: Identification of cytochrome P-450 1A (CYP1A) genes from two teleost fish, toa

A/Reference number: S55317; MUID:95275266; PMID:7755595

A/Accession: S55318

A/Molecule type: mRNA

A/Residues: 1-521 <MOR>

A/Cross-references: GB:U14162; NID:G968923; PIDN:AAA74969.1; PID:G968924

A/Note: 107-Glu was also found

C/Genetics:

A/Gene: CYP1A

C/Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C/Keywords: chromoprotein; electron transfer; heme; iron; liver; metalloprotein; monoox

F/319-485/Domain: cytochrome P450 homology <P45>

F/463/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 13.5%; Score 69; DB 2; Length 521;

Best Local Similarity 27.0%; Pred. No. 16;  
Matches 27; Conservative 17; Mismatches 32; Indels 24; Gaps 5;





Db 153 SOYPDLVRVGKDVANWDRTOGHDKMQLLQANPD 186

## RESULT 11

S51557

cytochrome P450, 3-methylcholanthrene-responsive - rainbow trout

C/Species: Oncorhynchus mykiss (rainbow trout)

C/Date: 01-Aug-1995 #sequence\_revision 10-Nov-1995 #text\_change 28-Jul-2000

C/Accession: S51557

R;Berndtson, A.K.; Chen, T.T.

Arch. Biochem. Biophys. 310, 187-195, 1994

A/Title: Two unique CYP1 genes are expressed in response to 3-methylcholanthrene treatment

A/Reference number: S51557; MUID:94213487; PMID:8161204

A/Accession: S51557

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-522 &lt;BER&gt;

A/Cross-references: EMBL:S69278; NID:g546373; PIDN:AAD14036.1; PID:g4261736

C/Genetics:

A/Introns: 280/3; 323/1; 353/1; 394/2; 423/2

C/Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C/Keywords: chromoprotein; heme; iron; metalloprotein

F;319-485/Domain: cytochrome P450 homology &lt;P45&gt;

F;463/Binding site: heme iron (Cys) (axial ligand) #status predicted

## Query Match

Best Local Similarity 13.3%; Score 68; DB 2; Length 522;

Matches 28; Conservative 15; Mismatches 33; Indels 24; Gaps 5;

Oy 1 MKIPVLPAVVLISLVLSA---QGATLGGPEESTIENTYASRPEAFNTPFLNIDKLSA 57

Db 81 IQIGMRPVVVLSGNETVRQALIKQG-----EDFAGRPDLYSFKFIN-DGKSLA 127

Oy 58 EKADEFLNWHALFESIKRKLPLNWDAPFKLKGLRSATPD 97

Db 128 FSTDKAGVWRA-----RRKLAMSALRSFATLEG--TTPE 159

## RESULT 12

B64234

hypothetical protein MG309 - Mycoplasma genitalium

C/Species: Mycoplasma genitalium

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 07-Dec-1999

C/Accession: B64234

R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;

M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.

, C.A.; Venter, J.C.

Science 270, 397-403, 1995

A/Title: The minimal gene complement of Mycoplasma genitalium.

A/Reference number: A64200; MUID:96026346; PMID:7569993

A/Accession: B64234

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-1225 &lt;TIGR&gt;

A/Cross-references: GB:U39712; GB:L43967; NID:g1046005; PID:g1046009; TIGR:MG309

A/Experimental source: strain G-37

C/Genetics:

A/Genetic code: SGC3

C/Superfamily: Mycoplasma hypothetical protein MG309

## Query Match

Best Local Similarity 13.3%; Score 68; DB 1; Length 1225;

Matches 25; Conservative 19; Mismatches 23; Indels 36; Gaps 6;

Oy 1 MKIPVLPA-----VVL-----SLVLHSAQATLGGPEESTI-ENYASRPEAF 44

Db 681 LKVSVIPSPQYSQIILVDTKLSSDPRTSLALNALNALVSSDELONTIRRDY----- 733

Oy 45 NTPFLNIDKLSAFKAD--FLNWHALFESIKRKLPLNWDAP 85

Db 734 ---FVNDQFKQALIDLKLTFTKWNNSLNNE-----NMNIF 765

## RESULT 13

A75097

hypothetical protein PAB1598 - Pyrococcus abyssi (strain Orsay)

C/Species: Pyrococcus abyssi

C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000

C/Accession: A75097

R;anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str

A/Reference number: A75001

A/Accession: A75097

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-459 &lt;KAW&gt;

A/Cross-references: GB:AF248286; GB:AL096836; NID:g5458366; PIDN:CAB50078.1; PID:g54585

A/Experimental source: strain Orsay

C/Genetics:

A/Gene: PAB1598

C/Superfamily: Methanobacterium thermoautotrophicum conserved hypothetical protein MTH1

## Query Match

Best Local Similarity 13.2%; Score 67.5; DB 2; Length 459;

Matches 20; Conservative 8; Mismatches 17; Indels 15; Gaps 3;

Oy 23 ATLG-----PEESTIENTYASR-PEAFNTPFLNIDKLSAFKADFLNWHALFESIKRK 76

Db 48 AEVGIYLLAESEITVEDEFSERLAEYFNDPFLKENPLR-----NWGAFFAYLAGK 98

## RESULT 14

AF0278

probable ribose-binding periplasmic protein (partial) YPO2285 [imported] - Yersinia pes

C/Species: Yersinia pestis

C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001

C/Accession: AF0278

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titchell, R.W.; Holden, M.T.G.; Prentice, M.B

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

H., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, J.

Nature 413, 523-527, 2001

A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A/Reference number: AB0001; MUID:21470413; PMID:11586360

A/Accession: AF0278

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-208 &lt;KUR&gt;

A/Cross-references: GB:AL590842; PIDN:CAC91090.1; PID:g15980281; GSPDB:GN00175

C/Genetics:

A/Gene: YPO2285.

## Query Match

Best Local Similarity 13.1%; Score 67; DB 2; Length 208;

Matches 23; Conservative 17; Mismatches 39; Indels 8; Gaps 3;

Oy 15 LVLHSAQATLGGPEESTIENTYASRPEAFNTPFLNIDKLSAFKADFLNWHALFESIK 74

Db 20 LVSNNAGGALGAIQWVKTGDSGKYVELVGAPSDN---NAATRANGYSSVLSOYPDLK 75

Oy 75 R-KLPFLNWD--AFPKLGLRSATPD 97

Db 76 RVGKEVANWMDRTQGYNKQSMQLQANPD 102

## RESULT 15

S23009

insulin-like growth factor-binding protein 1 precursor - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C/Accession: S23009

R;Sheyers, M.; Kettmann, R.; Maasart, S.; Renaville, R.; Burny, A.; Portetelle, D.

DNA Seq. 1, 407-408, 1991

A/Title: Cloning and characterization of a cDNA encoding the bovine insulin-like growth

A/Reference number: S23009; MUID:92119331; PMID:1722724

A/Accession: S23009

A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-263 <SNE>  
A;Cross-references: EMBL:X54979; NID:g435; PIDN:CAA38723.1; PID:g436  
A;Note: the authors translated the codon TGG for residue 30 as Cys  
C;Superfamily: insulin-like growth factor binding protein 1, thyroglobulin type I repeat  
F;180-255/Domain: thyroglobulin type I repeat homology <THY1>

Query Match 13.1%; Score 67; DB 1; Length 263;  
Best Local Similarity 29.6%; Pred. No. 11;  
Matches 24; Conservative 12; Mismatches 35; Indels 10; Gaps 4;

QY	14	LLVLSAQGATLGPEESTIENTYASRPEAFNTPLNIDKLSAFKADFL-NTHALFES	72
		:           :           :	
Db	96	LHALTRGQACMTSPCDEATDTKDTSPS-----NVSPESSEITQEQQLDNFHLMAES	148
QY	73	IKRKLPFLNWDAPFKLGKRS	93
		:           :	
Db	149	-SEDLPL-WNAISNYESLRA	167

Search completed: November 28, 2003, 07:57:40  
Job time : 31 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 07:33:16 ; Search time 17 Seconds

(without alignments)  
273.861 Million cell updates/sec

Title: US-10-059-395-142

Perfect score: 510  
Sequence: 1 MKIPVLPAAVLLSLVLSA.....LNMDAFPKLGLRSATPDAQ 99

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	14.9	234	1 TRMD_CAMJE	Q9PPJ4 campylobact
2	74	14.5	807	1 SUSI_HORVU	P31922 hordeum vul
3	71	13.9	521	1 CP11_PLAPE	Q9YH64 platichtys
4	69	13.5	521	1 CP11_PLEPL	Q92100 pleuronecte
5	69	13.5	521	1 CP11_SPAU	O42457 sparus aura
6	68.5	13.4	413	1 ACDS_PIG	P79273 sus scrofa
7	68	13.3	522	1 CP11_ONCMY	Q92110 oncorhynch
8	68	13.3	1225	1 Y309_MYCCE	P47551 mycoplasma
9	67	13.1	263	1 IBP1_BOVIN	P24591 bos taurus
10	67	13.1	521	1 CP11_LIMLI	O42430 limanda lim
11	67	13.1	521	1 CP11_STECH	Q92116 stenotomus
12	66.5	13.0	366	1 YHP7_YEAST	P38809 saccharomyc
13	66	12.9	1044	1 BUB1_SCHPO	O94751 schizosacch
14	65.5	12.8	506	1 YNM3_YEAST	P53867 saccharomyc
15	65.5	12.8	1053	1 TP2M_CABEL	P34534 caenorhabdi
16	65	12.7	353	1 YG98_HABIN	O05083 haemophilus
17	65	12.7	368	1 Y165_RICPR	Q9ZDZ8 rickettsia
18	64.5	12.6	519	1 TKTC_CRABL	Q42676 cratereostig
19	64.5	12.6	568	1 GAGJ_DROME	P21330 drosophila
20	64.5	12.6	1349	1 NOS_DROME	Q27571 drosophila
21	64	12.5	252	1 PMG2_MOUSE	O70250 mus musculu
22	64	12.5	252	1 PMG2_MOUSE	P16290 rattus norv
23	63	12.4	1709	1 CHD1_HUMAN	O14646 homo sapien
24	62.5	12.3	520	1 CP11_DICLA	P79716 dicentrarch
25	62	12.2	399	1 OYE1_YEAST	Q02899 saccharomyc
26	62	12.2	437	1 EF1G_HUMAN	P26641 homo sapien
27	62	12.2	437	1 EF1G_MOUSE	Q9D8N0 mus musculu
28	62	12.2	437	1 EF1G_MOUSE	P29694 oryctolagus
29	62	12.2	525	1 Y107_MERJA	Q57571 methanococc
30	62	12.2	1711	1 CHD1_MOUSE	P40201 mus musculu
31	61.5	12.1	339	1 IC11_TRIHA	P34055 trichoderma
32	61.5	12.1	433	1 UROK_MOUSE	P06869 mus musculu
33	61.5	12.1	872	1 IP3L_RAT	P42335 rattus norv

34	61.5	12.1	1233	1 HCVA_OCTDO	P12659 octopus dof
35	61.5	12.1	1247	1 NOS_ANOST	O61608 anopheles s
36	61.5	12.1	2896	1 HCYG_OCTDO	O61363 octopus dof
37	61	12.0	521	1 CP11_LIZAU	O42231 liza aurata
38	61	12.0	521	1 CP11_LIZSA	Q9W683 liza salien
39	61	12.0	669	1 CYK2_YEAST	Q05080 saccharomyc
40	61	12.0	3061	1 POLG_PVYHU	Q02963 p genome po
41	60.5	11.9	248	1 GPMA_METAC	Q8tn93 methanosarc
42	60.5	11.9	384	1 TMPB_TREPH	P29720 treponema p
43	60.5	11.9	563	1 YAS8_SCHPO	Q10144 schizosacch
44	60.5	11.9	1216	1 PIB1_BOVIN	P10894 bos taurus
45	60.5	11.9	1216	1 PIB1_HUMAN	Q9nq66 homo sapien

## ALIGNMENTS

RESULT 1	TRMD_CAMJE	STANDARD;	PRT;	234 AA.
ID	TRMD_CAMJE			
AC	Q9PPJ4;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31) (MIG-			
DE	methyltransferase) (tRNA [GM37] methyltransferase).			
GN	TRMD OR CJ0713.			
OS	Campylobacter jejuni.			
OC	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;			
OC	Campylobacteraceae; Campylobacter.			
OX	NCBI_TaxID=197;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RP	STRAIN=NCTC 11168;			
RX	MEDLINE=20150912; PubMed=10688204;			
RA	Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,			
RA	Basham D., Chillingworth T., Davies R.M., Feltham T., Holtroyd S.,			
RA	Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,			
RA	Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,			
RA	Whitehead S., Barrell B.G.;			
RT	"The genome sequence of the food-borne pathogen Campylobacter jejuni			
RT	reveals hypervariable sequences."			
RL	Nature 403:665-668(2000).			
CC	-1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs			
CC	(By similarity).			
CC	-1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-			
CC	homocysteine + tRNA containing N(1)-methylguanine.			
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).			
CC	-1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.			
CC	-----			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; AL139076; CAB72987.1; -			
DR	PIR; D81342; D81342.			
DR	HAMAP; MF_00605; -; 1.			
DR	InterPro; IPR002649; tRNA_m1G_MT.			
DR	Pfam; PF01746; tRNA_m1G_MT; 1.			
DR	ProDom; PD004978; tRNA_m1G_MT; 1.			
DR	TIGRFAMs; TIGR00088; tRMD; 1.			
KW	Transferase; Methyltransferase; tRNA processing; Complete proteome.			
SQ	SEQUENCE 234 AA; 27110 MW; 6A69B63BDEC8EFC CRC64;			

Query Match 14.9%; Score 76; DB 1; Length 234;

Best Local Similarity 33.0%; Pred. No. 0.51;

Matches 29; Conservative 10; Mismatches 39; Indels 10; Gaps 5;

OY 6 LPAVLLSLVLSAQAATLGGPE--ESTIENYASRPAFNTPLINDKLRSAFRADEF 63

Db 142 LPALVWCD-AILRVNG-VLGNMESLEESFENLLLEAPAFSKPFIPEKNNKFFTPSEF 199  
QY 64 LNW-HALFESIKR-----KLPFLNWDAP 85  
Db 200 LKGNHARIASLKTTLASCKTKFFRPDLF 227

## RESULT 2

SUS1\_HORVU STANDARD; PRT; 807 AA.  
ID\_ SUS1\_HORVU STANDARD; PRT; 807 AA.  
AC P31922;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Sucrose synthase 1 (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase 1).  
GN SS1.  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Hordeum.  
OC NCBI\_TaxID=4513;  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Abyssinian 2231; TISSUE=Endosperm;  
RX MEDLINE=92405741; PubMed=1388123;  
RA Sanchez de la Hoz P., Vicente-Carabajosa J., Mena M., Carbonero P.;  
RT "Homologous sucrose synthase genes in barley (Hordeum vulgare) are  
RT located in chromosomes 7H (syn. 1) and 2H. Evidence for a gene  
RT translocation?";  
RL FEBS Lett. 310:46-50(1992).  
RN [2]  
RP SEQUENCE OF 223-807 FROM N.A.  
RC STRAIN=cv. Pallas;  
RA Brandt J., Thordal-Christensen H., Collinge D.B.;  
RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: SUCROSE-CLEAVING ENZYME THAT PROVIDES UDP-GLUCOSE AND  
CC -1- FRUCTOSE FOR VARIOUS METABOLIC PATHWAYS.  
CC -1- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.  
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN DEVELOPING ENDOSPERM AND  
CC IN ROOTS AND, AT LOWER LEVELS, IN COLEOPTILES AND ALEURONE.  
CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1. PLANT  
CC SUCROSE SYNTHASE SUBFAMILY.

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CC -----

CC EMBL; X65871; CAA46701.1; -.  
DR EMBL; X66728; CAA47264.1; -.  
DR PIR; S29242; S29242.  
DR InterPro; IPR001296; Glyco\_trans\_1.  
DR InterPro; IPR000368; Sucrose\_synth.  
DR Pfam; PF00534; Glycos\_transf\_1; 1.  
DR Pfam; PF00862; Sucrose\_synth; 1.  
KW Transferase; Glycosyltransferase; Multigene family.  
FT CONFLICT 370 370 I -> IL (IN REF. 2).  
FT CONFLICT 374 374 I -> Y (IN REF. 2).  
FT CONFLICT 392 393 NE -> KO (IN REF. 2).  
SQ SEQUENCE 807 AA; 92211 MW; A863A8C876A060C8 CRC64;

Query Match 14.5%; Score 74; DB 1; Length 807;  
Best Local Similarity 27.7%; Pred. No. 3.2;  
Matches 26; Conservative 12; Mismatches 32; Indels 24; Gaps 3;

QY 30 EESTIENYASRP-----EAFNTPFLNIDKLSAFKADFLNWH---ALFESIKRKLFP 79  
Db 116 KEQGVDEHASRKFLVLELDFEPFNASFPSPMSKSYGKGVFLNRHLSSKLFQDKESLYPL 175

QY 80 LNW-----DAFPKLGLRSATPPAQ 99  
Db 176 LNFLKAHNYKGTMTILNDRIQSLRGLQSAIRKAE 209

## RESULT 3

CP11\_PLAFE STANDARD; PRT; 521 AA.  
ID CP11\_PLAFE STANDARD; PRT; 521 AA.  
AC Q9YH64;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1).  
GN CYP1A1 OR CYP1A.  
OS Platichthys flesus (European flounder).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
OC Pleuronectoidae; Pleuronectidae; Platichthys.  
OC NCBI\_TaxID=8260;  
OX NCBI\_TaxID=8260;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=North Sea population; TISSUE=Liver;  
RX MEDLINE=21353730; PubMed=11460673;  
RA Williams T.D., Lee J.S., Shearer D.L., Chipman J.K.;  
RT "The cytochrome P450 1A gene (CYP1A) from European flounder  
RT (Platichthys flesus), analysis of regulatory regions and development  
RT of a dual luciferase reporter gene system.";  
RL Mar. Environ. Res. 50:1-6(2000).  
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE  
CC MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED  
CC COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.  
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +  
CC oxidized flavoprotein + H(2)O.  
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.  
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.

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CC -----

CC EMBL; AJ132353; CAA10645.1; -.  
DR HSSP; P00179; 1DT6.  
DR InterPro; IPR001128; Cytochrome\_P450.  
DR Pfam; PF00067; P450; 1.  
DR PRINTS; PR00385; P450.  
DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;  
KW Microsome; Endoplasmic reticulum.  
FT METAL 463 463 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
SQ SEQUENCE 521 AA; 59009 MW; 58BA7DC3913C9091 CRC64;

Query Match 13.9%; Score 71; DB 1; Length 521;  
Best Local Similarity 27.0%; Pred. No. 4.3;  
Matches 27; Conservative 17; Mismatches 32; Indels 24; Gaps 5;

QY 1 MKIPVLPVVLISLVLSA---QGATLGPBEEESTIENYASRPFAFNTPFLNIDKLSA 57  
Db 81 IQIGMRPVVVLGSGSETVRQALIKQG-----DDFAGRPDLYSRPFINAGK-SLA 127

QY 58 FKADEFNLNHALFESIKRKLPLFNWDAPPKLGLRSATPD 97  
Db 128 FSTDQAGWRA-----RKLAYALSRSFNLG--TTPE 159

RESULT 4  
CP11\_PLEPL STANDARD; PRT; 521 AA.  
ID CP11\_PLEPL STANDARD; PRT; 521 AA.  
AC Q92100;

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DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1).
GN CYP1A1.
OS Pleuronectes platessa (Plaice).
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectidae; Pleuronectes.
OX NCBI_TaxID=8262;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94251288; PubMed=8193668;
RA Leaver M.J., Pirrit L., George S.G.;
RT "Cytochrome P450 1A1 cDNA from plaice (Pleuronectes platessa) and
RT induction of P450 1A1 mRNA in various tissues by 3-methylcholanthrene
RT and isosafrole.";
RL Mol. Mar. Biol. Biotechnol. 2:338-345(1993).
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
CC COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- INDUCTION: BY 3-METHYLCHOLANTHRENE (3MC) AND ISOSAFROLE (ISF).
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
CC -----
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CC -----
DR EMBL; X73631; CA52010.1; -.
DR PIR; S34184; S34184.
DR HSSP; P00179; 1DT6.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KM Microsome; Endoplasmic reticulum.
FT METAL. 463 463 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 521 AA; 59061 MW; AA7A97CB4578F9B6 CRC64;

Query Match 13.5%; Score 69; DB 1; Length 521;
Best Local Similarity 27.0%; Pred. No. 7;
Matches 27; Conservative 16; Mismatches 33; Indels 24; Gaps 5;

QY 1 MKIPVLPVAVLLSLVLSA---QGATLGGPEESTIENYASRPEAFNTPFLNIDKLSA 57
Db 81 IQIGMRPVVVLSTGTVRQALIKG-----DEFAGRDPDLYSFRFINAGK-SLA 127

QY 58 FKADFLNMWHLFESIKRKLPLNWDAPFKLGKLSATPD 97
Db 128 FSTDQAGWRA-----RRKLAYSALRSFSTLEG---TTPE 159

RESULT 5
CP11_SPAU STANDARD; PRT; 521 AA.
AC 042457; 042458;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1).
GN CYP1A1.
OS Sparus aurata (Gilthead sea bream).
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Sparus.
OX NCBI_TaxID=8175;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Cousinou M., Lopez-Barea J., Dorado G.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 175-521 FROM N.A.
RC TISSUE=Liver;
RA Tom M.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
CC COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
CC -----
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CC -----
DR EMBL; AF011223; AAB64297.1; -.
DR EMBL; AF005719; AAB62887.1; -.
DR HSSP; P00179; 1DT6.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KM Microsome; Endoplasmic reticulum.
FT METAL. 463 463 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT CONFLICT 175 177 LVK -> A (IN REF. 2).
FT CONFLICT 209 209 G -> A (IN REF. 2).
FT CONFLICT 212 212 Y -> S (IN REF. 2).
SQ SEQUENCE 521 AA; 59122 MW; 8FE00D86460B303B CRC64;

Query Match 13.5%; Score 69; DB 1; Length 521;
Best Local Similarity 27.0%; Pred. No. 7;
Matches 27; Conservative 17; Mismatches 32; Indels 24; Gaps 5;

QY 1 MKIPVLPVAVLLSLVLSA---QGATLGGPEESTIENYASRPEAFNTPFLNIDKLSA 57
Db 81 IQIGMRPVVVLSTGTVRQALIKG-----DDFAGRDPDLYSFRFIN-DGKSLA 127

QY 58 FKADFLNMWHLFESIKRKLPLNWDAPFKLGKLSATPD 97
Db 128 FSTDQAGWRA-----RRKLAYSALRSFSTLEG---TTPE 159

RESULT 6
ACDS_PIG STANDARD; PRT; 413 AA.
AC P79273;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acyl-CoA dehydrogenase, short-chain specific, mitochondrial precursor
DE (EC 1.3.99.2) (SCAD) (Butyryl-CoA dehydrogenase).
GN ACADS.
OS Sus scrofa (Pig).
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]

```



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RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Suzuki H., Itoh T., Kimura M., Murakami Y., Hamasima N., Yasue H.;
RT "Isolation of the pig short-chain acyl-CoA dehydrogenase gene and
RL assignment to chromosome 14q16.2-q23.2.";
CC Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Butanoyl-CoA + ETF = 2-butenoyl-CoA + reduced
CC ETF.
CC -1- COFACTOR: FAD.
CC -1- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
CC step.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- MISCELLANEOUS: A NUMBER OF STRAIGHT-CHAIN ACYL-COA DEHYDROGENASES
CC OF DIFFERENT SUBSTRATE SPECIFICITIES ARE PRESENT IN MAMMALIAN
CC TISSUES.
CC -1- SIMILARITY: BELONGS TO THE ACYL-COA DEHYDROGENASE FAMILY.
CC -----
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CC -----
DR EMBL; D89477; BAA13964.1; -.
DR HSSP; Q06319; 1BUC.
DR InterPro; IPR006089; Acyl-CoA dh.
DR InterPro; IPR006090; Acyl-CoA dh_C.
DR InterPro; IPR006091; Acyl-CoA dh_M.
DR InterPro; IPR006092; Acyl-CoA dh_N.
DR Pfam; PF00441; Acyl-CoA dh; 1.
DR Pfam; PF02770; Acyl-CoA dh_M; 1.
DR Pfam; PF02771; Acyl-CoA dh_N; 1.
DR PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR PROSITE; PS00073; ACYL_COA_DH_2; 1.
DR Oxidoreductase; Flavoprotein; FAD; Fatty acid metabolism;
KW Mitochondrion; Transit peptide.
FT TRANSIT 1 24 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 25 413 ACYL-COA DEHYDROGENASE, SHORT-CHAIN
FT SPECIFIC.
FT ACT_SITE 393 393 BASE (BY SIMILARITY).
SQ SEQUENCE 413 AA; 44850 MW; B8C480ADEDF7E98 CRC64;

Query Match 13.4%; Score 68.5; DB 1; Length 413;
Best Local Similarity 26.9%; Pred. No. 6.2;
Matches 18; Conservative 8; Mismatches 34; Indels 7; Gaps 1;

OY 36 NYASRPEAFNTPLNIDKLR-----SAFKADEFLNWHALFESIKRLPFLNWDAPPKL 88
DB 292 NYAENRRAFGVPLTKLQGIQFKLADMALLESARLLTWRAAMLKDNKNPFKEPAMAKL 351
OY 89 KGLRSAT 95
DB 352 AASEAAT 358

RESULT 7
CP11_ONCMY STANDARD; PRT; 522 AA.
AC 092110; 042195; P10609; P79830;
DT 01-JUL-1989 (Rel. 11, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1) (CYP1A2).
GN CYP1A1.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94213487; PubMed=8161204;
RA Berndtson A.K., Chen T.T.;
RT "Two unique CYP1 genes are expressed in response to 3-
RL methylcholanthrene treatment in rainbow trout.";
RL Arch. Biochem. Biophys. 310:187-195(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Bailey G., You L., Harttig U.;
RT "Cloning, sequencing and functional expression of two trout CYP1A
RT CDNAs in yeast.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Bailey G., You L., Harttig U.;
RT "Cloning, sequencing and aflatoxin B1 metabolism by multiple rainbow
RT trout CYP1A CDNAs expressed in yeast.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89078171; PubMed=3203599;
RA Heilmann L.J., Sheen Y.-Y., Bigelow S.W., Nebert D.W.;
RT "Trout P4501A1: cDNA and deduced protein sequence, expression in
RT liver, and evolutionary significance.";
RL DNA 7:379-387(1988).
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
CC COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- TISSUE SPECIFICITY: LIVER.
CC -1- INDUCTION: By 3-methylcholanthrene (3MC).
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
CC -1- CAUTION: THE SEQUENCE FROM REF.4 WAS A CHIMERA: ITS N-TERMINAL
CC PART HAS BEEN SHOWN TO BE DERIVED FROM WHAT IS NOW KNOWN AS THE
CC CYP1A3. CYP1A1 HAS ALSO BEEN CALLED CYP1A2.
CC -----
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CC -----
DR EMBL; S69278; AAD14036.1; -.
DR EMBL; U62797; AAB40627.1; -.
DR EMBL; AF015660; AAB69383.1; -.
DR EMBL; M21310; AAA49550.1; ALT_SEQ.
DR PIR; A28789; A28789.
DR PIR; S51557; S51557.
DR HSSP; P00179; 1DT6.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT METAL 463 463 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT CONFLICT 51 51 L -> P (IN REF. 3).
FT CONFLICT 97 97 V -> D (IN REF. 3).
FT CONFLICT 124 124 K -> N (IN REF. 3).
FT CONFLICT 306 306 Q -> H (IN REF. 3).
FT CONFLICT 390 390 T -> I (IN REF. 3).
FT CONFLICT 459 459 D -> G (IN REF. 2).
FT CONFLICT 470 470 Y -> H (IN REF. 3).
FT CONFLICT 474 474 Y -> F (IN REF. 1).
FT CONFLICT 483 483 R -> K (IN REF. 2).
SQ SEQUENCE 522 AA; 59344 MW; 9D063B5891102CE9 CRC64;

```

Query Match 13.3%; Score 68; DB 1; Length 522;  
 Best Local Similarity 28.0%; Pred. No. 9.1;  
 Matches 28; Conservative 15; Mismatches 33; Indels 24; Gaps 5;

QY 1 MKIPVLPVAVLLSLVLSA---QGATLGGPEESTIENYASRPEAFNTPFLNIDKLSA 57  
 Db 81 IQIGMRPVVLSGNETFVQALIKQG-----EDFAGRPLDYSFKFIN-DGKSLA 127

QY 58 FKADEFINWHALESIKRKLPLNWDAPFKLKGSRATPD 97  
 Db 128 FSTDKAGVWRA-----RRKLMSALRSFATLEG---TTPE 159

RESULT 8  
 Y309\_MYCGE STANDARD; PRT; 1225 AA.  
 AC P47551; Q49317;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical lipoprotein MG309 precursor.  
 GN MG309.  
 OS Mycoplasma genitalium.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 OX NCBI\_TaxID=2097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 33530 / G-37;  
 RX MEDLINE=96026346; PubMed=7569993;  
 RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,  
 RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,  
 RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,  
 RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,  
 RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,  
 RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;  
 RT "The minimal gene complement of Mycoplasma genitalium.";  
 RL Science 270:397-403 (1995).  
 RN [2]  
 RP SEQUENCE OF 1138-1224 FROM N.A.  
 RC STRAIN=ATCC 33530 / G-37;  
 RX MEDLINE=94075230; PubMed=8253680;  
 RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;  
 RT "A survey of the Mycoplasma genitalium genome by using random  
 sequencing.";  
 RL J. Bacteriol. 175:7918-7930 (1993).  
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  
 (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE MG307 / MG309 / MG338 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; U39711; AAC71531.1; -;  
 DR EMBL; U02200; AAD12488.1; -;  
 DR PIR; B64234; B64234.  
 DR TIGR; MG309; -;  
 DR PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.  
 DR KW Hypothetical protein; Lipoprotein; Membrane; Signal;  
 KM Complete proteome.  
 FT SIGNAL 1 27 POTENTIAL.  
 FT CHAIN 28 1225 HYPOTHETICAL LIPOPROTEIN MG309.  
 FT LIPID 28 28 N-ACYL DIGLYCERIDE (POTENTIAL).  
 FT CONFLICT 1185 1185 L -> V (IN REF. 2).  
 FT SEQUENCE 1225 AA; 138375 MW; C3E4BF5B4319B6E8 CRC64;

Query Match 13.3%; Score 68; DB 1; Length 1225;  
 Best Local Similarity 24.3%; Pred. No. 23;  
 Matches 25; Conservative 19; Mismatches 23; Indels 36; Gaps 6;

QY 1 MKIPVLPVAVLLSLVLSA---QGATLGGPEESTIENYASRPEAF 44  
 Db 681 LKSVIPSPQYSCQIILVDTKLSSDPRNTSLALNALNAVLSSDELQNTIRRDY----- 733

QY 45 NTPFLNIDKLSAFKAD-FLNWHALFESIKRKLPLNWDAP 85  
 Db 734 ---FVNDDQFKQAIIDLDKLTFTKNWNSLNNE-----NMNIF 765

RESULT 9  
 IBP1\_BOVIN STANDARD; PRT; 263 AA.  
 AC P24591;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Insulin-like growth factor binding protein 1 precursor (IGFBP-1)  
 DE (IBP-1) (IGF-binding protein 1).  
 GN IGFBP1.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Holstein-Friesian; TISSUE=Liver;  
 RX MEDLINE=92119331; PubMed=1722724;  
 RA Sneyers M., Kettmann R., Massart S., Renaville R., Burny A.,  
 RA Portetelle D.;  
 RT "Cloning and characterization of a cDNA encoding the bovine  
 RT insulin-like growth factor binding protein 1 (IGFBP-1).";  
 RL DNA Seq. 1:407-408 (1991).  
 CC -1- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs  
 CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH  
 CC PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE  
 CC INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- MISCELLANEOUS: BINDS EQUALLY WELL IGF-I AND IGF-II.  
 CC -1- SIMILARITY: Contains 1 IGFBP domain.  
 CC -1- SIMILARITY: Contains 1 thyroglobulin type-I domain.  
 CC -----  
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 CC -----  
 DR EMBL; X54979; CAA38723.1; -;  
 DR PIR; S23009; S23009.  
 DR HSSP; P24593; 1BOE.  
 DR InterPro; IPR000867; Insul\_gro\_fac\_pr.  
 DR InterPro; IPR000716; Thyroglobulin\_1.  
 DR Pfam; PF00219; IGFBP\_1.  
 DR Pfam; PF00086; thyroglobulin\_1; 1.  
 DR SMART; SM00121; IB; 1.  
 DR SMART; SM00211; TY; 1.  
 DR PROSITE; PS00222; IGF BINDING; 1.  
 DR PROSITE; PS00484; THYROGLOBULIN\_1; 1.  
 DR KW Growth factor binding; Signal.  
 FT SIGNAL 1 25  
 FT CHAIN 26 263 INSULIN-LIKE GROWTH FACTOR BINDING  
 FT DOMAIN 206 255 PROTEIN 1.  
 FT SITE 250 252 THYROGLOBULIN TYPE I.  
 FT DISULFID 73 86 CELL ATTACHMENT SITE.  
 FT DISULFID 80 106 BY SIMILARITY.  
 FT DISULFID 180 210 BY SIMILARITY.  
 FT SEQUENCE 263 AA; 28796 MW; 0403B642DDDC45B6 CRC64;

```
Query Match      13.1%; Score 67; DB 1; Length 263;  
Best Local Similarity 29.6%; Pred. No. 5.5;  
Matches 24; Conservative 12; Mismatches 35; Indels 10; Gaps 4
```

OY      14 LLVLHSAQATLGGPEEESTIENVASRPEAFNTPLINIDKLSAFAKADFL-NWHALFES 72  
         | ||| : |::| :||| :||| ::||| :||  
DB      96 LHALTRGQGACMTSPCDEATDTXDTTSPE-----NVSPESSEITQEQLLDNFHLMAES 148  
         | ||| : |::| :||| :||| ::||| :||  
  
OY      73 IKRKLPFLNMDAFPKLKGLRS 93  
         ||| |:| :||| :|||  
DB      149 -SEDLPIL-WNAISNYESIARA 167

```

RESULT 10
CP11_LIMLI
ID_CP11_LIMLI STANDARD; PRT; 521 AA.
AC 042430;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1).
GN CYP1A1.
OS Limanda limanda (Dab).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Pleuronectidae; Limanda.
OX NCBI_TaxID=27771;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21315588; PubMed=11423384;
RA Craft J.A., Robertson F.E., McPhail M.E., Brown E., Stagg R.M.;
RT "Measurement of cytochrome P4501A induction in dab (Limanda limanda)
RT and other teleosts with species-specific cDNA probes: isolation and
RT characterisation of dab cDNA and its use in expression studies with
RT beta-naphthoflavone-treated fish.";
RL Comp. Biochem. Physiol. 129C:115-127(2001).
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
CC COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
CC -----
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CC -----
DR EMBL; AJ001724; CAA04953.1; -.
DR HSSP; P00179; 1DT6.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT METAL 463 463 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 521 AA; 59063 MW; 11DE326C8A7FBDP9 CRC64;
Query Match 13.1%; Score 67; DB 1; Length 521;
Best Local Similarity 27.0%; Pred. No. 12;
Matches 27; Conservative 17; Mismatches 32; Indels 24; Gaps 5;

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QY      58 EKADEFINWHA LFESIKRKLPLFNWDAPKLGSRATPD   97
       | | : | | : | | : | | : | | : | | : | | :
Db     128 FSTDKAGIWRA-----RKLAYSALRSFATLEG--TTPE 159
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RESULT 11
CP11_STECH          STANDARD;      PRT;    521 AA.
ID_CP11_STECH
AC_Q92116;
DT_15-DEC-1998 (Rel. 37, Created)
DT_15-DEC-1998 (Rel. 37, Last sequence update)
DT_28-FEB-2003 (Rel. 41, Last annotation update)
DE_Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1).
DN_CYP1A1.
OS_Stenotomus chrysops (Scup).
OC_Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC_Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC_Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
OC_Sparidae; Stenotomus.
OX_NCBJ_TaxID=35579;
RN [1]
RP_SEQUENCE FROM N.A.
RC_TISSUE=Liver;
RX_MEDLINE=95275266; Pubmed=7755595;
RA_Morrisson H.G., Oleksiak M.F., Cornell N.W., Sogin M.L., Stegeman J.J.;
RT "Identification of cytochrome P-450 1A (CYP1A) genes from two teleost
RT fish, coadfish (Opsanus tau) and scup (Stenotomus chrysops), and
RT phylogenetic analysis of CYP1A genes.";
RL_Biochem. J. 308:97-104(1995).
CC -I- FUNCTION: CYTOCHROMES P450 ARE A GROUP OFHEME-THIOLATE
CC MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
CC COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
CC -I- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -I- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -I- SIMILARITY: Belongs to the cytochrome P450 family.
-----
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-----
DR_EMBL: U14162; AAA74969.1; -.
DR_HSSP: P00179; 1DT6.
DR_InterPro: IPR001128; Cytochrome_P450.
DR Pfam: PF00067; p450; 1.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
KW_Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT_METAL 463 463 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ_SEQUENCE 521 AA; 59019 MW; 8BDC4312074025D4 CRC64;
Query Match 13.1%; Score 67; DB 1; Length 521;
Best Local Similarity 27.0%; Pred. No. 12;
Matches 27; Conservative 16; Mismatches 33; Indels 24; Gaps 5;
QY Db QY 1 MKIPVLPAVLLSLVLHSA---QGATLGGBBESTITENYASRPEAFNTPLNDKLSA 57
::|:||||| : || | : | | | | | | |
Db 81 IQGMRPVVVLSGSFTRQALIKG-----DXFAGRPDLYSFRRIN-DGKSIA 127
| |:| : ||| : | | | | | | |
QY 58 FKADFELNWHALFSIRKKLPFLNMDAFPKLKGISATPD 97
| | : | | | | | | | | | | |
DB 128 ESTDAQGVWRA----RKLAYSALRSFATLEG--TTPE 159
| | : | | | | | | | | | | |
RESULTS 12
YHP7_YEAST STANDARD; PRT; 366 AA.
AC P38809;
```





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Db      | :|:|:|
        489 L-ENVKREQPF 498

RESULT 14
YMW3_YEAST
ID_YMW3_YEAST      STANDARD;      PRT;      506 AA.
AC      P53867;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      01-OCT-1996 (Rel. 34, Last annotation update)
DE      Hypothetical 56.6 kDa protein in URE2-SSU72 intergenic region.
GN      YNL223W OR N1274.
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OX      Saccharomycetales; Saccharomycetaceae; Saccharomyces.
RN      NCBI_TaxID=4932;
RP      SEQUENCE FROM N.A.
RX      MEDLINE=97051596; PubMed=8896273;
RA      Pandolfo D., de Antoni A., Lanfranchi G., Valle G.;
RT      "The DNA sequence of cosmid 14-5 from chromosome XIV reveals 21 open
RT      reading frames including a novel gene encoding a globin-like
RT      domain."
RL      Yeast 12:1071-1076 (1996).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Duesterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D., Hilbert H.,
RA      Moestl D.;
RL      Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE OF 13-506 FROM N.A.
RA      Sun Z., Hampsey M.;
RL      Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; Z69381; CAA93375.1; -
DR      EMBL; Z71499; CAA96126.1; -
DR      EMBL; U20390; AAA86498.1; -
DR      PIR; S63181; S63181.
DR      MEROPS; C54.001; -.
DR      SGD; S0005167; AUT2.
DR      GO; GO:0005875; C:microtubule associated complex; IPI.
DR      GO; GO:0008017; F:microtubule binding activity; IPI.
DR      GO; GO:0006914; P:autophagy; IMP.
DR      GO; GO:0006623; P:protein-vacuolar targeting; IMP.
DR      InterPro; IPR005078; Peptidase C54.
DR      Pfam; PF03416; Peptidase_C54; 2.
KW      Hypothetical protein.
SQ      SEQUENCE 506 AA; 56553 MW; 95EB599D6CDBB6F9 CRC64;

Query Match      12.8%; Score 65.5; DB 1; Length 506;
Best Local Similarity 25.8%; Pred. No. 16;
Matches 25; Conservative 13; Mismatches 26; Indels 33; Gaps 3;

QY      2 KIPVLPAVVLSTLVLSAGATLGPEESTIENYASRPEAFNTPF----- 48
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB      119 RAPDGPSPSLNLLV-----RTNPSTIEDYIANDCFNTDIGWCMIRTGSQL 168
QY      49 ---LNIIDKLSAFKADFLNWHALFESIKRKLPLNLW 82
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB      169 GNALQIHLGRDFRVNG-----NESLERSKFWNV 198

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ID      TP2M CAEEL      STANDARD;      PRT;      1053 AA.
AC      P34534;
DT      01-FEB-1994 (Rel. 28, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Putative DNA topoisomerase II, mitochondrial precursor (EC 5.99.1.3).
GN      R05D3.1.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OX      Rhabditidae; Peloderinae; Caenorhabditis.
RN      NCBI_TaxID=6239;
RP      SEQUENCE FROM N.A.
RX      STRAIN=Bristol N2;
RX      MEDLINE=94150718; PubMed=7906398;
RA      Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA      Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA      Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA      Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA      Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA      Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA      Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA      Sims M., Smaildon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA      Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA      Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA      Wohldman P.;
RT      "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT      elegans."
RL      Nature 368:32-38 (1994).
RN      [2]
RP      REVISIONS.
RA      Waterston R.;
RL      Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT
CC      BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II
CC      MAKES DOUBLE-STRAND BREAKS (BY SIMILARITY).
CC      -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC      of double-stranded DNA.
CC      -1- SUBUNIT: Homodimer (By similarity).
CC      -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
CC      -1- SIMILARITY: Belongs to the type II topoisomerase family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; L07144; AAM54162.1; -
DR      HSSP; P06786; 1BGW.
DR      WormPep; R05D3.1; CE31047.
DR      InterPro; IPR003594; ATPbind_ATPase.
DR      InterPro; IPR001241; DNA_topoisomI.
DR      InterPro; IPR002205; DNA_topoisomIV.
DR      Pfam; PF00204; DNA_gyraseB; 1.
DR      Pfam; PF00521; DNA_topoisomIV; 1.
DR      Pfam; PF02518; HATPase_C; 1.
DR      PRINTS; PR01158; TOPISMRASEII.
DR      PRINTS; PR00418; TP12FAMILY.
DR      ProDom; PD000742; DNA_topoisomIV; 1.
DR      SMART; SM00433; TOP2C; 1.
DR      SMART; SM00434; TOP4C; 1.
DR      PROSITE; PS00177; TOPOISOMERASE_II; 1.
KW      Hypothetical protein; Isomerase; Topoisomerase; DNA-binding;
KW      ATP-binding; Mitochondrion; Transit peptide.
FT      TRANSIT 1 ?
FT      CHAIN ? 1053 PUTATIVE DNA TOPOISOMERASE (POTENTIAL).
FT      NP_BIND 60 65 ATP (POTENTIAL).
FT      ACT_SITE 697 697 DNA_CLEAVAGE (BY SIMILARITY).
SQ      SEQUENCE 1053 AA; 120285 MW; BB167F2E01BFEA45 CRC64;

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RESULT 15  
TP2M CAEEL



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Query Match      12.8%; Score 65.5; DB 1; Length 1053;
Best Local Similarity 31.6%; Pred. No. 37;
Matches 18; Conservative 10; Mismatches 18; Indels 11; Gaps 2;

QY 42 EAFNTPFLNI--DKLSAFKADDFLNWHALFESIRKRLPLNWDAPKLGKRSAT 95
   ::|||::|||::|||::|||::|||::|||::|||::|||
Db 474 QSFRTPLLKAKKKDKYVSEFFSMNEYRKWADVEEGKWKIKY-----YKGLGTST 522

```

Search completed: November 28, 2003, 07:55:35  
Job time : 21 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 07:43:56 ; Search time 54 Seconds

(without alignments)  
473.096 Million cell updates/sec

Title: US-10-059-395-142

Perfect score: 510

Sequence: 1 MKIPVLPVAVLTLVLSLHSA.....LNWDAPPKLKGRLSATPDAQ 99

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77.5	15.2	1544	5 Q9VU57	Q9VU57 drosophila
2	75	14.7	254	5 Q95W96	Q95W96 heliocidari
3	74.5	14.6	407	11 Q8C4L6	Q8C4L6 mus musculu
4	73.5	14.4	1251	2 Q9ZBD1	Q9ZBD1 saccharopol
5	73	14.3	390	16 Q8UES9	Q8UES9 agrobacteri
6	72.5	14.2	634	10 Q22143	Q22143 arabidopsis
7	71.5	14.0	743	10 Q9FPB6	Q9FPB6 oryza sativ
8	71	13.9	439	13 Q98SG4	Q98SG4 scophthalmu
9	71	13.9	439	13 Q98SG7	Q98SG7 platichthys
10	70.5	13.8	251	16 Q935B8	Q935B8 salmonella
11	70	13.7	500	16 Q9X863	Q9X863 streptomyce
12	70	13.7	521	13 Q90WD4	Q90WD4 lithognathu
13	70	13.7	521	13 Q90XP1	Q90XP1 salmo salar
14	70	13.7	522	13 Q8QGFP	Q8QGFP salmo salar
15	70	13.7	522	13 Q9PRH3	Q9PRH3 oncorhynch
16	69	13.5	186	10 Q9SF44	Q9SF44 arabidopsis

17	69	13.5	674	16 Q8DSM6	Q8DSM6 vibrio vuln
18	68.5	13.4	203	4 Q9BSY6	Q9BSY6 homo sapien
19	68.5	13.4	439	13 Q9BSK5	Q9BSK5 ammodytes m
20	68.5	13.4	871	16 Q97K23	Q97K23 clostridium
21	68.5	13.4	899	5 Q9VIC5	Q9VIC5 drosophila
22	68.5	13.4	952	11 Q8CGB0	Q8CGB0 mus musculu
23	68	13.3	292	16 Q8YCU3	Q8YCU3 bruceella me
24	68	13.3	315	16 Q8FV13	Q8FV13 bruceella su
25	68	13.3	349	2 Q8VQL5	Q8VQL5 bruceella ab
26	68	13.3	727	5 Q8IS64	Q8IS64 locusta mig
27	67.5	13.2	173	16 Q8K6N5	Q8K6N5 streptococc
28	67.5	13.2	459	17 Q9UZH9	Q9UZH9 pyrococcus
29	67.5	13.2	519	13 Q9PTY6	Q9PTY6 anguilla ja
30	67.5	13.2	519	13 Q9PTY7	Q9PTY7 anguilla ja
31	67.5	13.2	519	13 Q8UW07	Q8UW07 brachydanio
32	67.5	13.2	519	13 Q8QGS5	Q8QGS5 brachydanio
33	67.5	13.2	521	13 Q8QG18	Q8QG18 anguilla an
34	67	13.1	208	16 Q8ZE97	Q8ZE97 yersinia pe
35	67	13.1	439	16 Q8XZR8	Q8XZR8 ralstonia s
36	67	13.1	912	5 Q8T034	Q8T034 drosophila
37	66.5	13.0	376	16 Q9KB87	Q9KB87 bacillus ha
38	66.5	13.0	531	5 Q9VHH1	Q9VHH1 drosophila
39	66.5	13.0	620	10 Q94IA8	Q94IA8 polygonum t
40	66.5	13.0	887	5 Q8T6I7	Q8T6I7 dictyosteli
41	66.5	13.0	1288	16 Q8EWX0	Q8EWX0 mycoplasma
42	66	12.9	346	8 Q8HJD9	Q8HJD9 acrocephalu
43	66	12.9	360	16 Q8YD10	Q8YD10 bruceella me
44	66	12.9	443	16 Q8YTT6	Q8YTT6 anabaena sp
45	66	12.9	519	13 Q9PT96	Q9PT96 dicentrarch

#### ALIGNMENTS

RESULT 1	Q9VU57	PRELIMINARY;	PRT;	1544 AA.
ID	Q9VU57	01-MAY-2000 (TREMREL. 13, Created)		
AC	Q9VU57	01-MAY-2000 (TREMREL. 13, last sequence update)		
DT	01-MAY-2000	(TREMREL. 13, last sequence update)		
DT	01-MAY-2000	(TREMREL. 13, last annotation update)		
DE	CG17687 protein.			
GN	CG17687.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BERKELEY;			
RX	MEDLINE=20196006; PubMed=10731132;			
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,			
RA	George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blazet R.G., Champe M., Pfeiffer B.D.,			
RA	Man K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,			
RA	Abri J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,			
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,			
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,			
RA	Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasner K.,			
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,			
RA	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Mlechina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhan G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195 (2000).  
DR EMBL; AE003538; AAF49833.1; -.  
DR FlyBase; FBgn0036348; CG17687.  
SQ SEQUENCE 1544 AA; 179386 MW; 98087CADFB9666E63 CRC64;

Query Match 15.2%; Score 77.5; DB 5; Length 1544;  
Best Local Similarity 32.6%; Pred. No. 13;  
Matches 30; Conservative 9; Mismatches 28; Indels 25; Gaps 4;

QY 2 KIPVPAVVLSTLVLSAQAATLGGPEESTIENTYASRPEAFNTPF-LNIDKLSAFKA 60  
Db 1168 KRPKLPGKVENSVLICMEASNKLSGKPE-----SHRTPEPLPDDVL----- 1207

QY 61 DEFLNWHALFESIKRKLPLF---NWDAPFKLK 89  
Db 1208 -EFLNYLAEFDQPKQCPNVDPRKSWDAFVKLR 1238

RESULT 2  
Q95W96 PRELIMINARY; PRT; 254 AA.  
ID Q95W96;  
AC Q95W96;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Primary mesenchyme-specific protein PM27.  
GN PM27.  
OS Helicoidaris erythrogramma (Sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;  
OC Helicoidaris.  
OX NCBI\_TaxID=7634;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Stander M.C., Raff R.A.;  
RT "Gene expression and skeleton formation in the sea urchin *Helicoidaris erythrogramma*.";  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF359343; AAL27536.1; -.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF00059; lectin\_c; 1.  
DR SMART; SM00034; CLECT; 1.  
DR PROSITE; PSS0041; C\_TYPE\_LLECTIN\_2; 1.  
SQ SEQUENCE 254 AA; 27430 MW; 48246B979666E554 CRC64;

Query Match 14.7%; Score 75; DB 5; Length 254;  
Best Local Similarity 24.4%; Pred. No. 2.8;  
Matches 21; Conservative 19; Mismatches 26; Indels 20; Gaps 3;

QY 4 PVLPAVLLSLVLHSAQAATLGGPEESTIENTY---ASRPEAFNTPF---LNIDKLS 56  
Db 96 PVLPGTW-----TADPQTSNAVINHLKSLSTPQALDIPFTGTLHNILTA 142

QY 57 AFKADEFNWHALFESIKRKLPLNW 82  
Db 143 LLERYEGWKWPSGWSSTTQALPFTNW 168

RESULT 3  
Q8C4L6 PRELIMINARY; PRT; 407 AA.  
ID Q8C4L6;  
AC Q8C4L6;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Inferred; RIKEN CDNA 1110014F24.  
OS *Mus musculus* (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Head;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
DR EMBL; AK081753; BAC38319.1; -.  
SQ SEQUENCE 407 AA; 42735 MW; 9D243DA7077983F6 CRC64;

Query Match 14.6%; Score 74.5; DB 11; Length 407;  
Best Local Similarity 25.9%; Pred. No. 5.6;  
Matches 22; Conservative 10; Mismatches 32; Indels 21; Gaps 3;

QY 18 HSAQAATLGGPEESTIENTYASRPEAFNTPF-LNIDKLSAFKA-DEFLNWH----- 68  
Db 241 YQGHGSGNGNIQKAEVNGLNTMSDASTLPF-NIDNFWENLKSXTRFINWDALNKGHAPS 299

QY 69 -----LFSIKRKLPLNW 82  
Db 300 PSTRALLYFRKLWENFKRSTPFFNW 324

RESULT 4  
Q9ZBD1 PRELIMINARY; PRT; 1251 AA.  
ID Q9ZBD1;  
AC Q9ZBD1;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Beta-galactosidase.  
OS *Saccharopolyspora rectivirgula*.  
OC Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;  
OC Pseudonocardiaceae; Pseudonocardiaceae; *Saccharopolyspora*.  
OX NCBI\_TaxID=28042;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98449763; PubMed=9774708;  
RA Inohara-Ochiai M., Nakayama T., Nakao M., Fujita T., Ueda T.,  
RA Ashikari T., Nishino T., Shibano Y.;  
RT "Unique primary structure of a thermostable multimeric beta-  
RT galactosidase from *Saccharopolyspora rectivirgula*.";  
RL Biochim. Biophys. Acta 1388:77-83 (1998).  
DR EMBL; D86429; BAA34817.1; -.  
DR HSSP; P00722; 1BGL.  
DR InterPro; IPR006101; Glyco\_hydro\_2.  
DR InterPro; IPR006102; Glyco\_hydro\_2ig.  
DR InterPro; IPR006104; Glyco\_hydro\_2SB.  
DR InterPro; IPR006103; Glyco\_hydro\_2TIM.  
DR InterPro; IPR004200; Glyco\_hydro\_42C.  
DR InterPro; IPR004199; Glyco\_hydro\_42N.  
DR InterPro; IPR006558; lamG\_like.  
DR Pfam; PF02930; Bgal\_small\_C; 1.  
DR Pfam; PF02929; Bgal\_small\_N; 1.  
DR Pfam; PF00703; Glyco\_hydro\_2; 1.  
DR Pfam; PF02836; Glyco\_hydro\_2\_C; 1.  
DR Pfam; PF02837; Glyco\_hydro\_2\_N; 1.  
DR PRINTS; PR00132; GLHYDLASE2.

DR SMART; SM00560; lamGL; 1.  
SQ SEQUENCE 1251 AA; 139978 MW; 825C3E825AF6D6AF CRC64;  
Query Match 14.4%; Score 73.5; DB 2; Length 1251;  
Best Local Similarity 29.2%; Pred. No. 28;  
Matches 33; Conservative 15; Mismatches 30; Indels 35; Gaps 7;  
QY 7 PAVVLSL-----LVHSAQATLGGPEESTIENYASRPE-----AFNTPFLNI 51  
Db 7 PAVLLATLAVTAGLLLPAAHAQPVDPSPDAIESYLEDPQRTGEGQPPHAFLRPYDA 66  
QY 52 DK-LRSAFK-----ADE-----FLN--WHALESIRKLP-----FLNWDA 84  
Db 67 EQALRSAREDLFAPADEPTPTWLSLNGRWQFOYADHYRDLPAWGQSGEWDA 119  
RESULT 5  
Q8UES9 PRELIMINARY; PRT; 390 AA.  
AC Q8UES9;  
DT 01-JUN-2002 (TReMBLrel. 21, Created)  
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE Para-aminobenzoate synthase component I.  
GN PAB OR ATU1676 OR AGR\_C3082.  
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Rhizobium.  
OX NCBI\_TaxID=176299;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21608550; PubMed=11743193;  
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,  
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,  
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,  
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,  
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,  
RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,  
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,  
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
RA Nester E.W.;  
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens  
C58.";  
RT Science 294:2317-2323 (2001).  
RL [2]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=21608551; PubMed=11743194;  
RX Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
RA Ouriollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,  
RA Houmlel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,  
RA Wollam C., Allinger M., Doughcy D., Scott C., Lappas C., Markelz B.,  
RA Planagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,  
RA Cielo C., Slater S.;  
RT "Genome sequence of the plant pathogen and biotechnology agent  
Agrobacterium tumefaciens C58.";  
RT Science 294:2323-2328 (2001).  
RL EMBL; AE009124; AAL42676.1; ALT\_INIT.  
DR EMBL; AE008089; AAK87448.1; -.  
DR InterPro; IPR005801; Anth\_synth\_chor.  
DR Pfam; PF00425; chorismate bind; 1.  
DR PRINTS; PR00095; ANTSNTHASEI.  
DR Prodom; PD000779; Anth\_synth\_chor; 1.  
KW Complete proteome.  
SQ SEQUENCE 390 AA; 43232 MW; 65EB9B0D09E7FF16 CRC64;  
Query Match 14.3%; Score 73; DB 16; Length 390;  
Best Local Similarity 33.7%; Pred. No. 7.8;  
Matches 30; Conservative 11; Mismatches 34; Indels 14; Gaps 5;  
QY 22 GATLGGPEESTIENYASRPEAFNTPFLNIDKLRSFAK-ADEFLNMHA--LFE----- 71  
Db 20 GTVTATFTPEBEII--VADEPEAFPTALQMBELRRAKGYLAGYMSYEAGFLPEPKLAPPA 77

QY 72 SIKRKLPLNMWDAF--PKLGLRSATPPDA 98  
Db 78 AEPRNVPLNFCVFSGFPQDEGRFARPD 106  
RESULT 6  
O22143 PRELIMINARY; PRT; 634 AA.  
AC O22143; Q93ZH6;  
DT 01-JAN-1998 (TReMBLrel. 05, Created)  
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE Putative transketolase (At2g45290/F4L23.20).  
GN AT2G45290.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,  
RA Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D., Somerville C.R.,  
RA Venter J.C.;  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RA Lin X.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RA Town C.D., Kaul S.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,  
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,  
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,  
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,  
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,  
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,  
RA Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,  
RA Ecker J.R.;  
RT "Arabidopsis cDNA clones.";  
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AC002387; AAB82634.2; -;  
DR EMBL; AY057528; AAL09768.1; -.  
DR HSSP; P23254; ITRK.  
DR InterPro; IPR005478; BactTransketolase.  
DR InterPro; IPR005476; Transketolase\_C.  
DR InterPro; IPR005475; Transketolase\_CR.  
DR InterPro; IPR005474; Transketolase\_N.  
DR Pfam; PF00456; transketolase\_1.  
DR Pfam; PF02780; transketolase\_C; 1.  
DR Pfam; PF02779; transket\_pyr; 1.  
DR TIGRFAMs; TIGR00232; tktlase\_bact; 1.  
DR PROSITE; PS00802; TRANSKETOLASE\_2; 1.  
SQ SEQUENCE 634 AA; 68851 MW; 42A8D1657C260113 CRC64;  
Query Match 14.2%; Score 72.5; DB 10; Length 634;  
Best Local Similarity 25.7%; Pred. No. 16;  
Matches 27; Conservative 15; Mismatches 26; Indels 37; Gaps 5;  
QY 18 HSAQATLGGPEESTIENYASRPEAFNTPFLNIDKLRS-----AFKADFLNMW 67  
Db 230 YSVHGAALGEKEVEATRNNTLGMPEFHPV-----EDVKSHWSRHTPEGAALBAD--WN 281  
QY 68 ALFESIKRKLPLF-----LNMWDAFPKLGLRSATPPDA 98

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Db      282 AKFAAYEKYPPEAAELKSIISGELPVGWE-----KALPTYTPDS 321

RESULT 7
Q9FPB6      PRELIMINARY;      PRT;      743 AA.
AC      Q9FPB6;
DT      01-MAR-2001 (TREMBLrel. 16, Created)
DT      01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT      01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE      Putative transketolase.
GN      P0679C08.28.
OS      Oryza sativa (Rice).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC      Ehrhartoideae; Oryzaceae; Oryza.
OX      NCBI_TaxID=4530;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=cv. Nipponbare;
RA      Sasaki T., Matsumoto T., Yamamoto K.;
RT      "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
RT      clone:P0679C08."
RL      Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AP002542; BAB19388.1; -.
DR      HSSP; P23254; 1TRK.
DR      Gramene; Q9FPB6; -.
DR      InterPro; IPR005478; BactTransketolase.
DR      InterPro; IPR005476; Transketolase_C.
DR      InterPro; IPR005475; Transketolase_CR.
DR      InterPro; IPR005474; Transketolase_N.
DR      Pfam; PF00456; transketolase; 1.
DR      Pfam; PF02780; transketolase_C; 1.
DR      Pfam; PF02779; transket_pyr; 1.
DR      TIGRFAMs; TIGR00232; tkltase_bact; 1.
DR      PROSITE; PS00801; TRANSKETOLASE_1; 1.
SQ      SEQUENCE 743 AA; 80028 MW; 8F6D6F68B8D3A26 CRC64;

Query Match      14.0%; Score 71.5; DB 10; Length 743;
Best Local Similarity 27.4%; Pred. No. 25;
Matches 29; Conservative 12; Mismatches 26; Indels 39; Gaps 6;

QY      18 HSAQATLGGPEESTIENYASRPEAFNTPFLNIDKLS-----AKFADEFLNWH 67
Db      340 XSVHGSALGTKEVEATRENIGWPEPFVP---EDVKSWSRHPQGAALFEAD---WN 391
QY      68 ALFESIKRKLPF-----LNM-DAPFKLGLRSATPDA 98
Db      392 AKFAAYEKYPEDAATLKSIIVSGELPAGWADALPKY-----TPES 431

RESULT 8
Q98SG4      PRELIMINARY;      PRT;      439 AA.
AC      Q98SG4;
DT      01-JUN-2001 (TREMBLrel. 17, Created)
DT      01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Cytochrome P4501A (Fragment).
GN      CYP1A.
OS      Scophthalmus maximus (turbot).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC      Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC      Pleuronectoidae; Scophthalmidae; Scophthalmus.
OX      NCBI_TaxID=52904;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Craft J.A., Robertson F.E., McPhail M.E., Brown E., Stagg R.M.;
RT      "Measurement of cytochrome P4501A induction in dab (Limanda limanda)
RT      and other teleosts with species-specific cDNA probes: isolation and
RT      characterization of dab cDNA and its use in expression studies with b-
RT      naphthoflavone-treated fish.";
```

```
RL      Comp. Biochem. Physiol. 129:115-127(2001).
CC      -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR      EMBL; AJ310694; CAC34401.1; -.
DR      HSSP; P00179; 1DT6.
DR      InterPro; IPR001128; Cytochrome_P450.
DR      Pfam; PF00067; P450; 1.
DR      PRINTS; PR00385; P450.
DR      PROSITE; PS00086; CYTOCHROME_P450; 1.
KW      Heme; Monooxygenase; Oxidoreductase.
FT      NON_TER 1
FT      NON_TER 439
SQ      SEQUENCE 439 AA; 49589 MW; 564ECC5864C696E5 CRC64;
```

```
Query Match      13.9%; Score 71; DB 13; Length 439;
Best Local Similarity 28.0%; Pred. No. 15;
Matches 28; Conservative 16; Mismatches 32; Indels 24; Gaps 5;
```

```
QY      1 MKIPVPAVVLISLVLSA---QGATLGGPEESTIENYASRPEAFNTPFLNIDKLSA 57
Db      52 IQIGMRPVVVLGSGDMVRQALIKG-----EEFAGRPDLYSFRFIN-DGKSLA 98
QY      58 FKADFLNWHALFESIKRKLPLNWDAPFKLGLRSATPD 97
Db      99 FSTDQAGVWRA-----RRKLAYSALRSFSTLEG--TTPE 130
```

## RESULT 9

```
Q98SG7      PRELIMINARY;      PRT;      439 AA.
AC      Q98SG7;
DT      01-JUN-2001 (TREMBLrel. 17, Created)
DT      01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Cytochrome P4501A (Fragment).
GN      CYP1A.
OS      Platicthys flesus (European flounder).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC      Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC      Pleuronectoidae; Platicthys.
OX      NCBI_TaxID=8260;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Craft J.A., Robertson F.E., McPhail M.E., Brown E., Stagg R.M.;
RT      "Measurement of cytochrome P4501A induction in dab (Limanda limanda)
RT      and other teleosts with species-specific cDNA probes: isolation and
RT      characterization of dab cDNA and its use in expression studies with b-
RT      naphthoflavone-treated fish."
RL      Comp. Biochem. Physiol. 129:115-127(2001).
CC      -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR      EMBL; AJ310693; CAC34310.1; -.
DR      HSSP; P00179; 1DT6.
DR      InterPro; IPR001128; Cytochrome_P450.
DR      Pfam; PF00067; P450; 1.
DR      PRINTS; PR00385; P450.
DR      PROSITE; PS00086; CYTOCHROME_P450; 1.
KW      Heme; Monooxygenase; Oxidoreductase.
FT      NON_TER 1
FT      NON_TER 439
SQ      SEQUENCE 439 AA; 49571 MW; A8CEB6449C8B12CA CRC64;
```

```
Query Match      13.9%; Score 71; DB 13; Length 439;
Best Local Similarity 27.0%; Pred. No. 15;
Matches 27; Conservative 17; Mismatches 32; Indels 24; Gaps 5;
```

```
QY      1 MKIPVPAVVLISLVLSA---QGATLGGPEESTIENYASRPEAFNTPFLNIDKLSA 57
Db      52 IQIGMRPVVVLGSGSETVRQALIKG-----DDFAGRPDLYSFRFINAGK-SLA 98
QY      58 FKADFLNWHALFESIKRKLPLNWDAPFKLGLRSATPD 97
Db      99 FSTDQAGVWRA-----RRKLAYSALRSFSTLEG--TTPE 130
```







GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 08:05:39 ; Search time 1715 Seconds

(without alignments)  
1402.999 Million cell updates/sec

Title: US-10-059-395-142  
Perfect score: 510  
Sequence: 1 MKIPYLPVLLSLVLHSA.....LNWDAFPKLGKRSATPDAG 99

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=x1h  
-Q=/cgn2\_1/USPTO\_spool/US10059395/runat\_25112003\_140713\_7115/app\_query.fasta\_1.263  
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bites -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10059395@CGN 1 1 2810 @runat\_25112003\_140713\_7115 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vr1:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	510	100.0	334 9	AA297512	AA297512 EST113061
2	510	100.0	432 13	BX112106	BX112106 BX112106
3	505	99.0	424 14	W69083	W69083 zd44b06.b1
4	484	94.9	394 14	W60320	W60320 zd29g01.b1
5	481	94.3	432 14	W69233	W69233 zd44c04.r1
6	477	93.5	431 14	W69227	W69227 zd44b06.r1
7	471.5	92.5	412 14	W60268	W60268 zd29g01.r1
8	458	89.8	373 9	AA722694	AA722694 zg82b06.s
9	456	89.4	381 14	W69108	W69108 zd44c04.b1
10	453.5	88.9	326 9	AA297513	AA297513 EST113062
11	450	88.2	348 9	AA238758	AA238758 xp03e08.x
12	440	86.3	377 9	AA582988	AA582988 nm72h02.s
13	413	81.0	339 9	AA778414	AA778414 zf39e05.s
14	381	74.7	345 9	AI217565	AI217565 qd43d02.x
15	380	74.5	359 10	BE466728	BE466728 hz24g06.x
16	380	74.5	362 9	AI140605	AI140605 qe05f03.x
17	379	74.3	376 14	W95920	W95920 ze08d01.r1
18	375	73.5	318 9	AA586846	AA586846 nm67e11.s
19	374	73.3	359 10	BG150312	BG150312 7j98g03.x
20	369	72.4	378 9	AI184682	AI184682 qd68b02.x
21	367	72.0	413 9	AA393296	AA393296 zt74f05.r
22	363	71.2	330 14	W95883	W95883 ze08d01.b1
23	357	70.0	358 9	AM003825	AM003825 wq83f12.x
24	353	69.2	436 9	AV597545	AV597545 AV597545
25	352	69.0	345 9	AA583942	AA583942 nm64f07.s
26	351.5	68.9	421 9	AV618771	AV618771 AV618771
27	351	68.8	334 9	AI217587	AI217587 qd43f04.x
28	322.5	63.2	461 12	BI285632	BI285632 UI-R-DDO-
29	317.5	62.3	454 12	BI282573	BI282573 UI-R-DDO-
30	313.5	61.5	448 12	BI282568	BI282568 UI-R-DDO-
31	308.5	60.5	452 12	BI277693	BI277693 UI-R-CZO-
32	306.5	60.1	444 12	BI286103	BI286103 UI-R-DDO-
33	306.5	60.1	446 12	BI283220	BI283220 UI-R-DDO-
34	305	59.8	368 9	AW260965	AW260965 EQUK0243
35	303.5	59.5	346 13	BY137356	BY137356 BY137356
36	303.5	59.5	409 9	AA572239	AA572239 v151g12.r
37	303.5	59.5	457 14	BY703646	BY703646 BY703646
38	303.5	59.5	467 9	AW105901	AW105901 um28f02.x
39	303.5	59.5	469 14	W30505	W30505 mc21f12.r1
40	303.5	59.5	470 9	AV007306	AV007306 AV007306
41	301	59.0	339 14	W52030	W52030 zd13b01.b1
42	300.5	58.9	938 14	CB192967	CB192967 AGENCOURT
43	300	58.8	241 9	AA595989	AA595989 nm64g08.s
44	298.5	58.5	327 13	BY140130	BY140130 BY140130
45	290.5	57.0	466 12	BI277761	BI277761 UI-R-CZO-

#### ALIGNMENTS

RESULT 1  
AA297512 334 bp mRNA linear EST 18-APR-1997  
LOCUS AA297512  
DEFINITION EST113061 Fetal skin Homo sapiens cDNA 5' end, mRNA sequence.  
ACCESSION AA297512  
VERSION AA297512.1 GI:1949866  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 334)  
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult

	TITLE	C.J., Lee,N.H., Kirkness,B.F., Weinstein,K.G., Gocayne,J.D., White ,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald ,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palancues,R.F., McDonald,L.A., Nguyen,D.T., Pelligriano,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meisner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon ,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
	JOURNAL MEDLINE PUBMED COMMENT	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995) 96026280 7566098 Other_ESTs: THCI51622 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index ( <a href="http://www.tigr.org/tdb/hgi/hgi.html">http://www.tigr.org/tdb/hgi/hgi.html</a> ) Seq primer: M13 Reverse.
FEATURES	source	Location/Qualifiers 1..334 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="ATCC (inhost):141532" /db_xref="taxon:9606" /tissue_type="epithelium" /cell_type="epithelial cell" /dev_stage="fetus" /clone_lib="Fetal skin" /note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI ; Site_2: XhoI"
BASE COUNT ORIGIN	77 a 100 c 78 g 78 t 1 others	
Alignment Scores:	Pred. No.: 1.6e-56 Length: 334	
Score:	510.00 Matches: 99	
Percent Similarity:	100.00% Conservative: 0	
Best Local Similarity:	100.00% Mismatches: 0	
Query Match:	100.00% Indels: 0	
DB:	Gaps: 0	
US-10-059-395-142 (1-99) x AA297512 (1-334)		
QY	1 MetlysiLeProValleuProAlaValleuLeuSerleuLeuValleuHisSerAla 20	
Db	14 ATGAAGATCCCGGTCTTCCCTGCGGTGGTGCTCCTCTCCCTCTGGTGCTCCACTGTGCC 73	
QY	21 GInGIyAIAthrleuglygylProgluGlugluSerThrilegluaAsnTyraLaSerArg 40	
Db	74 CAGGAGCCACCCCTGGGTGCTCTGAGGAAGAAGACCAATTGAGAATTATGCGTCACGA 133	
QY	41 ProgluAlapheaAsnthrProPheleuAsnilleAsplysleuArgSerAlaphelysAla 60	
Db	134 CCCGAGGCCTTTAACACCACCCGCTCTGAAACATCGACAATAATGCGATCTGCGTTAAGGCT 193	
QY	61 AspGluPheleuAsnTrpHisAlaleuPhegluSerIlleylsarglysleuProphelu 80	
Db	194 GATGAGTTCCTGAACCTGGCACGCCCTCTTTGAGTCTATCAAAAGAAAACCTTCCTTCCCTC 253	

DY  
Db

81 AsnTnpasPalaphProLysLeuLyegLYleuarGSerAlathrPrroAsPaalagln 99  
|||||  
||| |

RESULT 2  
BX112106

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BX112106           432 bp      mRNA     linear   EST 07-FEB-2003  
BX112106 Soares\_fetal\_heart\_NbhH19W Homo sapiens cDNA clone  
IMAGE9998D01781 ; IMAGE:342036, mRNA sequence.  
BX112106  
BX112106.1 GI:27878783  
EST.

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 432)  
Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,  
Radelof,U., Schneider,D. and Korn,B.  
Human Unigeneset - RZPD3  
Unpublished  
Contact: Ina Rolfs

254 AACTGGATGCCTTTCTTAAGCTGAAGA GAC TNA GCAGCGCA ACTCCTGTATGCC CAG 310

**FEATURES**  
 source  
 This clone is available royalty-free from RZPD;  
 contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 M13r, Primer sequence: TTTCCACACAGGAACAGCTATGAC.  
 Location/Qualifiers  
 1. .432

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE998D01781 ; IMAGE:342096"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_heart_NbHL19W"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5
TGTTACCAATCTGAAGTGGAGCGGCCGCATCTTTTCTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHL19W."

```

BASE COUNT	113 a	129 c	92 g	98 t
ORIGIN				
Alignment Scores:				
Pred. No.:	2,31e-56		length:	432
Score:	510.00		Matches:	99
Percent Similarity:	100.00%		Conservative:	0
Best Local Similarity:	100.00%		Mismatches:	0
Query Match:	100.00%		Indels:	0
DB:	13		Gaps:	0

US-10-059-395-142 (1-99) x BX112106 (1-432)

QY 1 MetLysIleProValIleuProAlaValIleuSerIleuLeuValIleuHisSerAla 20  
 DB 15 ATGAAGATCCCGGTCTCTCCGTGCTCTCTCCCTCTGCTGCTCCACTCTGCC 74  
 QY 21 GlnGlyAlaThrIleuGlyGlyProGluGluGluSerThrIleGluAsnTyraIaSerArg 40  
 DB 75 CAGGAGCCACCCCTGGGTGCTCTGAGGAAGAAGCACCATTGAGAAATTATGCTCACGA 134  
 QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
 DB 135 CCCGAGGCCCTTAACACCCCGTCTCTGAAACATCGACAATTGCGATCGCTTAAAGGCT 194  
 QY 61 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
 DB 195 GATGAGTTCCTGAAGTGGCAGCCCTCTTGAAGTCTATCAAAAGAACTCTCCCTC 254  
 QY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
 DB 255 AACTGGGATGCCCTTCTTAAGCTGAAGAGCTGAGAGCGCACTCTGATGCCAG 311

RESULT 3  
 LOCUS W69083 424 bp mRNA linear EST 16-OCT-1996  
 DEFINITION zd4b06.s1 Soares fetal\_heart\_NbHH19W Homo sapiens cDNA clone  
 IMAGE:343475 3', mRNA sequence.

ACCESSION W69083  
 VERSION W69083.1 GI:1378383  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 424)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman  
 ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,  
 Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston  
 ,R., Williamson,A., Wohlmann,P. and Wilson,R.  
 The WashU-Merck EST Project

TITLE Unpublished  
 JOURNAL  
 COMMENT

Contact: Wilson RK.  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Insert Length: 466 Std Error: 0.00  
 Seq primer: mob.REGA+ET

High quality sequence stop: 339.

# FEATURES

source  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:1268850"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:343475"  
 /sex="unknown"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares\_fetal\_heart\_NbHH19W"  
 /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a  
 modified polylinker; Site\_1: Site\_2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3']  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT7T3 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by  
 M.Fatima Bonaldo. This library was constructed from the  
 same fetus as the fetal lung library, Soares fetal lung  
 NbHL19W."

BASE COUNT 98 a 100 c 129 g 97 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.01e-55 Length: 424  
 Score: 505.00 Matches: 98  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.02% Indels: 0  
 DB: 14 Gaps: 0

US-10-059-395-142 (1-99) x W69083 (1-424)

QY 2 LysIleProValIleuProAlaValIleuSerIleuLeuValIleuHisSerAlaGln 21  
 DB 398 AAGATCCCGGTCTCTCCGTGCTCTCTCCCTCTGCTGCTCCACTCTGCCAG 339  
 QY 22 GlnAlaThrIleuGlyGlyProGluGluGluSerThrIleGluAsnTyraIaSerArgPro 41  
 DB 338 GGAGCCACCCCTGGGTGCTCTGAGGAAGAAGCACCATTGAGAAATTATGCTCACGACC 279  
 QY 42 GluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAlaAsp 61  
 DB 278 GAGGCTTAAACACCCCGTCTCTGAACATCGACAATTGCGATCTGCCCTTAAGCTGAT 219  
 QY 62 GluPheLeuAsnTrpHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeuAsn 81  
 DB 218 GAGTTCCTGAAGTGGCAGCCCTCTTGAAGTCTATCAAAAGAACTCTCTCTCAAC 159  
 QY 82 TrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
 DB 158 TGGGATGCCCTTCTTAAGCTGAAGAGCTGAGAGCGCACTCTGATGCCAG 105

RESULT 4  
 LOCUS W60320 394 bp mRNA linear EST 15-OCT-1996  
 DEFINITION zd29g01.s1 Soares fetal\_heart\_NbHH19W Homo sapiens cDNA clone  
 IMAGE:342096 3', mRNA sequence.

ACCESSION W60320  
 VERSION W60320.1 GI:1367079  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 394)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman  
 ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,  
 Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston  
 ,R., Williamson,A., Wohlmann,P. and Wilson,R.  
 The WashU-Merck EST Project

TITLE Unpublished  
 JOURNAL  
 COMMENT

Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Insert Length: 476 Std Error: 0.00  
 Seq primer: mob.REGA+ET

# FEATURES

source  
 1.394  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:1267471"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:342096"  
 /sex="unknown"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares\_fetal\_heart\_NbHH19W"



/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."

BASE COUNT 94 a 88 c 119 g 91 t 2 others  
ORIGIN

## Alignment Scores:

Pred. No.: 5.02e-53 Length: 394  
Score: 484.00 Matches: 94  
Percent Similarity: 98.95% Conservative: 0  
Best Local Similarity: 98.95% Mismatches: 1  
Query Match: 94.90% Indels: 0  
DB: 14 Gaps: 0

US-10-059-395-142 (1-99) x W60320 (1-394)

QY 5 ValLeuProAlaValLeuLeuSerLeuLeuValLeuHisSerAlaGlnGlyAlaThr 24  
Db 392 GTCCTTCCCTGCGGTGTCCTCTCCCTGTCGTCACCTGCCAGGAGCCACC 333  
QY 25 LeuGlyGlyProGluGluSerThrIleGluAsnTyraLaseArgProGluAlaPhe 44  
Db 332 CTGGGTGGTCTGAGGAGAAAGACCATTTGAGATTATGCGTCACGACCCGAGCCTTT 273  
QY 45 AsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeu 64  
Db 272 AACACCCCGTCTCTGACATCGACAAATTGCGATCTGCGTTTAAGGCTGATGATCTCTG 213  
QY 65 AsnTrpHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAla 84  
Db 212 AACTGGACGCGCTCTTGTAGTCTATCAAAAGAACTTCCTTCTCAACTGGGATGCC 153  
QY 85 PheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
Db 152 TTTCTTAAGCTGAAGAGACTGAGAGCGCAACTCTGATGCCAG 108

## RESULT 5

W69233 432 bp mRNA linear EST 16-OCT-1996  
LOCUS z44c04.r1 Soares fetal heart NbHL19W Homo sapiens cDNA clone  
DEFINITION IMAGE:343494 5', mRNA sequence.

W69233  
VERSION W69233.1 GI:1378493  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 432)  
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaaskis,B., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
Insert Length: 442 Std Error: 0.00

Seq primer: mob.REGA+ET  
High quality sequence stop: 341.  
Location/Qualifiers  
1..432

## FEATURES

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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:126869"  
/db\_xref="taxon:9606"  
/clone="IMAGE:343494"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal heart NbHL19W"  
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."

BASE COUNT 106 a 127 c 94 g 102 t 3 others  
ORIGIN

## Alignment Scores:

Pred. No.: 1.41e-52 Length: 432  
Score: 481.00 Matches: 98  
Percent Similarity: 98.99% Conservative: 0  
Best Local Similarity: 98.99% Mismatches: 1  
Query Match: 94.31% Indels: 1  
DB: 14 Gaps: 0

US-10-059-395-142 (1-99) x W69233 (1-432)

QY 1 MetLysIleProValLeuProAlaValLeuLeuSerLeuLeuValLeuHisSerAla 20  
Db 13 ATGAAGATCCCGGTCTTCTCTGCGGTGTCCTCTCCCTGTCGTCACCTGCC 72  
QY 21 GlnGlyAlaThrLeuGlyGlyProGluGluSerThrIleGluAsnTyraLaseArg 40  
Db 73 CAGGAGCACCCCTGGGTGT-CCTGAGGAGAAAGACCATTTGAGATTATGCGTCACGA 131  
QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
Db 132 CCCGAGCGCTTAAACCCCGTCTCTGACATCGACAAATTGCGATCTGCGTTTAAGGCT 191  
QY 61 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
Db 192 GATGAGTTCCTGAAGTGGACGCGCTCTTGTAGTCTATCAAAAGAACTTCCTTCTC 251  
QY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
Db 252 AACTGGGATGCTTCTTAAGCTGAAGAGACTGAGAGCGCAACTCTGATGCCAA 308

## RESULT 6

W69227 431 bp mRNA linear EST 16-OCT-1996  
LOCUS z44b06.r1 Soares fetal heart NbHL19W Homo sapiens cDNA clone  
DEFINITION IMAGE:343475 5', mRNA sequence.

W69227  
VERSION W69227.1 GI:1378487  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 431)  
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,

Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
The Washu-Merck EST Project  
Unpublished

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 466 Std Error: 0.00  
Seq primer: mob.REGA+ET  
High quality sequence stop: 410.  
Location/Qualifiers

# FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1268850"
/db_xref="taxon:9606"
/clone="IMAGE:343475"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_heart_NbHH19W"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCCGATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."
```

BASE COUNT 106 a 127 c 94 g 102 t 2 others  
ORIGIN

Alignment Scores:  
Pred. No.: 4.67e-52 Length: 431  
Score: 477.00 Matches: 98  
Percent Similarity: 97.03% Conservative: 0  
Best Local Similarity: 97.03% Mismatches: 1  
Query Match: 93.53% Indels: 2  
DB: 14 Gaps: 0

US-10-059-395-142 (1-99) x W69227 (1-431)

QY 1 MetLysIleProValLeuProAla-ValValLeuLeuSerLeuLeuValLeuHisSerAla 20  
DB 12 ATGAAGATCCCGGTCCTTCCTGCGCNGTGTGCTCTCTCCCTCGTGCTCCACTCTGC 71  
QY 20 aGInGlyAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAsnTyraLaseAr 40  
DB 72 CCAGGAGCCACCCCTGGTNGTCTCTGAGGAAGAAAGACACCATGAGATTATGCGTCACG 131  
QY 40 g-ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysA 60  
DB 132 ACCCGAGGCGCTTAACACCCGCTCTGACATCGACAAATTGCGATCTGCGTTAAGG 191  
QY 60 laAspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleLysArgLysLeuProPheL 80  
DB 192 CTGATGAGTTCCTGAACCTGACCGCCCTCTTGAAGTCTATCAAAAGAACTTCTTCC 251  
QY 80 euAsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
DB 252 TCAACTGGGATGCTTCTCTAAGCTGAAGAAAGAACTGAGAGCGCACTCTGATGCCAG 310

RESULT 7  
W60268

LOCUS W60268 412 bp mRNA linear EST 15-OCT-1996  
DEFINITION zd29g01.r1 Soares\_fetal\_heart\_NbHH19W Homo sapiens cDNA clone  
IMAGE:342096 5', mRNA sequence.  
ACCESSION W60268  
VERSION W60268.1 GI:1367169  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
The Washu-Merck EST Project  
Unpublished

# FEATURES

source

```
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 476 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 385.
Location/Qualifiers
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# FEATURES

source

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1.412
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/mol_type="mRNA"
/db_xref="GDB:1267471"
/db_xref="taxon:9606"
/clone="IMAGE:342096"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_heart_NbHH19W"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCCGATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."
```

BASE COUNT 96 a 127 c 88 g 98 t 3 others  
ORIGIN

Alignment Scores:  
Pred. No.: 2.29e-51 Length: 412  
Score: 471.50 Matches: 97  
Percent Similarity: 97.98% Conservative: 0  
Best Local Similarity: 97.98% Mismatches: 2  
Query Match: 92.45% Indels: 1  
DB: 14 Gaps: 0

US-10-059-395-142 (1-99) x W60268 (1-412)

QY 1 MetLysIleProValLeuProAlaValValLeuLeuSerLeuLeuValLeuHisSerAla 20  
DB 15 ATGAAGATCCCGGTCCTTCCTGCGGTGTGCTCTCTCCCTCGTGCTCCACTCTGCC 74  
QY 21 GInGlyAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAsnTyraLaseArg 40  
DB 75 CAGGAGCCACCCCTG--TGTCTGAGGAAGAAAGACCATGAGATTATGCGTCACGA 132

QY 41 ProgluAlaPheAsnThrProPheLeuAsnIleAspIlyLeuArgSerAlaPheIysAla 60  
 |||||  
 Db 133 CCCGAGCCTTTAACAACCCCGTCTGTAACATCGACAAATTGCGATCTGCGTTTAAGGCT 192

QY 61 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleIysArgIysLeuProPheLeu 80  
 |||||  
 Db 193 GATGAGTTCCTGAACCTGGACAGCCCTCTTGAAGTATCAAAAGAACTTCTTCTTC 252

QY 81 AsnTrpAspAlaPheProIlySleuIysGlyLeuArgSerAlaThrProAspAlaGln 99  
 |||||  
 Db 253 AACTGGATGCCCTTCTTAAGCTGAAGACTGAGAGCGCAGCACTCTGATGCCAG 309

RESULT 8  
 AA722694/c 373 bp mRNA linear EST 02-JAN-1998  
 LOCUS 2982b06.s1 Soares\_fetal\_heart\_NbH19W Homo sapiens cDNA clone  
 DEFINITION IMAGE:399827 3', mRNA sequence.  
 ACCESSION AA722694  
 VERSION AA722694.1 GI:2740401  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.  
 TITLE WashU-NCI human EST Project  
 JOURNAL Unpublished  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
 Seq primer: -40m13 fwd, 5T from Amer sham.

FEATURES  
 source  
 1..373  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:1307650"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:399827"  
 /sex="unknown"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lhb="Soares fetal heart NbH19W"  
 /note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dt) primer [5' TGTACCAATCTGAGTGGAGCGCGCGCATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Patima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbH19W."

BASE COUNT 89 a 81 c 113 g 90 t

ORIGIN

Alignment Scores:  
 Pred. No.: 1.15e-49 length: 373  
 Score: 458.00 Matches: 88  
 Percent Similarity: 98.88% Conservative: 0  
 Best Local Similarity: 98.88% Mismatches: 1  
 Query Match: 89.80% Indels: 0  
 DB: 9 Gaps: 0

US-10-059-395-142 (1-99) x AA722694 (1-373)

QY 11 LeuSerLeuLeuValIleuHisSerAlaGlnIlyAlaThrLeuGlyGlyProGluGlu 30  
 |||||  
 Db 373 CTCCTCTCCCTCTGTCCTCCACTCTGCCCCAGGAGTCAACCTGGTGTCTGAGGAA 314

QY 31 GluSerThrIleGluAsnTyrrAlaSerArgProGluAlaPheAsnThrProPheLeuAsn 50  
 |||||  
 Db 313 GAAAGCACCATTTGAAATTATGCGTCACGACCCGAGCCCTTTAACAACCCGTTCTGAAAC 254

QY 51 IleAspIlyLeuArgSerAlaPheIysAlaAspGluPheLeuAsnTrpHisAlaLeuPhe 70  
 |||||  
 Db 253 ATCGACAAATTGCGATCGCTTTAAGGCTGATGAGTTCCTGAACCTGGACAGCCCTCTTT 194

QY 71 GluSerIleIysArgIysLeuProPheLeuAsnTrpAspAlaPheProIlySleuIysGly 90  
 |||||  
 Db 193 GAGTCTATCAAAAGAACTTCTTCTCAACTGGGATGCCCTTCTTAAGCTGAAGAAAGA 134

QY 91 LeuArgSerAlaThrProAspAlaGln 99  
 |||||  
 Db 133 CTGAGGAGCGCAACTCTGATGCCAG 107

RESULT 9  
 W69108/c 381 bp mRNA linear EST 16-OCT-1996  
 LOCUS 2d44c04.s1 Soares fetal\_heart\_NbH19W Homo sapiens cDNA clone  
 DEFINITION IMAGE:343494 3', mRNA sequence.  
 ACCESSION W69108  
 VERSION W69108.1 GI:1378389  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
 TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
 Insert length: 442 Std Error: 0.00  
 Seq primer: mob.REGA+ET  
 High quality sequence stop: 347.

FEATURES  
 source  
 1..381  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:1268869"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:343494"  
 /sex="unknown"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lhb="Soares fetal\_heart\_NbH19W"  
 /note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dt) primer [5' TGTACCAATCTGAGTGGAGCGCGCGCATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by

M.Fatima Ronaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung MbHL19W."

BASE COUNT 91 a 86 c 114 g 89 t 1 others  
ORIGIN

## Alignment Scores:

Pred. No.: 2.16e-49 Length: 381  
Score: 456.00 Matches: 91  
Percent Similarity: 97.85% Conservative: 0  
Best Local Similarity: 97.85% Mismatches: 1  
Query Match: 89.41% Indels: 1  
DB: 14 Gaps: 0

US-10-059-395-142 (1-99) x W69108 (1-381)

QY 8 AlaValValLeuLeuSerLeuLeuValLeuHisSer-AlaGlnGlyAlaThrLeuGlyG1 27  
Db 381 GCCGTGTGNTCCCTCCCTCTGCTGCTCCACTCTTCCCGAGGAGCCACCCCTGGTGG 322

QY 27 YProGluGluGluSerThrIleGluAsnTyraIaSerArgProGluAlaPheAsnThrPr 47  
Db 321 TCCTGAGGAAGAAAGCACCATTGAGATTATGCGTCACGACCCGAGGCTTAAACACCC 262

QY 47 OPheLeuAsnIleAspIleuArgSerAlaPheIleuAlaAspGluPheLeuAsnThrPh 67  
Db 261 GTTCCTGAACATCGACAAATTCGATCTGCGTTAAGCTGATGATTCCTGAACGGCA 202

QY 67 sAlaLeuPheGluSerIleuArgIleuProPheLeuAsnTrpAspAlaPheProly 87  
Db 201 CGCCCTCTTGAAGTATCAAAAGAAACTCTTCCTCACTGGATGCCCTTCCTAA 142

QY 87 sLeuIysGlyLeuArgSerAlaThrProAspAlaGln 99  
Db 141 GCTGAAGAGACTGAGGAGCGCACTCTGATGCCAG 105

## RESULT 10

AA297513 326 bp mRNA linear EST 18-APR-1997

LOCUS AA297513 Fetal skin Homo sapiens cDNA 5' end, mRNA sequence.

DEFINITION AA297513

ACCESSION AA297513.1 GI:1949867

VERSION AA297513.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 326)

AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult

,C.J., Lee,N.H., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D., White

,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,

Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald

,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,

Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,

Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,

Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,

Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R.,

Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,

Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,

Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.,

Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,

Kunsch,C., Hungjun,J., Li,H., Weisner,P.S., Olsen,H., Raymond,L.,

Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon

,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and

Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns

JOURNAL based upon 83 million nucleotides of cDNA sequence

MEDLINE Nature 377 (6547 Suppl), 3-174 (1995)

PUBMED 96026280

COMMENT 7566098

Other\_ESTs: THCI51622

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423

Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
Seq primer: M13 Reverse.

## FEATURES

SOURCE

Location/Qualifiers  
1..326  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="ATCC (inhost):141549"  
/db\_xref="taxon:9606"  
/tissue\_type="epithelium"  
/cell\_type="epithelial cell"  
/dev\_stage="fetus"  
/clone\_lib="Fetal skin"  
/note="Organ: skin; Vector: pBluescript SK-; Site\_1: EcoRI  
; Site\_2: XhoI"

BASE COUNT 76 a 95 c 76 g 77 t 2 others  
ORIGIN

## Alignment Scores:

Pred. No.: 3.67e-49 Length: 326  
Score: 453.50 Matches: 91  
Percent Similarity: 92.86% Conservative: 0  
Best Local Similarity: 92.86% Mismatches: 6  
Query Match: 88.92% Indels: 1  
DB: 9 Gaps: 1

US-10-059-395-142 (1-99) x AA297513 (1-326)

QY 2 LysIleProValLeuProAlaValLeuLeuSerLeuValLeuHisSerAlaGln 21

Db 1 AAGATCCCGGTCTTCCCTGCGGTGCTCTCCCTCGTGTGCTCCACTGCCAG 60

QY 22 GlyAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAsnTyraIaSerArgPro 41

Db 61 GGAGCCACCCGTGGGTGCTCGAGGAGAAAGACCATGAGATTATGCGTCACGACC 120

QY 42 GluAlaPheAsnThrProPheLeuAsnIleAspIleuArgSerAlaPheIleuAlaAsp 61

Db 121 GAGGCTTTAACACCCCGTCTCGACATCGACAAATTGCGATCTCGTTAAGCTGAT 180

QY 62 GluPheLeuAsnTrpHisAlaLeuPheGluSerIleIleuArgIleuProPheLeuAsn 81

Db 181 GAGTTCCTGAAGTGGACGNCCTCTTGAAGTATCAAAAGAACTTCTTCCTCAAC 240

QY 82 TrpAspAlaPheProIleuIleuGlyLeuArgSerAla---ThrProAspAla 98

Db 241 TGGATGCCCTTCTTAAGCTGAAGAAAGACTTAAGAGCGCAATTCCTGATGCC 294

## RESULT 11

AW238758 348 bp mRNA linear EST 13-DEC-1999

LOCUS xp03e08.x1 NCI CGAP\_HN8 Homo sapiens cDNA clone IMAGE:2739302 3'

DEFINITION mRNA sequence.

ACCESSION AW238758

VERSION AW238758.1 GI:6571147

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 348)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL Tumor Gene Index

COMMENT Unpublished

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)



Tissue Procurement: Edward Shillitoe Ph.D., Silvio Gutkind Ph.D.,  
Chidchanok Leethanakul D.D.S., Michael Emmer-Buck M.D. Ph.D.  
CDNA Library Preparation: David B. Krizman, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: polyT not found  
Seq primer: -40UP from gibco  
High quality sequence stop: 331.

## FEATURES

source  
1. .348  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2739302"  
/tissue\_type="well-differentiated invasive carcinoma,  
floor of mouth"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP HN8"  
/note="Vector: PAMPI0; CDNA made by oligo-dT priming.  
Non-directionally cloned into the UDG sites of PAMPI0.  
Size-selected on agarose gel, average insert size 500 bp.  
Primary library; non-amplified. CDNA library  
Preparation: David B. Krizman, Ph.D (NCI). Reference:  
Krizman et al. (1996) Cancer Research 56:5380-5383."  
BASE COUNT 82 a 104 c 84 g 78 t  
ORIGIN

## Alignment Scores:

Pred. No.: 1.15e-48 Length: 348  
Score: 450.00 Matches: 86  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 88.24% Indels: 0  
DB: 9 Gaps: 0

US-10-059-395-142 (1-99) x AW238758 (1-348)

QY 14 LeuLeuValLeuHisSerAlaGlnGlyAlaThrLeuGlyGlyProGluGluSerThr 33  
Db 36 CTCCTGTGCTCCACTCTGCCAGGAGCCACTGGGTGCTCGAGAGAGAAAGCACC 95  
QY 34 ILeGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPheLeuAsnIleAspLys 53  
Db 96 ATTGAGATTATGATCAGCAGACCCGAGCCTTTAACACCCGTTCTCGAACATCGACAAA 155  
QY 54 LeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrPheAlaLeuPheGluSerIle 73  
Db 156 TTGGCATCTGCCGTTTAAAGCTGATGAGTTCTCTGAACCTGGCAGCCCTCTTGAGTCTATC 215  
QY 74 LysArgLysLeuProPheLeuAsnThrPaspAlaPheProLysLeuLysGlyLeuArgSer 93  
Db 216 AAAAGGAACCTTCCTTCTCAACTGGAGTGCCTTTCTTAAGCTGAAGGACTGAGGAGC 275  
QY 94 AlaThrProAspAlaGln 99  
Db 276 GCAACTCCTGATGCCAG 293

RESULT 12  
AA582988/c 377 bp mRNA linear EST 26-SEP-1997  
LOCUS nm72h02.s1 NCI\_CGAP\_lar1 Homo sapiens CDNA clone IMAGE:1089459 3',  
DEFINITION mRNA sequence.  
ACCESSION AA582988  
VERSION AA582988.1 GI:2360348  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 377)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.  
Emmer-Buck, M.D., Ph.D.  
CDNA Library Preparation: Stratagene, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert Length: 526 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham.

## FEATURES

source  
1. .377  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1089459"  
/tissue\_type="larynx"  
/lab\_host="SOLR (kanamycin resistant)"  
/clone\_lib="NCI CGAP lar1"  
/note="Organ: larynx; Vector: Bluescript SK-; Site 1:  
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:  
Oligo dT. larynx. 5' adaptor sequence: 5' GAATTCGACAGAG  
3' 3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'  
Average insert size: 0.9 kb."  
BASE COUNT 90 a 84 c 114 g 89 t  
ORIGIN

## Alignment Scores:

Pred. No.: 2.61e-47 Length: 377  
Score: 440.00 Matches: 91  
Percent Similarity: 98.91% Conservative: 0  
Best Local Similarity: 98.91% Mismatches: 1  
Query Match: 86.27% Indels: 1  
DB: 9 Gaps: 0

US-10-059-395-142 (1-99) x AA582988 (1-377)

QY 8 AlaValValLeuLeuSerLeuLeuValLeuHisSerAlaGlnGlyAlaThrLeuGlyGly 27  
Db 377 GCCGTGTGCTCTCTCCCTCTGCTCTCCACTGCTGCCAGGAGCCACCTGGTGGT 318  
QY 28 ProGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrPro 47  
Db 317 CCTGAGAGAGAAAGCACCATTGAGATTATGCGTCACGACCCGAGCCTTAACACCCCG 258  
QY 48 PheLeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrPhe 67  
Db 257 TTCCTGAACATCGACAATTGCCGATCTGCGTTAAGGCTGATGAGTTCTGAACG-CAC 199  
QY 68 AlaLeuPheGluSerIleLysArgLysLeuProPheLeuAsnThrPaspAlaPheProLys 87  
Db 198 GCCCTCTTGAGTCTATCAAAAAGAACTTCCTTCTCAACTGGAGTGCCTTCTTAAG 139  
QY 88 LeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
Db 138 CTGAAGGACTGAGGAGCGCAACTCTGATGCCAG 103

RESULT 13  
AA778414/c 339 bp mRNA linear EST 05-FEB-1998  
LOCUS zf39e05.s1 Soares fetal\_heart\_NbHH19w Homo sapiens CDNA clone  
DEFINITION IMAGE:379328 3', mRNA sequence.  
ACCESSION AA778414  
VERSION AA778414.1 GI:2837745  
KEYWORDS EST.  
SOURCE Homo sapiens (human)



ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 339)  
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.  
 TITLE WashU-NCI human EST Project  
 JOURNAL Unpublished  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: -40m13 fwd. ET from Amersham.  
 FEATURES  
 source  
 1. 339  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:1287584"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:379328"  
 /sex="unknown"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares\_fetal heart\_NbHL19W"  
 /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGGCATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."

BASE COUNT 79 a 77 c 96 g 87 t  
 ORIGIN

## Alignment Scores:

Pred. No.: 7 52e-44 Length: 339  
 Score: 413.00 Matches: 78  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 80.98% Indels: 0  
 DB: 9 Gaps: 0

US-10-059-395-142 (1-99) x AA778414 (1-339)

QY 22 G|Y|A|aThr|leu|G|y|G|y|Pro|G|u|G|u|Ser|Thr|I|le|G|u|Asn|Tyr|Ala|Ser|Arg|Pro 41  
 |||||  
 Db 337 GGAGCCACCCCTGGGTGCTCTGAGGAGAAAGCAACCATGAGATTATGCGTCACGACCC 278  
 QY 42 G|U|A|A|Phe|Asn|Thr|Pro|Phe|Leu|Asn|I|e|Asp|Lys|Leu|Arg|Ser|Ala|Phe|Lys|Ala|Asp 61  
 |||||  
 Db 277 GAGGCCTTAAACACCCCGTCTCTGACATCGACAATTTGCGATCTGCGTTTAAGGCTGAT 218  
 QY 62 G|U|Phe|Leu|Asn|T|P|H|I|S|A|L|e|u|Phe|G|u|Ser|I|e|Lys|A|R|g|Lys|Leu|P|ro|Phe|Leu|A|sn 81  
 |||||  
 Db 217 GAGTTCCTGAACCTGCGCCCTCTTGTAGCTATCAAAAGAACTTCTTCTTCTCAAC 158  
 QY 82 T|P|A|S|P|A|A|Phe|P|ro|Lys|Leu|Lys|G|Lys|Leu|Arg|Ser|Ala|Thr|Pro|Asp|Ala|Gln 99  
 |||||  
 Db 157 TGGGATGCCCTTCTTAAGCTGAAAGAGACTGAGAGCGCAACTCTGATGCCAG 104

RESULT 14  
 AI217565/c

LOCUS AI217565 345 bp mRNA linear EST 10-NOV-1998  
 DEFINITION qd43d02.x1 Soares\_fetal\_heart\_NbHL19W Homo sapiens cDNA clone  
 IMAGE:1732227 3', mRNA sequence.  
 ACCESSION AI217565  
 VERSION AI217565.1 GI:3797380  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 345)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaaps-r@mail.nih.gov  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert Length: 451 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 320.  
 FEATURES  
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 1. 345  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1732227"  
 /sex="unknown"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares\_fetal heart\_NbHL19W"  
 /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGGCATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."

BASE COUNT 79 a 77 c 99 g 89 t 1 others  
 ORIGIN

## Alignment Scores:

Pred. No.: 1.16e-39 Length: 345  
 Score: 381.00 Matches: 77  
 Percent Similarity: 96.25% Conservative: 0  
 Best Local Similarity: 96.25% Mismatches: 1  
 Query Match: 74.71% Indels: 2  
 DB: 9 Gaps: 0

US-10-059-395-142 (1-99) x AI217565 (1-345)

QY 22 G|Y|A|aThr|leu|G|y|G|y|Pro|G|u|G|u|Ser|Thr|I|le|G|u|Asn|Tyr|Ala|Ser|Arg|Pr 41  
 |||||  
 Db 342 GGAGCCACCCCTGGGTGCTCTGAGGAGAAAGCAACCATGAGATTATGCGTCACGACC 283  
 QY 41 O|G|U|A|A|Phe|Asn|Thr|Pro|Phe|Leu|Asn|I|e|Asp|Lys|Leu|Arg|Ser|Ala|Phe|Lys|Ala|A 61  
 |||||  
 Db 282 CGAGGCGCTTAAACACCCCGTCTCTGAAACATCGACAATTTGCGATCTGCGTTAAGGCTG 223  
 QY 61 S|P|G|U|Phe|Leu|Asn|T|P|H|I|S|A|L|e|u|Phe|G|u|Ser|I|e|Lys|A|R|g|Lys|Leu|P|ro|Phe|Leu|A 81  
 |||||  
 Db 222 ATGAGTTCCTGAACCTGCGCCCTCTTGTAGCTATCAAAAGAACTTCTTCTTCTCA 163  
 QY 81 S|N|T|P|A|S|P|A|A|Phe|P|ro|Lys|Leu|Lys|G|Lys|Leu|Arg|Ser|Ala|Thr|Pro|Asp|Ala|Gln 99  
 |||||  
 Db 162 ACTGGGATGCCCTTCTTAAGCTGAAAGAGACTGAGAGCGCAACTCTGATGCCAG 107

RESULT 15  
BE466728/c 359 bp mRNA linear EST 27-JUL-2000  
LOCUS hz24g06.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:3208954 3',  
DEFINITION mRNA sequence.  
ACCESSION BE466728  
VERSION BE466728.1 GI:9512503  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 359)  
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
info@image.llnl.gov  
Seq primer: -40UP from Gibco.  
Location/Qualifiers  
1. 359  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3208954"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_id="NCI\_CGAP\_GC6"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA  
from the normalized library NCI\_CGAP\_GC4 was prepared, and  
as circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (clonids  
1257096-1258631, 1469064-1470983, and 1475592-1476743).  
Subtraction by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 77 a 80 c 96 g 106 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 1.66e-39 Length: 359  
Score: 380.00 Matches: 73  
Percent Similarity: 96.05% Conservative: 0  
Best Local Similarity: 96.05% Mismatches: 3  
Query Match: 74.51% Indels: 0  
DB: 10 Gaps: 0  
US-10-059-395-142 (1-99) x BE466728 (1-359)  
QY 24 ThrLeuGlyGlyProGluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAla 43  
DB 347 ACCGGGGGAGACCGCGAGAGAAAGACCAATGAGAAATTATGCGTCACGACCGAGGCC 288  
QY 44 PheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPhe 63  
DB 287 TTTAACACCCCGTTCTGTAACATCGACAATATGCGTTAAAGGCTGATGAGTTC 228  
QY 64 LeuAsnTrpHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAsp 83  
DB 227 CTGAACCTGGACGCGCTCTTGAAGTCTATCAAAAGAACTTCCTTCTCACTGGGAT 168  
QY 84 AlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99

Db 167 GCCTTCTTAAGCTGAAAAGACTGAGAGCGCAACTCCTGATGCCAG 120

Search completed: November 28, 2003, 09:26:31  
Job time : 1723 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2003, 13:41:33 ; Search time 17 Seconds  
(without alignments)  
176.710 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Perfect score: 71

Sequence: 1 EESTIENYASRPEAFNTPE.....LNWDAFPKLGKRSATPDAQ 71

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

- Issued\_Patents\_AA:\*
- 1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*
  - 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*
  - 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*
  - 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*
  - 5: /cgn2\_6/ptodata/2/1aa/PTUS\_COMB.pep:\*
  - 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	100.0	99	4	US-09-996-243-201 Sequence 201, App
2	9	12.7	344	4	US-09-252-991A-22286 Sequence 22286, A
3	7	9.9	254	4	US-09-107-532A-4795 Sequence 4795, Ap
4	7	9.9	257	4	US-09-252-991A-26002 Sequence 26002, A
5	6	8.5	18	1	US-08-295-085-3 Sequence 3, Appli
6	6	8.5	18	1	US-08-295-085-4 Sequence 4, Appli
7	6	8.5	18	1	US-08-295-085-5 Sequence 5, Appli
8	6	8.5	18	5	PCT-US95-10741-3 Sequence 3, Appli
9	6	8.5	18	5	PCT-US95-10741-4 Sequence 4, Appli
10	6	8.5	18	5	PCT-US95-10741-5 Sequence 5, Appli
11	6	8.5	45	4	US-08-469-260A-483 Sequence 483, App
12	6	8.5	45	4	US-08-488-446-483 Sequence 483, App
13	6	8.5	45	4	US-08-467-344A-483 Sequence 483, App
14	6	8.5	105	4	US-09-252-991A-26885 Sequence 26885, A
15	6	8.5	117	4	US-09-252-991A-19208 Sequence 19208, A
16	6	8.5	122	2	US-09-109-266-8 Sequence 8, Appli
17	6	8.5	136	4	US-09-690-454-131 Sequence 131, App
18	6	8.5	177	4	US-09-252-991A-28186 Sequence 28186, A
19	6	8.5	178	4	US-09-328-352-5593 Sequence 5593, Ap
20	6	8.5	213	4	US-09-134-001C-3969 Sequence 3969, Ap
21	6	8.5	218	1	US-08-470-837-26 Sequence 26, Appli
22	6	8.5	218	4	US-08-868-452-26 Sequence 26, Appli
23	6	8.5	220	4	US-09-480-675A-4 Sequence 4, Appli
24	6	8.5	229	4	US-09-327-984A-8 Sequence 8, Appli
25	6	8.5	231	4	US-08-129-722A-2 Sequence 2, Appli
26	6	8.5	232	4	US-08-327-874A-6 Sequence 6, Appli
27	6	8.5	232	5	PCT-US94-09700-6 Sequence 6, Appli

28	6	8.5	233	4	US-09-107-532A-4966 Sequence 4966, Ap
29	6	8.5	245	4	US-09-613-303-23 Sequence 23, Appli
30	6	8.5	272	3	US-08-910-820-4 Sequence 4, Appli
31	6	8.5	272	3	US-08-910-820-6 Sequence 6, Appli
32	6	8.5	272	4	US-09-844-908-4 Sequence 4, Appli
33	6	8.5	272	4	US-09-844-908-6 Sequence 6, Appli
34	6	8.5	282	3	US-08-910-820-3 Sequence 3, Appli
35	6	8.5	282	3	US-08-910-820-5 Sequence 5, Appli
36	6	8.5	282	4	US-09-844-908-3 Sequence 3, Appli
37	6	8.5	282	4	US-09-844-908-5 Sequence 5, Appli
38	6	8.5	291	1	US-08-102-757-9 Sequence 9, Appli
39	6	8.5	291	1	US-08-102-757-11 Sequence 11, Appli
40	6	8.5	307	2	US-08-216-894-6 Sequence 6, Appli
41	6	8.5	307	3	US-09-115-746-6 Sequence 6, Appli
42	6	8.5	310	4	US-09-646-075-1 Sequence 1, Appli
43	6	8.5	324	4	US-09-613-303-25 Sequence 25, Appli
44	6	8.5	331	4	US-09-217-228-6 Sequence 6, Appli
45	6	8.5	346	2	US-08-476-254-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-996-243-201  
Sequence 201, Application US/09996243

Patent No. 6478825

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Baton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730P1C13

CURRENT APPLICATION NUMBER: US/09/996,243

PRIOR FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

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3	PRIOR APPLICATION NUMBER: 60/087106
4	PRIOR FILING DATE: 1998-05-28
5	PRIOR APPLICATION NUMBER: 60/087607
6	PRIOR FILING DATE: 1998-06-02
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9	PRIOR APPLICATION NUMBER: 60/087759
10	PRIOR FILING DATE: 1998-06-02
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12	PRIOR FILING DATE: 1998-06-03
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14	PRIOR FILING DATE: 1998-06-04
15	PRIOR APPLICATION NUMBER: 60/088025
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25	PRIOR APPLICATION NUMBER: 60/088033
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27	PRIOR APPLICATION NUMBER: 60/088326
28	PRIOR FILING DATE: 1998-06-04
29	PRIOR APPLICATION NUMBER: 60/088167
30	PRIOR FILING DATE: 1998-06-05
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42	PRIOR FILING DATE: 1998-06-10
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71	PRIOR APPLICATION NUMBER: 60/089599
72	PRIOR FILING DATE: 1998-06-17
73	PRIOR APPLICATION NUMBER: 60/089600

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2	PRIOR APPLICATION NUMBER: 60/089653
3	PRIOR FILING DATE: 1998-06-17
4	PRIOR APPLICATION NUMBER: 60/089801
5	PRIOR FILING DATE: 1998-06-18
6	PRIOR APPLICATION NUMBER: 60/089907
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17	PRIOR FILING DATE: 1998-06-22
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32	PRIOR APPLICATION NUMBER: 60/090444
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36	PRIOR APPLICATION NUMBER: 60/090472
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54	PRIOR APPLICATION NUMBER: 60/090695
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59	PRIOR FILING DATE: 1998-06-26
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61	PRIOR FILING DATE: 1998-06-26
62	PRIOR APPLICATION NUMBER: 60/091360
63	PRIOR FILING DATE: 1998-06-26
64	PRIOR APPLICATION NUMBER: 60/091478
65	PRIOR FILING DATE: 1998-07-01
66	PRIOR APPLICATION NUMBER: 60/091544
67	PRIOR FILING DATE: 1998-07-01
68	PRIOR APPLICATION NUMBER: 60/091519
69	PRIOR FILING DATE: 1998-07-02
70	PRIOR APPLICATION NUMBER: 60/091626
71	PRIOR FILING DATE: 1998-07-02
72	PRIOR APPLICATION NUMBER: 60/091633
73	PRIOR FILING DATE: 1998-07-02

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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
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Best Local Similarity 100.0%; Pred. No. 9.1e-68;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 KGLRSATPDAQ 71
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Db 89 KGLRSATPDAQ 99
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## RESULT 2

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US-09-252-991A-22286
; Sequence 22286, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22286
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22286
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Query Match      12.7%; Score 9; DB 4; Length 344;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 62 GLRSATPDA 70
    |||||
Db 210 GLRSATPDA 218
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## RESULT 3

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US-09-107-532A-4795
; Sequence 4795, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 893-5007
; TELEFAX: (781) 893-8277
; INFORMATION FOR SEQ ID NO: 4795:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...254
; SEQUENCE DESCRIPTION: SEQ ID NO: 4795:
US-09-107-532A-4795
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Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 46 KRKL PFL 52
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Db 33 KRKL PFL 39
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## RESULT 4

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US-09-252-991A-26002
; Sequence 26002, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26002
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26002
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Query Match      9.9%; Score 7; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 60 LKGLRSA 66
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Db 247 LKGLRSA 253
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## RESULT 5

```
US-08-295-085-3
; Sequence 3, Application US/08295085
; Patent No. 5582997
```



GENERAL INFORMATION:  
APPLICANT: Blondelle, Sylvie E.  
APPLICANT: Perez-Paya, Enrique  
APPLICANT: Houghten, Richard A.  
TITLE OF INVENTION: Lysine/Leucine Polypeptides, Mixture  
TITLE OF INVENTION: Sets and Libraries Thereof  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Edward P. Gamson  
STREET: 135 South LaSalle Street, Suite 1625  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/295,085  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Gamson, Edward P.  
REGISTRATION NUMBER: 29,381  
REFERENCE/DOCKET NUMBER: IMS017.0B 3418/61275  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 781-9470  
TELEFAX: (312) 781-9548  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-295-085-3

Query Match 8.5%; Score 6; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.5;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 PKLGL 63  
Db 9 PKLGL 14

RESULT 6  
US-08-295-085-4  
Sequence 4, Application US/08295085  
Patent No. 5582997  
GENERAL INFORMATION:  
APPLICANT: Blondelle, Sylvie E.  
APPLICANT: Perez-Paya, Enrique  
APPLICANT: Houghten, Richard A.  
TITLE OF INVENTION: Lysine/Leucine Polypeptides, Mixture  
TITLE OF INVENTION: Sets and Libraries Thereof  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Edward P. Gamson  
STREET: 135 South LaSalle Street, Suite 1625  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/295,085  
FILING DATE:

CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Gamson, Edward P.  
REGISTRATION NUMBER: 29,381  
REFERENCE/DOCKET NUMBER: IMS017.0B 3418/61275  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 781-9470  
TELEFAX: (312) 781-9548  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-295-085-4

Query Match 8.5%; Score 6; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.5;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 PKLGL 63  
Db 9 PKLGL 14

RESULT 7  
US-08-295-085-5  
Sequence 5, Application US/08295085  
Patent No. 5582997  
GENERAL INFORMATION:  
APPLICANT: Blondelle, Sylvie E.  
APPLICANT: Perez-Paya, Enrique  
APPLICANT: Houghten, Richard A.  
TITLE OF INVENTION: Lysine/Leucine Polypeptides, Mixture  
TITLE OF INVENTION: Sets and Libraries Thereof  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Edward P. Gamson  
STREET: 135 South LaSalle Street, Suite 1625  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/295,085  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Gamson, Edward P.  
REGISTRATION NUMBER: 29,381  
REFERENCE/DOCKET NUMBER: IMS017.0B 3418/61275  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 781-9470  
TELEFAX: (312) 781-9548  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-295-085-5

Query Match 8.5%; Score 6; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.5;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 PKLGL 63  
Db 9 PKLGL 14

Db 9 PKLKG 14

## RESULT 8

PCT-US95-10741-3

Sequence 3, Application PC/TUS9510741

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Lysine/Leucine Polypeptides, Mixture

TITLE OF INVENTION: Sets and Libraries Thereof

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Edward P. Gamson

STREET: 135 South LaSalle Street, Suite 1625

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/10741

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Gamson, Edward P.

REGISTRATION NUMBER: 29,381

REFERENCE/DOCKET NUMBER: IMS017.0B 3418/61275

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 781-9470

TELEFAX: (312) 781-9548

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US95-10741-3

Query Match 8.5%; Score 6; DB 5; Length 18;

Best Local Similarity 100.0%; Pred. No. 8.5;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 PKLKG 63

Db 9 PKLKG 14

## RESULT 9

PCT-US95-10741-4

Sequence 4, Application PC/TUS9510741

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Lysine/Leucine Polypeptides, Mixture

TITLE OF INVENTION: Sets and Libraries Thereof

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Edward P. Gamson

STREET: 135 South LaSalle Street, Suite 1625

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/10741

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Gamson, Edward P.

REGISTRATION NUMBER: 29,381

REFERENCE/DOCKET NUMBER: IMS017.0B 3418/61275

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 781-9470

TELEFAX: (312) 781-9548

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US95-10741-4

Query Match 8.5%; Score 6; DB 5; Length 18;

Best Local Similarity 100.0%; Pred. No. 8.5;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 PKLKG 63

Db 9 PKLKG 14

## RESULT 10

PCT-US95-10741-5

Sequence 5, Application PC/TUS9510741

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Lysine/Leucine Polypeptides, Mixture

TITLE OF INVENTION: Sets and Libraries Thereof

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Edward P. Gamson

STREET: 135 South LaSalle Street, Suite 1625

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/10741

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Gamson, Edward P.

REGISTRATION NUMBER: 29,381

REFERENCE/DOCKET NUMBER: IMS017.0B 3418/61275

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 781-9470

TELEFAX: (312) 781-9548

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US95-10741-5

Query Match 8.5%; Score 6; DB 5; Length 18;

Best Local Similarity 100.0%; Pred. No. 8.5;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 PKLKG 63

Db 9 PKLKG 14

RESULT 11  
US-08-469-260A-483  
; Sequence 483, Application US/08469260A  
; Patent No. 6451578  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUEHRHOF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIJK  
; APPLICANT: ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/469,260A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/424,550  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: POREMSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 483:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 45 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-469-260A-483

Query Match 8.5%; Score 6; DB 4; Length 45;  
Best local similarity 100.0%; Pred. No. 20;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 60 LKGLRS 65  
Db 37 LKGLRS 42

RESULT 12  
US-08-488-446-483  
; Sequence 483, Application US/08488446  
; Patent No. 6558898  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY

APPLICANT: ANTHONY SCOTT MUEHRHOF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIJK  
; APPLICANT: ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,446  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/424,550  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: POREMSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 483:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 45 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-488-446-483

Query Match 8.5%; Score 6; DB 4; Length 45;  
Best local similarity 100.0%; Pred. No. 20;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 60 LKGLRS 65  
Db 37 LKGLRS 42

RESULT 13  
US-08-467-344A-483  
; Sequence 483, Application US/08467344A  
; Patent No. 6586568  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUEHRHOF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIJK  
; APPLICANT: ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL

```
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,344A
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,550
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 483:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 483:
US-08-467-344A-483
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Query Match      8.5%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      60 LKGLRS 65
        |||||
Db      37 LKGLRS 42
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RESULT 14
US-09-252-991A-26885
; Sequence 26885, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26885
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26885
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Query Match      8.5%; Score 6; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      63 LRSATP 68
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Db      2 LRSATP 7
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RESULT 15
US-09-252-991A-19208
; Sequence 19208, Application US/09252991A
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; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19208
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19208
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Query Match      8.5%; Score 6; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      10 ASRPEA 15
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Db      7 ASRPEA 12
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Search completed: November 28, 2003, 13:44:08
Job time : 19 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 12:12:50 ; Search time 53 Seconds

(without alignments)  
591.287 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

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Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 1135135

Minimum DB seq length: 0

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-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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6: /cgn2\_6/ptodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	100.0	415	4	US-09-996-243-200 Sequence 200, App
2	9	12.7	666	4	US-09-252-991A-5754 Sequence 5754, Ap
3	9	12.7	837	4	US-09-252-991A-5702 Sequence 5702, Ap
4	9	12.7	1035	4	US-09-252-991A-5715 Sequence 5715, Ap
5	9	12.7	1245	4	US-09-252-991A-5725 Sequence 5725, Ap
6	7	9.9	765	4	US-09-107-532A-1141 Sequence 1141, Ap
7	7	9.9	774	4	US-09-252-991A-9431 Sequence 9431, Ap
8	7	9.9	2397	4	US-09-221-017B-272 Sequence 272, App
9	7	9.9	3964	4	US-09-620-312D-128 Sequence 128, App
10	7	9.9	5804	4	US-09-369-364A-12 Sequence 12, Appl
11	7	9.9	31208	4	US-09-852-067-3 Sequence 3, Appl1
12	7	9.9	34446	4	US-09-103-330-35 Sequence 35, Appl1

C 13	7	9.9	1230025	4	US-09-198-452A-1	Sequence 1, Appli
C 14	7	9.9	1664976	4	US-08-916-421B-1	Sequence 1, Appli
15	6	8.5	20	1	US-08-335-583C-20	Sequence 20, Appl
16	6	8.5	20	4	US-09-668-313A-170	Sequence 170, App
17	6	8.5	31	1	US-08-383-743A-9	Sequence 9, Appli
18	6	8.5	31	3	US-08-808-881-9	Sequence 9, Appli
19	6	8.5	31	3	US-09-017-631-9	Sequence 9, Appli
20	6	8.5	31	4	US-09-520-118-9	Sequence 9, Appli
21	6	8.5	31	5	PCT-US93-07116-9	Sequence 9, Appli
C 22	6	8.5	38	6	5185431-28	Patent No. 5185431
C 23	6	8.5	46	3	US-09-252-292-22	Sequence 22, Appl
24	6	8.5	62	3	US-08-483-511-13	Sequence 13, Appl
25	6	8.5	62	5	PCT-US93-01009-13	Sequence 13, Appl
26	6	8.5	74	3	US-08-258-287B-11	Sequence 11, Appl
27	6	8.5	74	3	US-08-368-704C-11	Sequence 11, Appl
28	6	8.5	75	3	US-09-060-756-146	Sequence 146, App
29	6	8.5	75	4	US-09-670-314-146	Sequence 146, App
C 30	6	8.5	164	1	US-08-480-552-1	Sequence 1, Appli
C 31	6	8.5	164	1	US-08-039-385-1	Sequence 1, Appli
C 32	6	8.5	164	3	US-08-929-208-1	Sequence 1, Appli
C 33	6	8.5	164	3	US-09-158-469-1	Sequence 1, Appli
C 34	6	8.5	164	3	US-09-561-844-1	Sequence 1, Appli
C 35	6	8.5	164	4	US-09-568-315-1	Sequence 1, Appli
C 36	6	8.5	164	4	US-09-562-226-1	Sequence 1, Appli
C 37	6	8.5	164	5	PCT-US91-07492-1	Sequence 1, Appli
38	6	8.5	165	3	US-08-836-261A-95	Sequence 95, Appl
39	6	8.5	240	6	5177308-2	Patent No. 5177308
C 40	6	8.5	255	4	US-09-134-001C-82	Sequence 82, Appl
41	6	8.5	277	1	US-08-391-339-12	Sequence 12, Appl
42	6	8.5	277	1	US-08-484-274A-12	Sequence 12, Appl
43	6	8.5	277	3	US-08-746-111-54	Sequence 54, Appl
C 44	6	8.5	305	4	US-09-313-294A-7107	Sequence 7107, Ap
45	6	8.5	318	4	US-09-252-991A-10314	Sequence 10314, A

#### ALIGNMENTS

RESULT 1  
US-09-996-243-200  
; Sequence 200, Application US/09996243  
; Patent No. 6478825  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C13  
; CURRENT APPLICATION NUMBER: US/09/996,243  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16





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; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-996-243-200 (1-415)

```
QY 1 GluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20
   |||||
Db 97 GAGGAAGAAGCACCATGAGATTATGCGTCACGACCGAGCGCTTTAAACACCCGCTTC 156
   |||||

QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40
   |||||
Db 157 CTGAACATCGACAATTGCGATCTGCCGTTTAAAGGCTGATGAGTCTTGAAGTGGCAGGCC 216
   |||||

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60
   |||||
Db 217 CTCTTGAGTCTATCAAAAGAACTCTTCTCTCAACTGGGATGCTTCTTAAGCTG 276
   |||||

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71
   |||||
Db 277 AAAGACTGAGGAGCGCAACTCCTGATGCCAG 309
   |||||
```

## RESULT 2

```
US-09-252-991A-5754/c
; Sequence 5754, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5754
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5754
```

Alignment Scores:  
Pred. No.: 0.508 Length: 666  
Score: 9.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	12.68%	Indels:	0
DB:	4	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-252-991A-5754 (1-666)

```
QY 62 GlyLeuArgSerAlaThrProAspAla 70
   |||||
Db 62 GGGCTGCGGAGCGCCACGCGCGAGCGCT 36
   |||||
```

## RESULT 3

```
US-09-252-991A-5702
; Sequence 5702, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5702
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5702
```

## Alignment Scores:

Pred. No.:	0.635	Length:	837
Score:	9.00	Matches:	9
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	12.68%	Indels:	0
DB:	4	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-252-991A-5702 (1-837)

```
QY 62 GlyLeuArgSerAlaThrProAspAla 70
   |||||
Db 218 GGGCTGCGGAGCGCCACGCGCGAGCGCT 244
   |||||
```

## RESULT 4

```
US-09-252-991A-5715
; Sequence 5715, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5715
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5715
```

Alignment Scores:  
Pred. No.: 0.781 Length: 1035  
Score: 9.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 12.68% Indels: 0  
DB: 4 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-252-991A-5715 (1-1035)

QY 62 GlyLeuArgSerAlaThrProAspAla 70  
|||||  
DB 628 GGGCTGGAGCGCGCACGCCGCGACGCT 654

RESULT 5  
US-09-252-991A-5725/c  
; Sequence 5725, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 5725  
; LENGTH: 1245  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5725

Alignment Scores:  
Pred. No.: 0.935 Length: 1245  
Score: 9.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 12.68% Indels: 0  
DB: 4 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-252-991A-5725 (1-1245)

QY 62 GlyLeuArgSerAlaThrProAspAla 70  
|||||  
DB 631 GGGCTGGAGCGCGCACGCCGCGACGCT 605

RESULT 6  
US-09-107-532A-1141  
; Sequence 1141, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571

; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arinello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781) 893-5007  
; TELEFAX: (781) 893-8277  
; INFORMATION FOR SEQ ID NO: 1141:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 765 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEITICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...765  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1141:  
US-09-107-532A-1141

Alignment Scores:  
Pred. No.: 80.3 Length: 765  
Score: 7.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 9.86% Indels: 0  
DB: 4 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-107-532A-1141 (1-765)

QY 46 LysArgLysLeuProPheLeu 52  
|||||  
DB 97 AAAAGAAATTACTTCTTG 117

RESULT 7  
US-09-252-991A-9431  
; Sequence 9431, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 9431  
; LENGTH: 774  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9431

Alignment Scores:  
Pred. No.: 81.2 Length: 774  
Score: 7.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 9.86% Indels: 0  
DB: 4 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-252-991A-9431 (1-774)

QY 60 LeuLysGlyLeuArgSerAla 66  
|||||

Db 739 CTCAGGCTGCGTAGCGCT 759

## RESULT 8

US-09-221-017B-272/c  
; Sequence 272, Application US/09221017B  
; Patent No. 6444799  
; GENERAL INFORMATION:  
; APPLICANT: ROSS, Bruce C.  
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
; NUMBER OF SEQUENCES: 1120  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/221,017B  
; FILING DATE: 23-DEC-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PP1182  
; FILING DATE: 31-DEC-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PP1546  
; FILING DATE: 30-JAN-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PP2911  
; FILING DATE: 09-APR-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/AU98/01023  
; FILING DATE: 10-DEC-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monroy, Gladys H  
; REGISTRATION NUMBER: 32,430  
; REFERENCE/DOCKET NUMBER: 27340-20021.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 272:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2397 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: UNKNOWN  
; ORIGINAL SOURCE:  
; ORGANISM: PORYPHYROMONAS GINGIVALIS  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1...2397  
US-09-221-017B-272

## Alignment Scores:

Pred. No.:	244	Length:	2397
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	9.86%	Indels:	0
DB:	4	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-221-017B-272 (1-2397)

QY 20 PheleuAsnIleApIysIeu 26

Db 647 TTCCTAATATAGATAATTA 627

## RESULT 9

US-09-620-312D-128  
; Sequence 128, Application US/09620312D  
; Patent No. 6569662  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yungqing  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: John Tillinghast  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and  
; FILE REFERENCE: 784CIP2B  
; CURRENT APPLICATION NUMBER: US/09/620,312D  
; CURRENT FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1105  
; SOFTWARE: pt\_FL\_genes Version 1.0  
; SEQ ID NO 128  
; LENGTH: 3964  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (174)..(2540)  
US-09-620-312D-128

## Alignment Scores:

Pred. No.:	399	Length:	3964
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	9.86%	Indels:	0
DB:	4	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-620-312D-128 (1-3964)

QY 10 AlAserArgProGluAlaPhe 16

Db 2273 GCTTCCAGGCCAGAGCCTTT 2293

## RESULT 10

US-09-369-364A-12  
; Sequence 12, Application US/09369364A  
; Patent No. 6391610  
; GENERAL INFORMATION:  
; APPLICANT: Apte, Suneel  
; APPLICANT: Hurskainen, Tiina L.  
; APPLICANT: Hirohata, Satoshi  
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
; FILE REFERENCE: 26473/4007/10-30-00  
; CURRENT APPLICATION NUMBER: US/09/369,364A  
; CURRENT FILING DATE: 1999-08-06  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1

```

; SEQ ID NO 12
; LENGTH: 5804
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(5648)
; NAME/KEY: misc feature
; LOCATION: (1406)
; OTHER INFORMATION: n=T
; NAME/KEY: misc_feature
; LOCATION: (1563)
; OTHER INFORMATION: n=T
US-09-369-364A-12

```

Alignment Scores:		
Pred. No.:	578	Length: 5804
Score:	7.00	Matches: 7
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	9.86%	Indels: 0
DB:	4	Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) X US-09-369-364A-12 (1-5804)

QY 45 ILeysaRGLysleuProPhe 51  
Db 2959 ATCAGAGAAAGTTACCATTC 2979

## RESULT 11

```

US-09-852-067-3
; Sequence 3, Application US/09852067
; Patent No. 6531297
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000897-CIP
; CURRENT APPLICATION NUMBER: US/09/852,067
; CURRENT FILING DATE: 2001-05-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 31208
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(31208)
; OTHER INFORMATION: n = A,T,C or G
US-09-852-067-3

```

Alignment Scores:		
Pred. No.:	2.97e+03	31208
Score:	7.00	7
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	9.86%	Indels: 0
DB:	4	Gaps: 0
US-10-059-395-142_COPY_29_99 (1-71)	x US-09-852-067-3 (1-31208)	

```

QY      46  LYSARGLYSLEUPROPHLEU 52
          |||||
Db      24241 AAGAGGAACCTCCCTTCTTG 24261

```

RESULT 12  
US-09-103-330-35  
; Sequence 35, Application US/091033330A  
; Patent No. 6319716  
; GENERAL INFORMATION:

```

; APPLICANT: TIKOO, SURESH K.
; APPLICANT: BABIUK, LORNE A.
; APPLICANT: REDDY, POLICE S.
; TITLE OF INVENTION: ISOLATION OF MUTANTS IN THE E3 REGION OF THE
; TITLE OF INVENTION: BOVINE ADENOVIRUS GENOME AND THEIR USE IN VACCINES
; FILE REFERENCE: 293102002121
; CURRENT APPLICATION NUMBER: US/09/103,330A
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 08/880,234
; EARLIER FILING DATE: 1997-06-23
; EARLIER APPLICATION NUMBER: 08/164,292
; EARLIER FILING DATE: 1993-12-09
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 34446
; TYPE: DNA
; ORGANISM: Bovine adenovirus type 3
US-09-103-330-35

```

! ORGANISM: Bovine adenovirus type 3  
US-09-103-330-35

Alignment Scores:	3.28e+03	Length:	34446
Pred. No.:			

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	9.86%	Indels:	0
DB:	4	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) X US-09-103-330-35 (1-34446)

Qy 62 GlyLeuArgSerAlaThrPro 68  
Db 14923 GGCCTACGGTCAGCAACACCG 14943

### RESULT 13

```

US-09-198-452A-1/c
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffalls, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(15000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (15001)..(30000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (30001)..(45000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (45001)..(60000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (60001)..(75000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (75001)..(90000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (90001)..(105000)
; OTHER INFORMATION: n=a or c or g or t

```





```
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (840001)..(855000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (855001)..(870000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (870001)..(885000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (885001)..(900000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (900001)..(915000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
```

```
Alignment Scores:
Pred. No.: 1.02e+05 Length: 1230025
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.86% Indels: 0
DB: 4 Gaps: 0
```

US-10-059-395-142\_COPY\_29\_99 (1-71) X US-09-198-452A-1 (1-1230025)

OY 16 PheAaThrProPheLeuAsn 22

Db 391689 TTCAACACACATTTTGAAT 391669

#### RESULT 14

```
; US-08-916-421B-1/c
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco
; Patent No. 6503729
; TITLE OF INVENTION: jannaschi
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschi
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (28257)..(28258)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84773)..(84773)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84808)..(84808)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84812)..(84812)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98120)..(98120)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98159)..(98159)
```

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; OTHER INFORMATION: n equals a, t, c, or g
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OTHER INFORMATION: n equals a, t, c, or g  
US-08-916-421B-1

Alignment Scores:  
Pred. No.: 1.34e+05 Length: 1664976  
Score: 7.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 9.86% Indels: 0  
DB: 4 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-08-916-421B-1 (1-1664976)  
QY 44 SerileysArglybLeupPro 50  
Db 1134223 AGCATAAAGAGAGTACTT 1134203

RESULT 15  
US-08-335-583C-20  
Sequence 20, Application US/08335583C  
Patent No. 5693779  
GENERAL INFORMATION:  
APPLICANT: Moos Jr., Malcolm  
APPLICANT: Wang, Shouwan  
APPLICANT: Krinks, Marie  
TITLE OF INVENTION: PRODUCTION AND USE OF  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson and Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: USA  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/335,583C  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: NIH104.001A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-760-0404  
TELEFAX: 714-760-9502  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
IMMEDIATE SOURCE:  
LIBRARY: GENWORKS, X57234  
US-08-335-583C-20

Alignment Scores:  
Pred. No.: 27.1 Length: 20  
Score: 6.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 8.45% Indels: 0  
DB: 1 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-08-335-583C-20 (1-20)  
QY 62 GlyleuArgSerAlaThr 67  
Db 3 GGACTTCGAAGTCAACC 20

Sat Nov 29 17:52:38 2003

us-10-059-395-142\_copy\_29\_99.011.rn1

Page 10

Search completed: November 28, 2003, 13:11:13  
Job time : 311 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 13:41:08 ; Search time 18 Seconds

(without alignments)  
379.332 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Perfect score: 71

Sequence: 1 EESSTIENYASRPEAFNTPF.....LNWDAFPKLGKLSATPDAQ 71

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 76:\*

1: pirl:\*

2: pirl:\*

3: pirl:\*

4: pirl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	11.3	184	2 AF0298	probable yfeABCD 1
2	8	11.3	428	2 D97010	5-enolpyruvylshikI
3	7	9.9	202	2 A83448	hypothetical prote
4	7	9.9	311	1 BYEBT	sulfate-binding pr
5	7	9.9	329	2 AG0942	periplasmic sulpha
6	7	9.9	361	2 I50505	gene wnt8 protein
7	7	9.9	372	1 WNVZCN	major envelope ant
8	7	9.9	372	2 C72155	E13L protein - var
9	7	9.9	372	2 H36840	C17L protein - var
10	7	9.9	372	2 T28475	hypothetical prote
11	7	9.9	437	2 D69519	tRNA nucleotidyltr
12	7	9.9	451	2 A38099	glycylpeptide N-te
13	7	9.9	816	2 T25555	hypothetical prote
14	7	9.9	867	2 D86393	hypothetical prote
15	6	8.5	25	2 S74108	hemolysin A - Vibri
16	6	8.5	52	2 S52069	hemolysin A - Vibri
17	6	8.5	99	2 A41605	p36 protein (CAK C
18	6	8.5	116	1 B46279	homeotic protein H
19	6	8.5	128	2 B46279	guanylin precursor
20	6	8.5	131	2 AG2115	kinetoplast DNA-as
21	6	8.5	164	2 B36951	hypothetical prote
22	6	8.5	172	2 T02229	hypothetical prote
23	6	8.5	178	2 F64931	protein BYJ15 - co
24	6	8.5	178	2 H90932	probable membrane
25	6	8.5	178	2 H90932	hypothetical prote
26	6	8.5	178	2 D85781	hypothetical prote
27	6	8.5	185	2 AE0707	probable membrane
28	6	8.5	186	2 T08279	hypothetical prote
29	6	8.5	187	2 AG0662	conserved hypothet

30	6	8.5	190	2 T31661	hypothetical prote
31	6	8.5	197	2 C95290	hypothetical prote
32	6	8.5	203	2 G86785	acetyltransferase
33	6	8.5	204	2 E95896	probable transcrip
34	6	8.5	219	2 A26484	glutathione transf
35	6	8.5	227	2 F96777	germin-like protei
36	6	8.5	231	2 A82084	MTA/SAH nucleosida
37	6	8.5	239	2 C81935	probable ribonucle
38	6	8.5	239	2 E81169	ribonuclease III N
39	6	8.5	239	2 E70800	probable transport
40	6	8.5	240	2 T25299	hypothetical prote
41	6	8.5	241	2 AG0857	hypothetical prote
42	6	8.5	244	2 T26265	hypothetical prote
43	6	8.5	245	2 F96913	glutamine ABC tran
44	6	8.5	261	2 C84776	hypothetical prote
45	6	8.5	261	2 E96036	probable phenylace

#### ALIGNMENTS

RESULT 1  
AF0298  
Probable yfeABCD locus regulator yfeE [imported] - Yersinia pestis (strain CO92)  
C/Species: Yersinia pestis  
C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Nov-2001  
C/Accession: AF0298  
R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
11, M.; Rutherford, K.; Skellern, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,  
Nature 413, 523-527, 2001  
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A/Reference number: AB0001; MUID:21470413; PMID:11586360  
A/Accession: AF0298  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-184 <KUR>  
A/Cross-references: GB:AL590842; PIDN:CAC91250.1; PID:g15980439; GSPDB:GN00175  
C/Genetics:  
A/Gene: yfeE  
C/Superfamily: Escherichia coli probable membrane protein b1726

Query Match 11.3%; Score 8; DB 2; Length 184;  
Best Local Similarity 100.0%; Pred. No. 0.68;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 FNTPLNI 23  
Db 63 FNTPLNI 70

RESULT 2  
D97010  
5-enolpyruvylshikimate-3-phosphate synthase [imported] - Clostridium acetobutylicum  
C/Species: Clostridium acetobutylicum  
C/Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 30-Sep-2001  
C/Accession: D97010  
R/Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1c  
A/Reference number: A96900; MUID:21359325; PMID:21359325  
A/Accession: D97010  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-428 <KUR>  
A/Cross-references: GB:AE001437; PIDN:AAK78871.1; PID:g15023793; GSPDB:GN00168  
A/Experimental source: Clostridium acetobutylicum ATCC824  
C/Genetics:  
A/Gene: CAC0895  
C/Superfamily: 3-phosphoshikimate 1-carboxyvinyltransferase; 3-phosphoshikimate 1-carbox

Query Match 11.3%; Score 8; DB 2; Length 428;



Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EESTIEN 8  
|||||||  
Db 35 EESTIEN 42

## RESULT 3

AB3448  
hypothetical protein PA1579 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: AB3448  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Berman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Iarbig, K.; Lam, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A:Reference number: AB2950; PMID:20437337; PMID:10984043  
A:Accession: AB3448  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-202 <STO>  
A:Cross-references: GB:AE004586; GB:AE004091; NID:g9947536; PIDN:AAG04968.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA1579

Query Match 9.9%; Score 7; DB 2; Length 202;  
Best Local Similarity 100.0%; Pred. No. 8.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 60 LKGLRSA 66  
|||||||  
Db 192 LKGLRSA 198

## RESULT 4

BYEBT  
sulfate-binding protein - Salmonella typhimurium  
C:Species: Salmonella typhimurium  
C:Date: 24-Sep-1981 #sequence\_revision 09-Aug-1997 #text\_change 09-Aug-1997  
C:Accession: A03403; S09675  
R:Ishihara, H.; Hogg, R.W.  
J. Biol. Chem. 255, 4614-4618, 1980  
A:Title: Amino acid sequence of the sulfate-binding protein from Salmonella typhimurium  
A:Reference number: A03403; PMID:80182123; PMID:6989815  
A:Accession: A03403  
A:Molecule type: protein  
A:Residues: 1-230,232-300,'D',302-311 <ISI>  
A:Experimental source: strain LT2  
R:Garrett, A.R.; Johnson, L.A.; Beacham, I.R.  
Mol. Microbiol. 3, 177-186, 1989  
A:Title: Isolation, molecular characterization and expression of the uisB gene of Salmonella typhimurium  
A:Reference number: S04172; PMID:89343621; PMID:2548058  
A:Accession: S09675  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 228-311 <GAR>  
A:Cross-references: EMBL:X13380  
C:Comment: This protein, isolated from the periplasmic space of the cell, specifically binds to sulfated ligands.  
C:Superfamily: sulfate-binding protein  
C:Keywords: periplasmic space; sulfate transport

Query Match 9.9%; Score 7; DB 1; Length 311;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 55 DAFPKLK 61  
|||||||  
Db 274 DAFPKLK 280

RESULT 5  
AG0942  
periplasmic sulphate binding protein [imported] - Salmonella enterica subsp. enterica s

C:Species: Salmonella enterica subsp. enterica serovar Typhimurium  
A:Note: this species has also been called Salmonella typhimurium  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AG0942  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.  
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium  
A:Reference number: AB0502; PMID:21534947; PMID:11677608  
A:Accession: AG0942  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-329 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD09561.1; PID:g16504675; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY3808  
C:Superfamily: sulfate-binding protein

Query Match 9.9%; Score 7; DB 2; Length 329;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 55 DAFPKLK 61  
|||||||  
Db 292 DAFPKLK 298

## RESULT 6

I50505  
gene wnt8 protein - zebra fish  
C:Species: Brachydanio rerio (zebra fish)  
C:Date: 13-Mar-1997 #sequence\_revision 13-Mar-1997 #text\_change 24-Nov-1999  
C:Accession: I50505  
R:Kelly, G.M.; Greenstein, P.; Erezylmaz, D.F.; Moon, R.T.  
Development 121, 1787-1799, 1995  
A:Title: Zebrafish wnt8 and wnt8b share a common activity but are involved in distinct signaling pathways  
A:Reference number: I50505; PMID:95324404; PMID:7600994  
A:Accession: I50505  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-361 <KEL>  
A:Cross-references: EMBL:U10869; NID:g968914; PID:g968915  
C:Genetics:  
A:Gene: wnt8  
C:Superfamily: int-1 transforming protein

Query Match 9.9%; Score 7; DB 2; Length 361;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 61 KGLRSAT 67  
|||||||  
Db 77 KGLRSAT 83

## RESULT 7

WMVZCN  
major envelope antigen - vaccinia virus (strain Copenhagen)  
C:Species: vaccinia virus  
A:Note: host Homo sapiens (man)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Jul-1999  
C:Accession: I42507  
R:Goebel, S.J.; Johnson, G.P.; Perkins, M.E.; Davis, S.W.; Winslow, J.P.; Paoletti, E.  
Virology 179, 517-563, 1990  
A:Title: Appendix to "The complete DNA sequence of vaccinia virus".  
A:Reference number: A42501  
A:Accession: I42507

A;Molecule type: DNA  
A;Residues: 1-372 <GOE>  
A;Cross-references: GB:M35027; NID:g335317; PIDN:AAA48031.1; PID:g335379  
R;Goebel, S.J.; Johnson, G.P.; Perkus, M.E.; Davis, S.W.; Winslow, J.P.; Paoletti, E.  
Virology 179, 247-266, 1990  
A;Title: The complete DNA sequence of vaccinia virus.  
A;Reference number: A42531; MUID:91021027; PMID:2219722  
A;Contents: annotation; possible protein-coding frames  
A;Note: neither amino acid nor nucleotide sequence is given  
C;Superfamily: vaccinia virus major envelope antigen  
C;Keywords: envelope protein; transmembrane protein

Query Match 9.9%; Score 7; DB 1; Length 372;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 IDKL RSA 29  
Db 224 IDKL RSA 230

RESULT 8  
C72155  
E13L protein - variola minor virus (strain Garcia-1966)  
C;Species: variola minor virus  
C;Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 20-Jun-2000  
C;Accession: C72155  
R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Saifonov, P.F.; Massung, R.F.; Lopat  
submitted to GenBank, March 1998  
A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor  
A;Reference number: A72150  
A;Accession: C72155  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-372 <SHC>  
A;Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54637.1; PID:g5830598  
A;Experimental source: strain Garcia-1966  
C;Genetics:  
A;Gene: E13L  
C;Superfamily: vaccinia virus major envelope antigen

Query Match 9.9%; Score 7; DB 2; Length 372;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 IDKL RSA 29  
Db 224 IDKL RSA 230

RESULT 9  
H36840  
C17L protein - variola virus (strain India-1967)  
C;Species: variola virus  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 23-Mar-2001  
C;Accession: H36840  
R;Blinov, V.M.  
submitted to GenBank, November 1992  
A;Reference number: A36859  
A;Accession: H36840  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-372 <BLI>  
A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA48978.1; PID:g297218  
C;Superfamily: vaccinia virus major envelope antigen  
C;Keywords: transmembrane protein

Query Match 9.9%; Score 7; DB 2; Length 372;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 224 IDKL RSA 230

RESULT 10  
T28475  
hypothetical protein C17L - variola major virus  
C;Species: variola major virus  
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000  
C;Accession: T28475  
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin  
Nature 366, 748-751, 1993  
A;Title: Potential virulence determinants in terminal regions of variola smallpox virus  
A;Reference number: Z20488; MUID:94088747; PMID:8264798  
A;Accession: T28475  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-372 <MAS>  
A;Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60785.1; PID:g438955  
A;Experimental source: strain Bangladesh-1975  
C;Superfamily: vaccinia virus major envelope antigen

Query Match 9.9%; Score 7; DB 2; Length 372;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 IDKL RSA 29  
Db 224 IDKL RSA 230

RESULT 11  
D69519  
cRNA nucleotidyltransferase (cca) homolog - Archaeoglobus fulgidus  
C;Species: Archaeoglobus fulgidus  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 06-Jan-2003  
C;Accession: D69519  
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, S.J.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo:  
A;Reference number: A69250; MUID:98049343; PMID:9389475  
A;Accession: D69519  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-437 <KLE>  
A;Cross-references: GB:AE000955; GB:AE000782; NID:g2689278; PIDN:AAB89084.1; PID:g264835;  
C;Superfamily: cRNA nucleotidyltransferase (CCA-adding enzyme)

Query Match 9.9%; Score 7; DB 2; Length 437;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 LRS AFKA 32  
Db 316 LRS AFKA 322

RESULT 12  
A38099  
glycylpeptide N-tetradecanoyltransferase (EC 2.3.1.97) - yeast (Candida albicans)  
C;Species: Candida albicans  
C;Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 28-Jul-2000  
C;Accession: A38099  
R;Wiegand, R.C.; Carr, C.; Minnerly, J.C.; Pauley, A.M.; Carron, C.P.; Langner, C.A.; Du  
J. Biol. Chem. 267, 8591-8598, 1992  
A;Title: The Candida albicans myristoyl-CoA:protein N-myristoyltransferase gene. Isolatic  
A;Reference number: A38099; MUID:92235090; PMID:1569105  
A;Accession: A38099  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA

A;Residues: 1-451 <MIB>  
A;Cross-references: GB:M80544; NID:g170883; PIDN:AAA34351.1; PID:g170884  
C;Superfamily: yeast glycylpeptide N-tetradecanoyltransferase  
C;Keywords: acyltransferase; coenzyme A

Query Match 9.9%; Score 7; DB 2; Length 451;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 58 PKLKGRLR 64  
|||||  
Db 262 PKLKGRLR 268

## RESULT 13

T25555  
hypothetical protein C17H11.6 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C;Accession: T25555  
R;Johnson, D.  
submitted to the EMBL Data Library, December 1996

A;Description: The sequence of C. elegans cosmid C17H11.  
A;Reference number: Z20049

A;Accession: T25555

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-816 <JOH>

A;Cross-references: EMBL:U80847; PIDN:AAB37987.1; GSPDB:GN00028; CESP:C17H11.6

A;Experimental source: strain Bristol N2; clone C17H11

C;Genetics:

A;Gene: CESP:C17H11.6

A;Map position: X

A;Introns: 47/3; 85/3; 122/3; 150/2; 187/2; 260/1; 331/1; 399/1; 448/1; 497/1; 534/3; 59

Query Match 9.9%; Score 7; DB 2; Length 816;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 56 APPKLKG 62  
|||||  
Db 104 APPKLKG 110

## RESULT 14

D86393

hypothetical protein TIK7.1 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2001

C;Accession: D86393

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hutzar, L.  
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: D86393

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-867 <STO>

A;Cross-references: GB:AE005172; NID:g9797740; PIDN:AAF98558.1; GSPDB:GN00141

C;Genetics:

A;Map position: 1

Query Match 9.9%; Score 7; DB 2; Length 867;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 60 LKGLRSA 66  
|||||  
Db 457 LKGLRSA 463

## RESULT 15

S74108  
hemolysin A - Vibrio cholerae (fragments)

C;Species: Vibrio cholerae

C;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999

C;Accession: S74108

R;Menzl, K.; Maier, E.; Chakraborty, T.; Benz, R.  
Eur. J. Biochem. 240, 646-654, 1996

A;Title: HlyA hemolysin of Vibrio cholerae O1 biotype El Tor. Identification of the hem

A;Reference number: S74108; MUID:97008956; PMID:8856066

A;Accession: S74108

A;Molecule type: protein

A;Residues: 1-15;16-25 <MEN>

A;Experimental source: strain O1 biotype El Tor

C;Keywords: channel-forming protein; toxin

Query Match 8.5%; Score 6; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 65 SATPDA 70  
|||||  
Db 9 SATPDA 14

Search completed: November 28, 2003, 13:43:46  
Job time : 21 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 13:40:38 ; Search time 11 Seconds

(without alignments)  
303.536 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Perfect score: 71

Sequence: 1 EEESTIENYASRPEAFNTPF.....LNWDAFPKLGIRSATPDQAQ 71

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	11.3	184	1	YFEE YERPE
2	8	11.3	428	1	AROQ_CLOAB
3	7	9.9	202	1	YF79_PSEAE
4	7	9.9	205	1	EF1B_YEAST
5	7	9.9	239	1	GIDB_CLOPE
6	7	9.9	325	1	CYK2_ORYSA
7	7	9.9	329	1	SUBI_SALTY
8	7	9.9	359	1	WNT8_BRARE
9	7	9.9	372	1	VENV_VACCC
10	7	9.9	372	1	VENV_VARV
11	7	9.9	437	1	CCA_ARCFU
12	7	9.9	451	1	NMT_CANAL
13	6	8.5	116	1	GUAN_MOUSE
14	6	8.5	164	1	YGAE_ERWAM
15	6	8.5	178	1	YNIB_ECOLI
16	6	8.5	189	1	MOBA_PASMU
17	6	8.5	191	1	AMPN_CANFA
18	6	8.5	218	1	GT26_SCHJA
19	6	8.5	227	1	GLT3_ARATH
20	6	8.5	234	1	AMPN_BOVIN
21	6	8.5	239	1	RNC_NEIMA
22	6	8.5	239	1	RNC_NEIMB
23	6	8.5	249	1	KDXA_XANAC
24	6	8.5	263	1	SURE_CHLTE
25	6	8.5	289	1	HXD8_MOUSE
26	6	8.5	306	1	YZ05_AQUAE
27	6	8.5	313	1	ENV1_MOUSE
28	6	8.5	313	1	Y135_TREPA
29	6	8.5	323	1	CYCH_XENLA
30	6	8.5	329	1	SUBI_ECOLI
31	6	8.5	334	1	ARGC_BUCAL
32	6	8.5	343	1	APL6_HUMAN
33	6	8.5	344	1	YD33_MYCTU

#### ALIGNMENTS

RESULT 1	YFEE_YERPE	STANDARD;	PRT;	184 AA.
AC	Q56956;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Putative yfearBCD regulator yfear.			
GN	YFEE OR YF02445 OR Y1891.			
OS	Yersinia pestis.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Yersinia.			
OX	NCBI_TaxID=632;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=KIM6;			
RA	Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.			
RL				
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CO-92 / Biovar Orientalis;			
RX	MEDLINE=21470413; PubMed=11586360;			
RA	Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,			
RA	Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,			
RA	Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,			
RA	Feltwell T., Hamlin N., Holtroyd S., Jagels K., Karlyshev A.V.,			
RA	Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,			
RA	Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;			
RT	"Genome sequence of Yersinia pestis, the causative agent of plague.";			
RL	Nature 413:523-527(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=KIMS / Biovar Mediaevalis;			
RX	MEDLINE=22137863; PubMed=12142430;			
RA	Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,			
RA	Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,			
RA	Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,			
RA	Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,			
RA	Perry R.D.;			
RT	"Genome sequence of Yersinia pestis KIM.";			
RL	J. Bacteriol. 184:4601-4611(2002).			
CC	-1- FUNCTION: PUTATIVE REGULATOR OF YFABCD, AN ABC TRANSPORTER LOCUS			
CC	INVOLVED IN INORGANIC IRON TRANSPORT.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).			
CC	-1- SIMILARITY: STRONG, TO E.COLI YNIB.			
CC				
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC				
DR	EMBL; U50903; AAC46151.1; ..			

DR EMBL; AJ414152; CAC91250.1; -.  
DR EMBL; AE013792; AAM85458.1; -.  
DR PIR; AF0298; AF0298.  
KW Transmembrane; Complete proteome.  
FT TRANSMEM 15 35 POTENTIAL.  
FT TRANSMEM 84 104 POTENTIAL.  
FT TRANSMEM 162 182 POTENTIAL.  
SQ SEQUENCE 184 AA; 20913 MW; 99860ED024E8A51A CRC64;

Query Match 11.3%; Score 8; DB 1; Length 184;  
Best Local Similarity 100.0%; Pred. No. 0.37;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 FNTPLNT 23  
| | | | | | | |  
| | | | | | | |  
Db 63 FNTPLNT 70

## RESULT 2

ARO\_A\_CLOAB STANDARD; PRT; 428 AA.

ID ARO\_A\_CLOAB STANDARD; PRT; 428 AA.  
AC Q97KM2;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).  
GN AROA OR CAC0895.  
OS Clostridium acetobutylicum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.  
OX NCBI\_TaxID=1488;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;  
RX MEDLINE=21359325; PubMed=11466286;  
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;  
RA "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";  
RT J. Bacteriol. 183:4823-4838(2001).  
RL -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.  
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway; sixth step.  
CC -1- SUBUNIT: Monomer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
CC -1- SIMILARITY: Belongs to the EPSP synthase family.  
-----  
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-----  
DR EMBL; AE007605; AAK78871.1; -.  
DR PIR; D97010; D97010.  
DR HAMAP; MF\_00210; -; 1.  
DR InterPro; IPR006264; AROA.  
DR InterPro; IPR001986; EPSP\_synthase.  
DR Pfam; PF00275; EPSP\_synthase; 1.  
DR ProDom; PD001867; EPSP\_synthase; 1.  
DR TIGRfam; TIGR01356; aroA; 1.  
DR PROSITE; PS00104; EPSP\_SYNTHASE\_1; FALSE\_NEG.  
DR PROSITE; PS00885; EPSP\_SYNTHASE\_2; 1.  
KW Aromatic amino acid biosynthesis; Transferase; Complete proteome.  
SQ SEQUENCE 428 AA; 46960 MW; D3A9BFF46E9C547 CRC64;

Query Match 11.3%; Score 8; DB 1; Length 428;

Best Local Similarity 100.0%; Pred. No. 0.77;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEESTIEN 8  
| | | | | | | |  
| | | | | | | |  
Db 35 EEESTIEN 42

## RESULT 3

YF79\_PSEAE STANDARD; PRT; 202 AA.  
ID YF79\_PSEAE STANDARD; PRT; 202 AA.  
AC Q913D8;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hypothetical protein PA1579.  
GN PA1579.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 15692 / PA01;  
RX MEDLINE=20437337; PubMed=10984043;  
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brady L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.;  
RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.";  
RT Nature 406:959-964(2000).  
RL [2]  
RN [2]  
RP POTENTIAL FUNCTION.  
RX MEDLINE=21173595; PubMed=11276083;  
RA Iyer L.M., Koonin E.V., Aravind L.;  
RA "Adaptations of the helix-grip fold for ligand binding and catalysis in the START domain superfamily.";  
RT Proteins 43:134-144(2001).  
RL -1- FUNCTION: May play a role in the interaction of the bacterium with animal cells.  
CC -1- SIMILARITY: Contains 1 START domain.  
-----  
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-----  
DR EMBL; AE004586; AAG04968.1; -.  
DR PIR; A83448; A83448.  
DR InterPro; IPR002913; START.  
DR Pfam; PF01852; START; 1.  
DR PROSITE; PS50848; START; 1.  
KW Hypothetical protein; Complete proteome.  
FT DOMAIN 1 202 START.  
SQ SEQUENCE 202 AA; 22110 MW; 9F1C9B71F61ED95E CRC64;

Query Match 9.9%; Score 7; DB 1; Length 202;  
Best Local Similarity 100.0%; Pred. No. 4.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 LKGIKSA 66  
| | | | | | | |  
| | | | | | | |  
Db 192 LKGIKSA 198

## RESULT 4

EF1B\_YEAST



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ID EF1B YEAST STANDARD; PRT; 205 AA.
AC P32471;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Elongation factor 1-beta (EF-1-beta).
GN EF1B OR TEF5 OR YAL003W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93131037; PubMed=8420802;
RA Hiraga K., Suzuki K., Tsuchiya E., Miyakawa T.;
RT "Cloning and characterization of the elongation factor EF-1 beta
RT homologue of Saccharomyces cerevisiae. EF-1 beta is essential for
RT growth."
RL FEBS Lett. 316:165-169(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=S288c / AB972;
RC MEDLINE=95028152; PubMed=7941740;
RA Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B.,
RA Delaney S., Ouellette B.F.F., Barton A.B., Kaback D.B., Bussey H.;
RT "Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of
RT the 42 kbp SPO7-CEN1-CDC15 region."
RL Yeast 10:535-541(1994).
RN [3]
RP SEQUENCE OF 167-177.
RC STRAIN=S288c;
RX MEDLINE=95203288; PubMed=7895733;
RA Garrels J.I., Fletcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
RT Saccharomyces cerevisiae."
RL FEBS Microbiol. Lett. 137:1-8(1996).
RN [5]
RP ACETYLATION, AND PHOSPHORYLATION.
RA Garrels J.I., Fletcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -1- FUNCTION: EF-1-BETA AND EF-1-DELTA STIMULATE THE EXCHANGE OF
CC GDP BOUND TO EF-1-ALPHA TO GTP.
CC -1- SUBUNIT: EF-1 IS COMPOSED OF FOUR SUBUNITS: ALPHA, BETA,
CC DELTA, AND GAMMA.
CC -1- PTM: PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO THE EF-1-BETA/EF-1-DELTA FAMILY.
CC -----
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CC -----
DR EMBL; D14080; BAA03165.1; -.
DR EMBL; L22015; AAC04954.1; -.
DR PIR; S43445; S43445.
DR PDB; 1F60; 22-NOV-00.
DR PDB; 1G7C; 30-MAY-01.
DR PDB; 1IJE; 06-JUN-01.
DR PDB; 1IJF; 06-JUN-01.
DR SWISS-2DPAGE; P32471; YEAST.

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DR SGD; S0000003; EF1B.
DR InterPro; IPR001326; EF1_BD.
DR InterPro; IPR004046; GST_Cterm.
DR Pfam; PF00736; EF1BD; 1.
DR PROSITE; PS00824; EF1BD_1; 1.
DR PROSITE; PS00825; EF1BD_2; 1.
KW Elongation factor; Protein biosynthesis; Acetylation; Phosphorylation;
KW 3D-structure.
FT INIT MET 0 0
FT MOD_RES 1 1 ACETYLATION.
FT CONFLICT 48 48 F -> S (IN REF. 2).
FT CONFLICT 56 56 F -> S (IN REF. 2).
FT CONFLICT 97 97 W -> L (IN REF. 2).
FT CONFLICT 167 167 L -> E (IN REF. 3).
SQ SEQUENCE 205 AA; 22689 MW; E47782908998DED6 CRC64;

```

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Query Match 9.9%; Score 7; DB 1; Length 205;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 29 AFKADEF 35
Db 55 AFKADEF 61

```

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RESULT 5
GIDB_CLOPE STANDARD; PRT; 239 AA.
ID GIDB_CLOPE
AC Q8XH32;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methyltransferase gidb (EC 2.1.1.-) (Glucose inhibited division
DE protein B).
GN GIDB OR CPE2653.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC -1- FUNCTION: Probable S-adenosyl-L-methionine dependent
CC methyltransferase specific for a sterol and/or lipid substrate (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO THE GIDB FAMILY.
CC -----
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CC -----
DR EMBL; AP003194; BAB82359.1; -.
DR HAMAP; MF_00074; -.
DR InterPro; IPR003682; GIDB.
DR Pfam; PF03527; GIDB; 1.
DR ProDom; PD004441; GIDB; 1.
DR TIGRFAMs; TIGR00138; gidb; 1.
KW Transferase; Methyltransferase; Complete proteome.
SQ SEQUENCE 239 AA; 26886 MW; 5F1024A3E3C1C71E CRC64;

```

```

Query Match 9.9%; Score 7; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DR EMBL; AE008889; AA22903.1; -.

DR EMBL; X13380; -; NOT\_ANNOTATED\_CDS.

DR PIR; A03403; BYEBT.

DR PDB; 1SBP; 31-OCT-93.

DR StGene; SG10382; sbp.

DR InterPro; IPR000957; Sulphate bind.

DR InterPro; IPR005669; Thiosulph\_bind.

DR Pfam; PF01547; SBP\_bac\_1; 1.

DR ProDom; PD008688; Sulphate bind; 1.

DR TIGRFAMs; TIGR00971; 3a0106s03; 1.

DR PROSITE; PS00401; PROK\_SULFATE\_BIND\_1; 1.

DR PROSITE; PS00757; PROK\_SULFATE\_BIND\_2; 1.

KW Sulfate transport; Transport; Periplasmic; Signal; 3D-structure;

KW Complete proteome.

FT SIGNAL 1 19

FT CHAIN 20 329

FT CONFLICT 58 58

FT CONFLICT 63 64

FT CONFLICT 70 70

FT CONFLICT 79 79

FT CONFLICT 89 89

FT CONFLICT 129 129

FT CONFLICT 175 175

FT CONFLICT 249 249

FT CONFLICT 319 319

FT STRAND 21 28

FT TURN 31 32

FT TURN 31 32

FT HELIX 33 51

FT STRAND 54 61

FT HELIX 64 69

FT HELIX 71 73

FT TURN 74 75

FT STRAND 80 83

FT HELIX 86 94

FT TURN 95 96

FT TURN 100 101

FT HELIX 102 105

FT HELIX 107 110

FT STRAND 113 115

FT STRAND 117 122

FT TURN 123 124

FT TURN 126 127

FT HELIX 132 136

FT TURN 138 139

FT STRAND 142 143

FT TURN 147 149

FT HELIX 151 167

FT TURN 168 170

FT HELIX 172 184

FT TURN 185 185

FT STRAND 186 188

FT HELIX 193 201

FT TURN 202 202

FT STRAND 208 212

FT HELIX 213 221

FT TURN 222 227

FT STRAND 228 231

FT STRAND 235 237

FT STRAND 239 239

FT STRAND 242 245

FT HELIX 247 253

FT TURN 254 254

FT HELIX 256 267

FT HELIX 269 277

FT TURN 278 279

FT STRAND 281 282

FT HELIX 285 290

FT TURN 291 291

FT HELIX 292 294

SULFATE-BINDING PROTEIN.

R -> D (IN REF. 2).

GS -> SQ (IN REF. 2).

S -> SS (IN REF. 2).

V -> T (IN REF. 2).

D -> N (IN REF. 2).

H -> T (IN REF. 2).

Q -> E (IN REF. 2).

MISSING (IN REF. 2).

N -> D (IN REF. 2).

FT STRAND 299 301

FT HELIX 303 307

FT HELIX 310 317

FT TURN 318 318

FT TURN 320 321

FT HELIX 323 328

SQ SEQUENCE 329 AA; 36540 MW; AFE24D81D758CAFD CRC64;

Query Match 9.9%; Score 7; DB 1; Length 329;

Best Local Similarity 100.0%; Pred. No. 6.8;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 DAFPKLK 61

Db 292 DAFPKLK 298

RESULT 8

WNT8\_BRARE

ID WNT8\_BRARE STANDARD; PRT; 359 AA.

AC P51028; Q90YL9;

DT 01-OCT-1996 (Rel. 34, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Wnt-8 protein precursor.

GN WNT8.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI\_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RX MEDLINE=95324404; PubMed=7600994;

RA Kelly G.M., Erezylmaz D.F., Greenstein P.B., Moon R.T.;

RT "Zebrafish wnt8 and wnt8b share a common activity but are involved in distinct developmental pathways.";

RL Development 121:1787-1799(1995).

RN [2]

RP SEQUENCE FROM N.A., REVISIONS, AND DEVELOPMENTAL STAGE.

RX MEDLINE=21563308; PubMed=11703928;

RA Lekven A.C., Thorpe C.J., Waxman J.S., Moon R.T.;

RT "Zebrafish wnt8 encodes two wnt8 proteins on a bicistronic transcript and is required for mesoderm and neuroectoderm patterning.";

RL Dev. Cell 1:103-114(2001).

CC -!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS. MAY BE INVOLVED IN THE SPECIFICATION OF THE SPATIAL PATTERNS OF EXPRESSION OF GSC AND OTHER REGULATORY GENES LEADING TO THE ESTABLISHMENT OF THE EMBRYONIC AXIS.

CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the extracellular matrix.

CC -!- TISSUE SPECIFICITY: IN FUTURE MESODERM.

CC -!- DEVELOPMENTAL STAGE: Required for mesoderm and neural ectoderm patterning during gastrulation.

CC -!- SIMILARITY: Belongs to the Wnt family.

CC -----

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CC -----

DR EMBL; U10869; AAC59697.2; -.

DR EMBL; AY032749; AAK70223.1; -.

DR ZFIN; ZDB-GENE-980526-332; wnt8.

DR InterPro; IPR005817; Wnt.

DR InterPro; IPR005816; Wnt\_growthfactor.

DR Pfam; PF00110; wnt; 1.

```

DR PRINTS; PR01349; WNTPROTEIN.
DR SMART; SM00097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
KW Wnt signaling pathway; Developmental protein; Glycoprotein; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 359 WNT-8 PROTEIN.
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 359 AA; 40289 MW; C192475B9D48C3C2 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 359;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 61 KGLRSAT 67
DB 77 KGLRSAT 83

RESULT 9
ID VENV_VACCC STANDARD; PRT; 372 AA.
AC P20638;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Major envelope protein (37 kDa protein) (p37K).
GN F13L.
OS Vaccinia virus (strain Copenhagen).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10249;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91021027; PubMed=2219722;
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
RA Paoletti E.;
RT "The complete DNA sequence of vaccinia virus.";
RL Virology 179:247-266(1990).
RN [2]
RP COMPLETE GENOME.
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
RA Paoletti E.;
RT "Appendix to 'The complete DNA sequence of vaccinia virus.'";
RL Virology 179:517-563(1990).
CC -1- FUNCTION: THIS PROTEIN IS THE MAJOR ANTIGEN ON THE ENVELOPE OF
CC EXTRACELLULAR VACCINIA VIRUS.
CC -1- PTM: ACYLATED BY PALMITIC ACID GROUP(S).
CC -1- SIMILARITY: Contains 1 PLD phosphodiesterase domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M35027; AAA48031.1; -.
DR PIR; I42507; WMVZCN.
DR InterPro; IPR001736; PLD.
DR Pfam; PF00614; PLDC; 2.
DR SMART; SM00155; PLDC; 2.
DR PROSITE; PS50035; PLD; 1.
KW Late protein; Antigen; Lipoprotein; Palmitate.
FT DOMAIN 307 334 PLD PHOSPHODIESTERASE.
SQ SEQUENCE 372 AA; 41823 MW; B488783DC82EFB83 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 372;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 23 IDKLRSA 29
DB 224 IDKLRSA 230

RESULT 10
ID VENV_VARV STANDARD; PRT; 372 AA.
AC P33815;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Major envelope protein (37 kDa protein) (p37K).
GN F13L OR C17L.
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=India-1967 / Isolate Ind3;
RX MEDLINE=94152154; PubMed=8109158;
RA Shchelkunov S.N., Blinov V.M., Resenchuk S.M., Totmenin A.V.,
RA Sandakhchiev L.S.;
RT "Analysis of the nucleotide sequence of a 43 kbp segment of the
RT genome of variola virus India-1967 strain.";
RL Virus Res. 30:239-258(1993).
RN [2]
RP COMPLETE GENOME.
RC STRAIN=India-1967 / Isolate Ind3;
RX MEDLINE=93202261; PubMed=8384129;
RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RT "Genes of variola and vaccinia viruses necessary to overcome the host
RT protective mechanisms.";
RL FEBS Lett. 319:80-83(1993).
CC -1- FUNCTION: THIS PROTEIN IS THE MAJOR ANTIGEN ON THE ENVELOPE OF
CC EXTRACELLULAR VACCINIA VIRUS.
CC -1- PTM: ACYLATED BY PALMITIC ACID GROUP(S).
CC -1- SIMILARITY: Contains 1 PLD phosphodiesterase domain.
CC -----
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CC -----
DR EMBL; X69198; CAA48978.1; -.
DR PIR; H36840; H36840.
DR InterPro; IPR001736; PLD.
DR Pfam; PF00614; PLDC; 2.
DR SMART; SM00155; PLDC; 2.
DR PROSITE; PS50035; PLD; 1.
KW Late protein; Antigen; Lipoprotein; Palmitate.
FT DOMAIN 307 334 PLD PHOSPHODIESTERASE.
SQ SEQUENCE 372 AA; 41902 MW; C769B05DD48EC944 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 372;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 IDKLRSA 29
DB 224 IDKLRSA 230

RESULT 11
ID CCA_ARCFU STANDARD; PRT; 437 AA.
AC 028126;
DT 15-DEC-1998 (Rel. 37, Created)

```

DT 15-DEC-1998 (Rel. 37, last sequence update)  
DT 16-OCT-2001 (Rel. 40, last annotation update)  
DE tRNA nucleotidyltransferase (EC 2.7.7.25) (tRNA adenylyltransferase)  
DE (tRNA CCA-pyrophosphorylase) (CCA-adding enzyme).  
GN CCA OR AF2156.  
OS Archaeoglobus fulgidus.  
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;  
OC Archaeoglobaceae; Archaeoglobus.  
OX NCBI\_TaxID=2234;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;  
RX MEDLINE=98049343; PubMed=9389475;  
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.B.,  
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,  
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,  
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,  
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,  
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,  
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,  
RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,  
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,  
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
RA Venter J.C.;  
RT "The complete genome sequence of the hyperthermophilic, sulphate-  
RT reducing archaeon Archaeoglobus fulgidus.";  
RL Nature 390:364-370(1997).  
CC -!- FUNCTION: THIS ENZYME CARRIES OUT SYNTHESIS OF THE TRNA CCA  
CC TERMINUS.  
CC -!- CATALYTIC ACTIVITY: ATP + {tRNA}(N) = diphosphate + {tRNA}(N+1).  
CC -!- SIMILARITY: BELONGS TO THE TRNA NUCLEOTIDYLTRANSFERASE / POLY(A)  
CC POLYMERASE FAMILY.  
CC -----  
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CC -----  
DR EMBL; AE000955; AAB89084.1; -.  
DR PIR; D69519; D69519.  
DR TIGR; AF2156; -.  
DR InterPro; IPR002934; NTP transf.  
DR Pfam; PF01909; NTP\_transf\_2; 1.  
DR PIRSF; PIRSF005335; CCA-adding\_enz; 1.  
KW Transferase; Nucleotidyltransferase; RNA-binding; tRNA processing;  
KW Complete proteome.  
SQ SEQUENCE 437 AA; 51385 MW; C5D57122F63CAC97 CRC64;  
  
Query Match 9.9%; Score 7; DB 1; Length 437;  
Best Local Similarity 100.0%; Pred. No. 8.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 26 LRSAFKA 32  
Db 316 LRSAFKA 322  
  
RESULT 12  
NMT\_CANAL  
ID NMT\_CANAL STANDARD; PRT; 451 AA.  
AC P30418;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Glycylpeptide N-tetradecanoyltransferase (EC 2.3.1.97) (Peptide  
DE N-myristoyltransferase) (Myristoyl-CoA:protein N-myristoyltransferase)  
DE (NMT).  
GN NMT1.  
OS Candida albicans (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=5476;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92235090; PubMed=1569105;  
RA Wiegand R.C., Carr C., Minerly J.C., Pauley A.M., Carron C.P.,  
RA Langner C.A., Duronio R.J., Gordon J.I.;  
RT "The Candida albicans myristoyl-CoA:protein N-myristoyltransferase  
RT gene. Isolation and expression in Saccharomyces cerevisiae and  
RT Escherichia coli.";  
RL J. Biol. Chem. 267:8591-8598(1992).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.45 ANGSTROMS).  
RX MEDLINE=98162557; PubMed=9501915;  
RA Weston S.A., Camble R., Colls J., Rosenbrock G., Taylor I.,  
RA Egerton M., Tucker A.D., Tunnicliffe A., Mistry A., Mancía F.,  
RA de la Fortelle E., Irwin J., Bricogne G., Paupic R.A.;  
RT "Crystal structure of the anti-fungal target N-myristoyl  
RT transferase.";  
RL Nat. Struct. Biol. 5:213-221(1998).  
CC -!- FUNCTION: Adds a myristoyl group to the N-terminal glycine residue  
CC of certain cellular proteins.  
CC -!- CATALYTIC ACTIVITY: Tetradecanoyl-CoA + glycyl-peptide = CoA + N-  
CC tetradecanoylglycyl-peptide.  
CC -!- SUBUNIT: Monomer.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: BELONGS TO THE NMT FAMILY.  
CC -----  
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CC -----  
DR EMBL; M80544; AAA34351.1; -.  
DR PIR; A38099; A38099.  
DR PDB; 1NMT; 16-FEB-99.  
DR PDB; 1YK; 30-DEC-02.  
DR PDB; 1YVL; 30-DEC-02.  
DR InterPro; IPR000903; Nmt.  
DR Pfam; PF01233; NMT; 1.  
DR Pfam; PF02799; NMT\_C; 1.  
DR PROSITE; PS00975; NMT\_1; 1.  
DR PROSITE; PS00976; NMT\_2; 1.  
KW Transferase; Acyltransferase; 3D-structure.  
KW STRAND  
FT 61 62  
FT HELIX  
FT 69 71  
FT TURN  
FT 81 82  
FT STRAND  
FT 83 87  
FT TURN  
FT 90 91  
FT HELIX  
FT 93 106  
FT TURN  
FT 109 110  
FT TURN  
FT 113 114  
FT STRAND  
FT 115 117  
FT HELIX  
FT 121 128  
FT TURN  
FT 131 132  
FT HELIX  
FT 135 137  
FT STRAND  
FT 138 143  
FT TURN  
FT 144 146  
FT STRAND  
FT 149 162  
FT TURN  
FT 163 166  
FT STRAND  
FT 167 179  
FT HELIX  
FT 181 183  
FT TURN  
FT 184 185  
FT HELIX  
FT 189 202  
FT TURN  
FT 203 204  
FT STRAND  
FT 208 212  
FT STRAND  
FT 221 229  
FT HELIX  
FT 232 237  
FT TURN  
FT 238 239  
FT TURN  
FT 245 246



FT HELIX 249 256  
FT TURN 265 266  
FT STRAND 267 269  
RT HELIX 272 274  
FT HELIX 275 285  
FT HELIX 286 288  
FT STRAND 291 294  
FT HELIX 297 305  
FT TURN 309 310  
FT STRAND 316 322  
FT TURN 324 325  
FT STRAND 328 336  
FT STRAND 339 341  
FT STRAND 349 350  
FT STRAND 352 360  
FT HELIX 361 364  
FT TURN 366 367  
FT HELIX 368 383  
FT HELIX 384 386  
FT TURN 387 387  
FT STRAND 390 394  
FT TURN 397 398  
FT HELIX 399 401  
FT TURN 402 402  
FT HELIX 403 406  
FT TURN 407 407  
FT STRAND 409 420  
FT TURN 421 421  
FT STRAND 422 423  
FT STRAND 431 431  
FT TURN 433 435  
FT STRAND 438 438  
FT TURN 440 441  
FT STRAND 446 446  
SQ SEQUENCE 451 AA; 51877 MW; 7D107CBC05458D2D CRC64;

Query Match  
Best Local Similarity 9.9%; Score 7; DB 1; Length 451;  
Matches 7; Conservativity 100.0%; Pred. No. 8.9;  
0; Mismatches 0; Indels 0; Gaps 0;

QY 58 PKLGLR 64  
Db 262 PKLGLR 268

RESULT 13  
GUAN\_MOUSE  
ID GUAN\_MOUSE STANDARD; PRT; 116 AA.  
AC P33680;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Guanylin precursor (Guanylate cyclase activator 2A).  
GN GUCA2A OR GUCA2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Small Intestine;  
RX MEDLINE=93028409; PubMed=1409606;  
RA de Sauvage F.J., Keshav S., Kuang W.J., Gillett N., Henzel W.,  
RA Goeddel D.V.;  
RT "Precursor structure, expression, and tissue distribution of human  
RT guanylin.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:9089-9093(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Kato J., Wiegand R.C., Currie M.G.;  
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.

RC STRAIN=129/Sv;  
RX MEDLINE=95229161; PubMed=7713512;  
RA Sciaky D., Kosiba J.L., Cohen M.B.;  
RT "Genomic sequence of the murine guanylin gene.";  
RL Genomics 24:583-587(1994).  
CC -1- FUNCTION: ENDOGENOUS ACTIVATOR OF INTESTINAL GUANYLATE CYCLASE.  
CC IT STIMULATES THIS ENZYME THROUGH THE SAME RECEPTOR BINDING REGION  
CC AS THE HEAT-STABLE ENTEROTOXINS.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: LOCALIZED IN BOTH CRYPTS AND VILLI IN THE  
CC SMALL INTESTINE AND TO SUPERFICIAL EPITHELIAL CELLS IN THE COLON.  
CC -1- SIMILARITY: BELONGS TO THE GUANYLIN FAMILY. ALSO SIMILAR TO HEAT-  
CC STABLE ENTEROTOXINS.  
CC -----  
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CC -----  
DR EMBL; M95175; AAA37758.1; -;  
DR EMBL; L05516; AAA37715.1; -;  
DR EMBL; U60528; AAB05758.1; -;  
DR PIR; A55643; B46279.  
DR HSSP; Q02747; IGNA.  
DR MGD; MGI:102738; Guca2.  
DR InterPro; IPR000879; Guanylin.  
DR Pfam; PF02058; Guanylin; 1.  
DR PRINTS; PR00774; GUANYLIN.  
DR ProDom; PD005588; Guanylin; 1.  
KW Signal.  
FT SIGNAL 1 23 POTENTIAL.  
FT PROPEP 24 101  
FT PEPTIDE 102 116 GUANYLIN.  
FT DISULFID 105 113 BY SIMILARITY.  
FT DISULFID 108 116 BY SIMILARITY.  
SQ SEQUENCE 116 AA; 12466 MW; 272E0D87C20869C7 CRC64;

Query Match  
Best Local Similarity 8.5%; Score 6; DB 1; Length 116;  
Matches 6; Conservativity 100.0%; Pred. No. 30;  
0; Mismatches 0; Indels 0; Gaps 0;

QY 59 KLKGLR 64  
Db 38 KLKGLR 43

RESULT 14  
YGAE\_ERWAM  
ID YGAE\_ERWAM STANDARD; PRT; 164 AA.  
AC P35675;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein in gale 3' region (Fragment).  
DE Erwinia amylovora.  
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Erwinia.  
OX NCBI\_TaxID=552;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BA7/74;  
RX MEDLINE=94117381; PubMed=7507102;  
RA Metzger M., Bellemann P., Bugert P., Geider K.;  
RT "Genetics of galactose metabolism of Erwinia amylovora and its  
RT influence on polysaccharide synthesis and virulence of the fire  
RT blight pathogen.";  
RL J. Bacteriol. 176:450-459(1994).  
CC -1- SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY.  
CC -----  
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DR EMBL; X76172; CAA53768.1; -.  
DR PIR; B36951; B36951.  
DR HSSP; P27830; 1BHK.  
DR InterPro; IPR001509; Epimerase\_Dh.  
DR Pfam; PF01370; Epimerase; 1.  
KW Hypothetical protein.  
FT NON\_TER 164 164  
SQ SEQUENCE 164 AA; 18161 MW; A817E62C1F5580AC CRC64;

Query Match 8.5%; Score 6; DB 1; Length 164;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 LNIDKL 26  
Db 29 LNIDKL 34

RESULT 15  
YNIB\_ECOLI

ID YNIB\_ECOLI STANDARD; PRT; 178 AA.

AC P76208;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein yniB.

GN YNIB OR B1726.

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI\_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1474(1997).

CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -|- SIMILARITY: STRONG, TO Y.PESTIS YFEE.

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CC -----

DR EMBL; AE000267; AAC74796.1; -.

DR PIR; F64931; F64931.

DR Ecogene; EG13987; yniB.

KW Hypothetical protein; Transmembrane; Complete proteome.

FT TRANSMEM 15 35 POTENTIAL.

FT TRANSMEM 80 100 POTENTIAL.

FT TRANSMEM 158 178 POTENTIAL.

SQ SEQUENCE 178 AA; 20367 MW; 2BAB6884D37E9E36 CRC64;

Query Match 8.5%; Score 6; DB 1; Length 178;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NTPFLN 22

Db 64 NTPFLN 69

Search completed: November 28, 2003, 13:43:20  
Job time : 14 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 13:42:24 ; Search time 29 Seconds

(without alignments)  
631.784 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Perfect score: 71

Sequence: 1 EEEETIENYASRPEAFNTPF.....LNWDAFPKLGKRSATPDAQ 71

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteria:\*
- 17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	11.3	390	16 Q8ETM3	Q8etm3 oceanobacil
2	7	9.9	173	16 Q8D808	Q8d808 vibrio vuln
3	7	9.9	238	10 Q9LTX0	Q9ltx0 arabidopsis
4	7	9.9	282	10 Q8W313	Q8w313 oryza sativ
5	7	9.9	284	5 Q9BLQ8	Q9blq8 leishmania
6	7	9.9	329	16 Q8Z2W5	Q8z2w5 salmonella
7	7	9.9	354	10 Q9FHE9	Q9fhe9 arabidopsis
8	7	9.9	354	13 Q90YL8	Q90yl8 brachydanio
9	7	9.9	354	13 Q90YL8	Q90yl8 brachydanio
10	7	9.9	372	12 Q8V2W9	Q8v2w9 camelopard
11	7	9.9	372	12 Q8V2W9	Q8v2w9 variola vir
12	7	9.9	437	11 Q9D496	Q9d496 mus musculu
13	7	9.9	477	2 Q9AQL1	Q9aql1 porphyromon
14	7	9.9	541	12 Q9EMJ0	Q9emj0 ambsacta moo
15	7	9.9	793	5 Q95Q83	Q95q83 caenorhabdi
16	7	9.9	796	5 Q95Q84	Q95q84 caenorhabdi

17	7	9.9	867	10 Q9FZE6	Q9fze6 arabidopsis
18	7	9.9	1077	13 Q8UTW6	Q8utw6 tribolodon
19	7	9.9	1088	13 Q8AYH7	Q8ayh7 oncornychnu
20	7	9.9	1566	5 Q8WZD0	Q8wzd0 drosophila
21	7	9.9	1566	5 Q9VJT4	Q9vjt4 drosophila
22	7	9.9	1577	5 Q9NKC7	Q9nkc7 drosophila
23	6	8.5	69	12 Q912H0	Q912h0 human echov
24	6	8.5	76	4 Q9PIC0	Q9pic0 homo sapien
25	6	8.5	76	12 Q912I5	Q912i5 human coxa
26	6	8.5	85	12 Q912F8	Q912f8 human echov
27	6	8.5	90	12 Q912I7	Q912i7 human coxa
28	6	8.5	96	12 Q912G3	Q912g3 human echov
29	6	8.5	96	15 Q83374	Q83374 murine leuk
30	6	8.5	99	12 Q912I6	Q912i6 human coxa
31	6	8.5	101	2 Q9Z5F2	Q9z5f2 pseudomonas
32	6	8.5	102	12 Q9JTA62	Q9ja62 human coxa
33	6	8.5	103	12 Q912G2	Q912g2 human echov
34	6	8.5	106	12 Q912G1	Q912g1 human echov
35	6	8.5	112	5 Q9VFU2	Q9vfuz drosophila
36	6	8.5	127	16 Q8FKP9	Q8fkp9 escherichia
37	6	8.5	129	11 Q9CQ03	Q9cqp3 mus musculu
38	6	8.5	131	5 Q9VUZ9	Q9vuz9 drosophila
39	6	8.5	131	16 Q8YU76	Q8yu76 anabaena sp
40	6	8.5	132	16 Q8NSE0	Q8nse0 corynebacte
41	6	8.5	133	5 Q9GYU7	Q9gyu7 drosophila
42	6	8.5	137	4 Q96EW8	Q96ew8 homo sapien
43	6	8.5	144	9 Q8W766	Q8w766 bacterioph
44	6	8.5	145	2 Q9EW39	Q9ew39 streptococ
45	6	8.5	149	10 Q9FSN5	Q9fsn5 oryza sativ

#### ALIGNMENTS

##### RESULT 1

Q8ETM3 PRELIMINARY; PRT; 390 AA.

AC Q8ETM3; 01-MAR-2003 (Tremblrel. 23, Created)

DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)

DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)

DE Hypothetical protein.

GN OB0237.

OS Oceanobacillus iheyensis.

OC Bacteria; Firmicutes; Bacillales; Oceanobacillus.

OX NCBI\_TaxID=182710;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=HTE831 / DSM 14371 / JCM 11309;

RX MEDLINE=22220767; PubMed=12235376;

RA Takami H., Takaki Y., Uchiyama I.;

RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments.";

RT Nucleic Acids Res. 30:3927-3935(2002).

DR EMBL; AP004593; BAC12193.1; -.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 390 AA; 43262 MW; B2CE189BE0A63D2B CRC64;

Query Match 11.3%; Score 8; DB 16; Length 390;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 PFLNIDKL 26  
|||  
Db 200 PFLNIDKL 207

RESULT 2

Q8D808 PRELIMINARY; PRT; 173 AA.

AC Q8D808; 01-MAR-2003 (Tremblrel. 23, Created)

DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
DE Hypothetical protein.  
GN V13186.  
OS *Vibrio vulnificus*.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; *Vibrio*.  
OX NCBI\_TaxID=672;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CMCP6;  
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,  
RA Choy H.E.;  
RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.";  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB016807; AA01501.1; -  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 173 AA; 19836 MW; EE70E83D96A7CE3F CRC64;  
  
Query Match 9.9%; Score 7; DB 16; Length 173;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Oy 23 IDKLRS 29  
Db 59 IDKLRS 65  
  
RESULT 3  
O9LTXO PRELIMINARY; PRT; 238 AA.  
AC O9LTXO;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)  
DE Hypothetical protein (AT3912650/T2E22\_103).  
GN T2E22.4.  
OS *Arabidopsis thaliana* (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; *Arabidopsis*.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COLUMBIA;  
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COLUMBIA;  
RA MEDLINE=20277480; PubMed=10819329;  
RA Nakamura Y.;  
RT "Structural analysis of *Arabidopsis thaliana* chromosome 3. I. Sequence  
RT features of the regions of 4,504,864 bp covered by sixty p1 and TAC  
RT clones.";  
RL DNA Res. 7:131-135(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RA MEDLINE=21016720; PubMed=11130713;  
RA Salanoubat M., Lemcke K., Rieger M., Ansgorge W., Unsel M.,  
RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,  
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,  
RA De Simone V., Choise N., Artiguenave F., Robert C., Broctier P.,  
RA Wincker P., Catolico L., Weissenbach J., Saurin W., Quetier F.,  
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,  
RA Wurmbach E., Drzonek H., Erle H., Jordan N., Bangert S.,  
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,  
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,  
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,  
RA Reichelt J., Scharfe M., Schoen O., Baryes M., Terol J., Clement J.,  
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,  
RA Cooke R., Laudie M., Berger-Llauro C., Furnelle B., Maury D.,

RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,  
RA Monfort A., Argiou A., Flores M., Liguori R., Vitale D.,  
RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,  
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,  
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,  
RA Creasy T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,  
RA Pai G., Miltscher J., Sellers P., Gill J.E., Feldblyum T.V.,  
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,  
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,  
RA Sasamoto S., Kimura T., Ideasa K., Kawashima K., Kishida Y.,  
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,  
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;  
RT "Sequence and analysis of chromosome 3 of the plant *Arabidopsis*  
RT *thaliana*.";  
RL Nature 408:820-822(2000).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,  
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,  
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,  
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,  
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,  
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,  
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,  
RA Ecker J.R.;  
RT "Arabidopsis cDNA clones.";  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Kim C.J., Chen H., Cheuk R., Shin P., Banh J., Bowser L.,  
RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,  
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,  
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,  
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,  
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;  
RT "Arabidopsis ORF clones.";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB024033; BAB02408.1; -  
DR EMBL; AC069474; AAG51037.1; -  
DR EMBL; AY057658; AAL15289.1; -  
DR EMBL; AY113015; AAM47323.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 238 AA; 26887 MW; EB2A551B3C005D7C CRC64;  
  
Query Match 9.9%; Score 7; DB 10; Length 238;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Oy 22 NIDKLRS 28  
Db 57 NIDKLRS 63  
  
RESULT 4  
O8W313 PRELIMINARY; PRT; 282 AA.  
AC O8W313;  
DT 01-MAR-2002 (Tremblrel. 20, Created)  
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
DE Cysteine synthase, 5'-partial (Fragment).  
GN OSJNBA0069E14.1.  
OS *Oryza sativa* (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; *Oryza*.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Nipponbare;  
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,

```
RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA Tseltrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G.,
RA Vanaken S.E., Uteback T.R., Feldblum T.V., Kalb E., Quackenbush J.,
RA Salzberg S.L., White O., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSJNBa0069E14 genomic sequence.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC091811; AAL58961.1; -.
DR Gramene; Q8W313; -.
DR InterPro; IPR001926; B6_enzyme_beta.
DR InterPro; IPR005859; Cys_synthK.
DR InterPro; IPR005856; Cys_synthK.
DR Pfam; PF00291; PALP; 1.
DR TIGRFAMs; TIGR01139; cysK; 1.
DR TIGRFAMs; TIGR01136; cysKM; 1.
FT NON_TER 1
SQ SEQUENCE 282 AA; 29892 MW; 3503D2F3CA80EF5 CRC64;

Query Match
Best Local Similarity 9.9%; Score 7; DB 10; Length 282;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 LFESIKR 47
Db 267 LFESIKR 273

RESULT 5
Q9BLQ8 PRELIMINARY; PRT; 284 AA.
AC Q9BLQ8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE 6-pass transmembrane protein L654.12.
GN L654.12.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RA Tosato V., Ciaroni L., Bianchetti G., Bruschi C.V., Ivens A.C.,
RA Quail M., Rajandream M.A., Barrell B.G.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL; AL512294; CAC29460.1; -.
DR InterPro; IPR002076; GNS1_SUR4.
DR Pfam; PF01151; ELO; 1.
KW Transmembrane.
SQ SEQUENCE 284 AA; 32575 MW; B845BEE11D6CE9A0 CRC64;

Query Match
Best Local Similarity 9.9%; Score 7; DB 5; Length 284;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 KRKLPL 52
Db 137 KRKLPL 143

RESULT 6
Q8Z2W5 PRELIMINARY; PRT; 329 AA.
AC Q8Z2W5;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
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DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Periplasmic sulphate binding protein.
GN STY3808.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagers K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
DR EMBL; AL627279; CAD09561.1; -.
DR InterPro; IPR006059; SBP_bac_1.
DR InterPro; IPR000957; Sulphate_bind.
DR InterPro; IPR005669; Thiosulph_bind.
DR Pfam; PF01547; SBP_bac_1; 1.
DR Prodom; PD008688; Sulphate_bind; 1.
DR TIGRFAMs; TIGR00971; Jaa106s03; 1.
DR PROSITE; PS00401; PROK_SULFATE_BIND_1; 1.
DR PROSITE; PS00757; PROK_SULFATE_BIND_2; 1.
KW Complete proteome.
SQ SEQUENCE 329 AA; 36496 MW; 100FD9CC32C050AF CRC64;

Query Match
Best Local Similarity 9.9%; Score 7; DB 16; Length 329;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 DAFPKLK 61
Db 292 DAFPKLK 298

RESULT 7
Q9FHE9 PRELIMINARY; PRT; 354 AA.
AC Q9FHE9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Similarity to disease resistance protein.
OS Arabidopsis thaliana (mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones."
RL DNA Res. 7:31-63(2000).
DR EMBL; AB019224; BAB09490.1; -.
DR InterPro; IPR000157; TIR_domain.
DR Pfam; PF01582; TIR; 1.
DR SMART; SMO0255; TIR; 1.
DR PROSITE; PS50104; TIR; 1.
SQ SEQUENCE 354 AA; 40106 MW; 2E2A1B525B377997 CRC64;
```



Query Match 9.9%; Score 7; DB 10; Length 354;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 58 PKLGLR 64  
|||  
149 PKLGLR 155

Db

RESULT 8

O90YL8 PRELIMINARY; PRT; 354 AA.

AC Q90YL8;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Wnt8-like protein 2.  
GN WNT8.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lekven A.C., Thorpe C.J., Waxman J.S., Moon R.T.;  
RT "Zebrafish wnt8 encodes two Wnt8 proteins on a bicistronic transcript and is required for mesoderm and neuroectoderm patterning.";  
RL Dev. Cell 1:0-0(2001).  
DR EMBL; AY032749; AAK70224.1; -.  
DR InterPro; IPR005817; Wnt.  
DR Pfam; PF00110; wnt; 1.  
DR PRINTS; PR01349; WNTPROTEIN.  
DR SMART; SM00097; WNT1; 1.  
SQ SEQUENCE 354 AA; 40109 MW; F42951A27AC38A67 CRC64;

Query Match 9.9%; Score 7; DB 13; Length 354;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 61 KGLRSAT 67  
|||  
76 KGLRSAT 82

Db

RESULT 9

O90YJ8 PRELIMINARY; PRT; 354 AA.

AC Q90YJ8;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Wnt8-like protein 2.  
GN WNT8.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lekven A.C., Thorpe C.J., Waxman J.S., Moon R.T.;  
RT "Zebrafish wnt8 encodes two Wnt8 proteins on a bicistronic transcript and is required for mesoderm and neuroectoderm patterning.";  
RL Dev. Cell 1:0-0(2001).  
DR EMBL; AY032749; AAK70224.1; -.  
DR InterPro; IPR005817; Wnt.  
DR Pfam; PF00110; wnt; 1.  
DR PRINTS; PR01349; WNTPROTEIN.  
DR SMART; SM00097; WNT1; 1.  
SQ SEQUENCE 354 AA; 40109 MW; F42951A27AC38A67 CRC64;

Query Match 9.9%; Score 7; DB 13; Length 354;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 61 KGLRSAT 67  
|||  
76 KGLRSAT 82

Db

RESULT 10

O8V2W9 PRELIMINARY; PRT; 372 AA.

AC Q8V2W9;  
DT 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Putative EBV envelope lipase (CMP48L).  
GN CMP48L.  
OS Camel痘 virus (strain CP-1).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=203174;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Alfonso C.L., Tulman E.R., Lu Z., Zsak L., Zaitsev V.L.,  
RC STRAIN=M-96;  
RA Kerembekova U.Z., Sandybaev N.T., Kutish G.F., Rock D.L.;  
RT "The genome of camel痘 virus.";  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CMS;  
RX PubMed=11907336;  
RA Gubser C., Smith G.L.;  
RT "The sequence of camel痘 virus shows it is most closely related to variola virus, the cause of smallpox.";  
RL J. Gen. Virol. 83:855-872(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CMS;  
RA Gubser C., Smith G.L.;  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF438165; AAL73755.1; -.  
DR EMBL; AY009089; AAG37509.1; -.  
DR InterPro; IPR001736; PLD.  
DR Pfam; PF00614; PLDC; 2.  
DR SMART; SM00155; PLDC; 2.  
DR PROSITE; PS50035; PLD; 1.  
SQ SEQUENCE 372 AA; 41914 MW; DFC025644501B151 CRC64;

Query Match 9.9%; Score 7; DB 12; Length 372;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 IDKLSA 29  
|||  
224 IDKLSA 230

Db

RESULT 11

O85369 PRELIMINARY; PRT; 372 AA.

AC Q85369;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Homolog of VACCINIA virus CDS F13L.

DR InterPro; IPR005816; Wnt\_grchfactor.  
DR Pfam; PF00110; wnt; 1.  
DR PRINTS; PR01349; WNTPROTEIN.  
DR SMART; SM00097; WNT1; 1.  
SQ SEQUENCE 354 AA; 40065 MW; B25CEDFB7453FD37 CRC64;

Query Match 9.9%; Score 7; DB 13; Length 354;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 61 KGLRSAT 67  
|||  
76 KGLRSAT 82

Db

RESULT 10

O8V2W9 PRELIMINARY; PRT; 372 AA.

AC Q8V2W9;  
DT 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Putative EBV envelope lipase (CMP48L).  
GN CMP48L.  
OS Camel痘 virus (strain CP-1).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=203174;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Alfonso C.L., Tulman E.R., Lu Z., Zsak L., Zaitsev V.L.,  
RC STRAIN=M-96;  
RA Kerembekova U.Z., Sandybaev N.T., Kutish G.F., Rock D.L.;  
RT "The genome of camel痘 virus.";  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CMS;  
RX PubMed=11907336;  
RA Gubser C., Smith G.L.;  
RT "The sequence of camel痘 virus shows it is most closely related to variola virus, the cause of smallpox.";  
RL J. Gen. Virol. 83:855-872(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CMS;  
RA Gubser C., Smith G.L.;  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF438165; AAL73755.1; -.  
DR EMBL; AY009089; AAG37509.1; -.  
DR InterPro; IPR001736; PLD.  
DR Pfam; PF00614; PLDC; 2.  
DR SMART; SM00155; PLDC; 2.  
DR PROSITE; PS50035; PLD; 1.  
SQ SEQUENCE 372 AA; 41914 MW; DFC025644501B151 CRC64;

Query Match 9.9%; Score 7; DB 12; Length 372;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 IDKLSA 29  
|||  
224 IDKLSA 230

Db

RESULT 11

O85369 PRELIMINARY; PRT; 372 AA.

AC Q85369;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Homolog of VACCINIA virus CDS F13L.

```

GN C17L OR E13L.
OS Variola virus, and
OS Variola minor virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255, 53258;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Variola virus; STRAIN=BANGLADESH-1975;
RX MEDLINE=94088747; PubMed=8264798;
RA Masung R.F., Esposito J.J., Liu L.I., Qi J., Utterback T.R.,
RA Knight J.C., Aubin L., Yuran T.B., Parsons J.M., Loparev V.N.;
RT "Potential virulence determinants in terminal regions of variola
RT smallpox virus genome.";
RL Nature 366:748-751(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=variola minor virus; STRAIN=GARCIA-1966;
RA Shchelkunov S.N., Tolmenin A.V., Gutorov V.V., Safronov P.F.,
RA Masung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
RA Esposito J.J., Sosnovtsev S.;
RT "Analysis of the complete coding sequence of DNA of alastrim variola
RT minor virus strain Garcia-1966.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; L22579; AAA60785.1; -
DR EMBL; Y16780; CAB54637.1; -
DR InterPro; IPR001736; PLD.
DR Pfam; PF00614; PLDC; 2.
DR SMART; SM00155; PLDC; 2.
DR PROSITE; PS50035; PLD; 1.
SQ SEQUENCE 372 AA; 41929 MW; C7711FBA9C212E14 CRC64;

Query Match
Best Local Similarity 9.9%; Score 7; DB 12; Length 372;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 IDKLRSA 29
Db 224 IDKLRSA 230

RESULT 12
Q9D496 PRELIMINARY; PRT; 437 AA.
AC Q9D496;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 4930548H24Rik protein.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gueirincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,

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RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK016690; BAB30382.1; -
DR MGD; MGI:1914906; 4930548H24Rik.
SQ SEQUENCE 437 AA; 50470 MW; F1C862ED6B16526B CRC64;

Query Match
Best Local Similarity 9.9%; Score 7; DB 11; Length 437;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ESIXRKL 49
Db 384 ESIXRKL 390

RESULT 13
Q9AQL1 PRELIMINARY; PRT; 477 AA.
AC Q9AQL1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE DNA gyrase B subunit (Fragment).
GN GYRB.
OS Porphyromonas levi.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=28114;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29147;
RA Suzuki M., Takadera T., Harayama S., Yamamoto S.;
RT "Diversity of marine Cytophaga-like bacteria: Phylogenetic analysis
RT using gyrb sequences and their carotenoids profiles.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
DR EMBL; AB048189; BAB33156.1; -
DR HSSP; P06982; 1A56.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR001241; DNA_topoisom.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF01751; Toprim; 1.
DR PRINTS; PR00418; TP12FAMILY.
DR SMART; SM00433; TOP2C; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
KW ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 477 AA; 53457 MW; C88B7FA1536E16D CRC64;

Query Match
Best Local Similarity 9.9%; Score 7; DB 2; Length 477;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 LINDKLR 27
Db 388 LINDKLR 394

RESULT 14
Q9EMJ0 PRELIMINARY; PRT; 541 AA.
AC Q9EMJ0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE AMV216.
GN AMV216.

```

OS Amsacta moorei entomopoxvirus (AMEPV).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;  
OC Entomopoxvirus B.  
OX NCBI\_TaxID=28321;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20396580; PubMed=10936094;  
RA Bawden A.L., Glassberg K.J., Diggs J., Shaw R., Farmerie W.,  
Moyer R.W.;  
RT "Complete Genomic Sequence of the Amsacta moorei Entomopoxvirus:  
RT Analysis and Comparison with Other Poxviruses.";  
RL Virology 274:120-139(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Bawden A.L., Glassberg K.J., Diggs J., Shaw R., Farmerie W.,  
Moyer R.W.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF250284; AAG02922.1; -  
SQ SEQUENCE 541 AA; 63508 MW; 669A703BA055EF84 CRC64;

Query Match 9.9%; Score 7; DB 12; Length 541;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ESTIENY 9  
Db 477 ESTIENY 483

## RESULT 15

O95Q83 PRELIMINARY; PRT; 793 AA.  
ID O95Q83  
AC O95Q83;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Hypothetical 87.4 kDa protein.  
GN C17H11.6.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RA None;  
RT "Genome sequence of the nematode C. elegans: a platform for  
RT investigating biology. The C. elegans Sequencing Consortium.";  
RL Science 282:2012-2018(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Johnson D.;  
RT "The sequence of C. elegans cosmid C17H11.";  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Waterston R.;  
RT "Direct Submission.";  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
DR EMBL; U80847; AAK68189.1; -  
DR WormPep; C17H11.6a; CE27704.  
DR InterPro; IPR006895; zf-Sec23\_Sec24.  
DR InterPro; IPR002867; znf\_C6HC.  
DR InterPro; IPR001841; znf\_ring.  
DR Pfam; PF01485; IIR; 1.  
DR Pfam; PF00097; zf-C3HC4; 1.  
DR Pfam; PF04810; zf-Sec23\_Sec24; 1.  
DR SMART; SMO0647; IIR; 2.  
DR SMART; SMO0184; RING; 2.

DR PROSITE; PSS0089; ZF\_RING\_2; 1.  
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.  
SQ SEQUENCE 793 AA; 87408 MW; 6FD1C98F1809C9D4 CRC64;

Query Match 9.9%; Score 7; DB 5; Length 793;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 56 AFPKLKG 62  
Db 96 AFPKLKG 102

Search completed: November 28, 2003, 13:44:48  
Job time : 34 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 12:18:06 ; Search time 1605 Seconds  
(without alignments)  
1075.151 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99  
Perfect score: 71  
Sequence: 1 EEBSTIENYASRPEAFNTPF.....LNMDAFPKLGKLSATPDAQ 71

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Word size: 1

Total number of hits satisfying chosen parameters: 45562437

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=x1h  
-Q=/cgn2\_1/USPTO\_spool/US10059395/runat\_25112003\_140940\_8064/app\_query.fasta\_1.263  
-DB=EST -QFMT=fastap -SUFFIX=ol1.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10059395 @CGN 1 1 2810 @runat\_25112003\_140940\_8064 -NCPU=6 -ICPU=3  
-NO\_MMALP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : EST: \*  
1: em\_estba: \*  
2: em\_esthum: \*  
3: em\_estin: \*  
4: em\_estmu: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_htc: \*  
9: gb\_est1: \*  
10: gb\_est2: \*  
11: gb\_htc: \*  
12: gb\_est3: \*  
13: gb\_est4: \*  
14: gb\_est5: \*  
15: em\_estfun: \*  
16: em\_estom: \*  
17: em\_gss\_hum: \*  
18: em\_gss\_inv: \*  
19: em\_gss\_pln: \*  
20: em\_gss\_vrt: \*  
21: em\_gss\_fun: \*  
22: em\_gss\_mam: \*  
23: em\_gss\_mus: \*  
24: em\_gss\_pro: \*  
25: em\_gss\_rtd: \*  
26: em\_gss\_phg: \*  
27: em\_gss\_vrt: \*  
28: gb\_gss1: \*

29: gb\_gss2: \*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	71	100.0	318	9 AA586846	AA586846 nm67e11.s
2	71	100.0	334	9 AA297512	AA297512 EST113061
C 3	71	100.0	339	9 AA778414	AA778414 zf39e05.s
4	71	100.0	348	9 AW238758	AW238758 xp03e08.x
C 5	71	100.0	359	10 BE466728	BE466728 hz24g06.x
C 6	71	100.0	362	9 AI140605	AI140605 qe05f03.x
C 7	71	100.0	373	9 AA722694	AA722694 zg82b06.s
C 8	71	100.0	381	14 W69108	W69108 zd44c04.s1
C 9	71	100.0	394	14 W60320	W60320 zd29g01.s1
10	71	100.0	412	14 W60268	W60268 zd29g01.r1
C 11	71	100.0	424	14 W69083	W69083 zd44b06.s1
12	71	100.0	432	13 BX112106	BX112106 BX112106
13	71	100.0	432	14 W69233	W69233 zd44c04.r1
14	59	83.1	431	14 W69227	W69227 zd44b06.r1
15	58	81.7	413	9 AA393296	AA393296 zt74f05.r
C 16	57	80.3	345	9 AI217565	AI217565 qd43d02.x
C 17	56	78.9	241	9 AA595989	AA595989 nm64g08.s
C 18	53	74.6	359	10 BG150312	BG150312 7j98g03.x
C 19	51	71.8	334	9 AI217587	AI217587 qd43f04.x
20	43	60.6	345	9 AA583942	AA583942 nm64f07.s
21	43	60.6	376	14 W95920	W95920 ze08d01.r1
C 22	39	54.9	221	9 AA584333	AA584333 nm73a09.s
23	39	54.9	326	9 AA297513	AA297513 EST113062
C 24	37	52.1	358	9 AW003825	AW003825 wg83f12.x
C 25	37	52.1	377	9 AA582988	AA582988 nm72h02.s
C 26	35	49.3	330	14 W95883	W95883 ze08d01.s1
C 27	33	46.5	218	9 AA398638	AA398638 zt74f05.s
C 28	33	46.5	239	9 AA595930	AA595930 nm66a07.s
C 29	27	38.0	339	14 W52030	W52030 zd13b01.s1
C 30	27	38.0	378	9 AI184682	AI184682 qd68b02.x
C 31	24	33.8	368	9 AW260965	AW260965 EQUK0243
C 32	24	33.8	436	9 AV597545	AV597545 AV597545
C 33	18	25.4	163	9 AA776980	AA776980 zf23d05.s
34	15	21.1	377	9 AW260982	AW260982 EQUK0196
35	14	19.7	421	9 AV618771	AV618771 AV618771
C 36	12	16.9	323	10 BE715771	BE715771 MR2-HT075
C 37	8	11.3	271	10 BE701465	BE701465 PM2-NN017
38	8	11.3	304	9 AI894297	AI894297 ms66b04.x
39	8	11.3	310	14 CD036743	CD036743 mgsu011xd
40	8	11.3	353	10 BF366304	BF366304 CML-NT008
41	8	11.3	365	10 BF735391	BF735391 CML-AN008
42	8	11.3	378	10 BF522420	BF522420 UI-R-C3-t
43	8	11.3	382	12 BI881645	BI881645 fm88g05.y
44	8	11.3	399	12 BI881568	BI881568 fm87c01.y
45	8	11.3	404	14 R80137	R80137 yi95c09.r1

ALIGNMENTS

RESULT 1  
AA586846/c 318 bp mRNA linear EST 26-SEP-1997  
LOCUS nm67e11.s1 NCI\_CGAP\_Lar1 Homo sapiens CDNA clone IMAGE:1088972 3',  
DEFINITION mRNA sequence.  
ACCESSION AA586846  
VERSION AA586846  
KEYWORDS AA586846.1 GI:2397660  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 318)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP);  
JOURNAL Tumor Gene Index  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmerit-Buck, M.D., Ph.D.  
CDNA Library Preparation: Stratagene, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/BLNL at: [www-bio.lnl.gov/bbrp/image/image.html](http://www-bio.lnl.gov/bbrp/image/image.html)  
Insert length: 465 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham.  
Location/Qualifiers  
1..318  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1088972"  
/tissue\_type="larynx"  
/lab\_host="SOLR (kanamycin resistant)"  
/clone\_lib="NCI\_CGAP\_Lar1"  
/note="Organ: larynx; Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Larynx. 5' adaptor sequence: 5' CTCGAGTTT TTT TTT TTT TTT 3', 3' adaptor sequence: 5' CTCGAGTTT TTT TTT TTT TTT 3', Average insert size: 0.9 kb."  
BASE COUNT 76 a 67 c 90 g 85 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 5.07e-68 Length: 318  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AA586846 (1-318)  
QY 1 GUGUGUSeThrIleGluAsnTYrAlaSerArpProGluAlaPheAsnThrProPhe 20  
Db 316 GAGGAAGAAAGCACCATTTGAGATTATGCGTCACGACCGAGCCCTTAACACCCGCTTC 257  
QY 21 LeuAsnIleAspIlySleuArgSerAlaPheIlySAlaAspGluPheLeuAsnTrpHisAla 40  
Db 256 CTGAACATCGACAATTGCCATCTCGCTTAAGCGCTGATGATTCTCTGAACCTGGCAGCC 197  
QY 41 LeuPheGluSerIleIySArgIySleuProPheLeuAsnTrpAspAlaPheProIySleu 60  
Db 196 CTCTTGAGTCTATCAAAAGGAACTTCCTTCTCACTGGGATGCCCTTCTTAAGCTG 137  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 136 AAAGGACTGAGAGCGCACTCTGATGCCAG 104  
RESULT 2  
AA297512 334 bp mRNA linear EST 18-APR-1997  
LOCUS: AA297512 Fetal skin Homo sapiens cDNA 5' end, mRNA sequence.  
DEFINITION: AA297512  
ACCESSION: AA297512 GI:1949866  
VERSION: AA297512.1  
KEYWORDS: EST.  
SOURCE: Homo sapiens (human)  
ORGANISM: Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 334)  
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult ,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White

,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald ,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., HungJun,J., Li,H., Meisner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon ,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.  
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  
Nature 377 (6547 Suppl), 3-174 (1995)  
96026280  
MEDLINE  
PUBMED  
7566098  
COMMENT Other\_ESTs: THC151622  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: [arkerlav@tigr.org](mailto:arkerlav@tigr.org)  
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
Seq primer: M13 Reverse.  
FEATURES  
Source  
Location/Qualifiers  
1..334  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="ATCC (inhost):141532"  
/db\_xref="taxon:9606"  
/tissue\_type="epithelium"  
/cell\_type="epithelial cell"  
/dev\_stage="fetus"  
/clone\_lib="Fetal skin"  
/note="Organ: skin; Vector: pBluescript SK-; Site 1: EcoRI ; Site 2: XhoI"  
BASE COUNT 77 a 100 c 78 g 78 t 1 others  
ORIGIN  
Alignment Scores:  
Pred. No.: 5.35e-68 Length: 334  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AA297512 (1-334)  
QY 1 GUGUGUSeThrIleGluAsnTYrAlaSerArpProGluAlaPheAsnThrProPhe 20  
Db 98 GAGGAAGAAAGCACCATTTGAGATTATGCGTCACGACCGAGCCCTTAACACCCGCTTC 157  
QY 21 LeuAsnIleAspIlySleuArgSerAlaPheIlySAlaAspGluPheLeuAsnTrpHisAla 40  
Db 158 CTGAACATCGACAATTGCCATCTCGCTTAAGCGCTGATGATTCTCTGAACCTGGCAGCC 217  
QY 41 LeuPheGluSerIleIySArgIySleuProPheLeuAsnTrpAspAlaPheProIySleu 60  
Db 218 CTCTTGAGTCTATCAAAAGGAACTTCCTTCTCACTGGGATGCCCTTCTTAAGCTG 277  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 278 AAAGGACTNAGAGCGCACTCTGATGCCAG 310



```
RESULT 3
AA778414/c      339 bp      mRNA      linear      EST 05-FEB-1998
LOCUS          2f39e05.s1 Soares fetal heart_NbHH19W Homo sapiens cDNA clone
DEFINITION     IMAGE:379328 3', mRNA sequence.
ACCESSION      AA778414
VERSION        AA778414.1 GI:2837745
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 339)
AUTHORS        Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
                Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
                , J., Moore, B., Scheilenberg, K., Steptoe, M., Tan, F., Theising, B.,
                White, Y., Wylie, T., Waterston, R. and Wilson, R.
TITLE          WashU-NCI human EST Project
JOURNAL        Unpublished
COMMENT        Contact: Wilson RK
                Washington University School of Medicine
                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                Tel: 314 286 1800
                Fax: 314 286 1810
                Email: est@watson.wustl.edu
                This clone is available royalty-free through LNL ; contact the
                IMAGE Consortium (info@image.llnl.gov) for further information.
                Seq primer: -40m3 fwd. ET from Amersham.
FEATURES       location/Qualifiers
Source         1. 339
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="GDB:1287584"
                /db_xref="taxon:9606"
                /clone="IMAGE:379328"
                /sex="unknown"
                /dev_stage="19 weeks"
                /lab_host="DH10B (ampicillin resistant)"
                /clone_lib="Soares_fetal_heart_NbHH19W"
                /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
                modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                strand cDNA was primed with a Not I - oligo(dt) primer [5'
                TGTTACCAATCTGAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'],
                double-stranded cDNA was size selected, ligated to Eco RI
                adapters (Pharmacia), digested with Not I and cloned into
                the Not I and Eco RI sites of a modified pT7T3 vector
                (Pharmacia). Library went through one round of
                normalization to a Cot = 5. Library constructed by
                M.Fatima Bonaldo. This library was constructed from the
                same fetus as the fetal lung library, Soares fetal lung
                NbHL19W."
BASE COUNT     79 a      77 c      96 g      87 t
ORIGIN
Alignment Scores:
Pred. No.:      5.44e-68      Length:      339
Score:          71.00         Matches:      71
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels: 0
DB:             9            Gaps: 0
US-10-059-395-142_COPY_29_99 (1-71) x AA778414 (1-339)
QY             1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20
Db             316 GAGGAAGAAAGCACCATTCGATATGCGTCACGACCGAGCCCTTTAACACCCCGTTC 257
QY             21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnTrpHisAla 40
Db             256 CTGAACATCGACAATTCGATCTCGCTTAAGGCTGATGAGTTCCTGAACTGGCAGCC 197
QY             41 LeuPheGluSerIleIysArgIysLeuProPheLeuAsnTrpAspAlaPheProIysLeu 60
```

```
RESULT 4
AW238758      348 bp      mRNA      linear      EST 13-DEC-1999
LOCUS          xp03e08.x1 NCI_CGAP_HN8 Homo sapiens cDNA clone IMAGE:2739302 3',
DEFINITION     mRNA sequence.
ACCESSION      AW238758
VERSION        AW238758.1 GI:6571147
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 348)
AUTHORS        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                Tumor Gene Index
JOURNAL        Unpublished
COMMENT        Contact: Robert Strausberg, Ph.D.
                Email: cga@bbs-r@mail.nih.gov
                Tissue Procurement: Edward Shillitoe Ph.D., Silvio Gutkind Ph.D.,
                Chidchanok Leethanakul D.D.S., Michael Emmert-Buck M.D. Ph.D.
                cDNA Library Preparation: David B. Krizman, Ph.D.
                DNA Sequencing by: Washington University Genome Sequencing Center
                Clone distribution: NCI-CGAP clone distribution information can be
                found through the I.M.A.G.E. Consortium/LNL at:
                www-bio.llnl.gov/bbrp/image/image.html
FEATURES       Possible reversed clone: polyT not found
                Seq primer: -40UP from Gibco
                High quality sequence stop: 331.
                location/Qualifiers
Source         1. 348
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:2739302"
                /tissue_type="well-differentiated invasive carcinoma,
                floor of mouth"
                /lab_host="DH10B"
                /clone_lib="NCI CGAP HN8"
                /note="Vector: pAMP10; cDNA made by oligo-dT priming.
                Non-directionally cloned into the UDG sites of pAMP10.
                Size-selected on agarose gel, average insert size 500 bp.
                Primary library; non-amplified. cDNA library
                Preparation: David B. Krizman, Ph.D (NCI). Reference:
                Krizman et al. (1996) Cancer Research 56:5380-5383."
BASE COUNT     82 a      104 c      84 g      78 t
ORIGIN
Alignment Scores:
Pred. No.:      5.6e-68      Length:      348
Score:          71.00         Matches:      71
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels: 0
DB:             9            Gaps: 0
US-10-059-395-142_COPY_29_99 (1-71) x AW238758 (1-348)
QY             1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20
Db             81 GAGGAAGAAAGCACCATTCGATATGCGTCACGACCGAGGCTTTAACACCCCGTTC 140
QY             21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnTrpHisAla 40
```

Db 141 CTGAACATCGACAATGCGATCTGCGTTTAAAGCTGATGAGTTCCTGAACTGGCAGCC 200

Qy 41 LeuPheGluSerIleYsArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
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Db 201 CTCTTGAGTCTATCAAAAGAACTTCCTTCTCAACTGGAGATGCCCTTCTTAAGCTG 260

Qy 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
|||||  
Db 261 AAAGGACTGAGGAGCGCAACTCTGATGCCAG 293

RESULT 5  
BE466728/c 359 bp mRNA linear EST 27-JUL-2000  
LOCUS h224G06.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:3208954 3',  
DEFINITION mRNA sequence.  
ACCESSION BE466728  
VERSION BE466728.1 GI:9512503  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 359)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL, send email to:  
info@image.lnl.gov  
Seq primer: -40UP from Gibco.  
FEATURES  
source  
1. 359  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3208954"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP GC6"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA  
from the normalized library NCI CGAP GC4 was prepared, and  
88 circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (cloneIDs  
1257096-1258631, 1469064-1470983, and 1475592-1476743).  
Subtraction by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 77 a 80 c 96 g 106 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 5.79e-68 Length: 359  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x BE466728 (1-359)

Qy 1 GluGluGluSerThrIleGluAsnTrpAlaSerArgProGluAlaPheAsnThrProPhe 20  
|||||  
Db 332 GAGAGAGAAAGCACCATGAGATATATGCGTCACGACCGCGCCCTTTAAACACCCCGTTTC 273

Qy 21 LeuAsnIleAspLysLeuArgSerAlaPheYsAlaAspGluPheLeuAsnTrpHisAla 40  
|||||  
Db 272 CTGAACATCGACAATGCGATCTGCGTTTAAAGCTGATGAGTTCCTGAAGTGGCAGCC 213

Qy 41 LeuPheGluSerIleYsArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
|||||  
Db 212 CTCTTGAGTCTATCAAAAGAACTTCCTTCTCAACTGGAGATGCCCTTCTTAAGCTG 153

Qy 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
|||||  
Db 152 AAAGGACTGAGGAGCGCAACTCTGATGCCAG 120

RESULT 6  
A1140605/c 362 bp mRNA linear EST 29-OCT-1998  
LOCUS ge05f03.x1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1738109  
DEFINITION 3', mRNA sequence.  
ACCESSION A1140605  
VERSION A1140605.1 GI:3648062  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 362)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgapbs-r@mail.nih.gov  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
www-bio.lnl.gov/bbrp/image/image.html  
Insert Length: 425 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham.  
FEATURES  
source  
1. 362  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1738109"  
/sex="male"  
/lab\_host="DH10B"  
/clone\_lib="Soares\_testis\_NHT"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech Laboratories  
, Inc., and primed with a Not I - oligo(dt) primer [5'  
TGTTACCAATCTGAGTGGAGCGCGCCCAATTATTTTATTTT 3'].  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. Library  
went through one round of normalization to Cots, and was  
constructed by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 77 a 81 c 99 g 105 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 5.84e-68 Length: 362  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x A1140605 (1-362)



M. Fatima Donald. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHL19W."

BASE COUNT 91 a 86 c 114 g 89 t 1 others

## Alignment Scores:

Pred. No.: 6.18e-68 Length: 381  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x W63108 (1-381)

OY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
|||  
DB 317 GAGGAAGAAAGCACCATTTGAGAAATATGCGTCACGACCCGAGGCTTTAAACACCCCGTTTC 258  
OY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTyrPheAla 40  
|||  
DB 257 CTGAACATCGACAAATTGCGATCTGCTTTAAGGCTGATGATGCTTGAAGTGGACGCC 198  
OY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTyrAspAlaPheProLysLeu 60  
|||  
DB 197 CTCCTTGAGTCTATCAAAAGAACTCTCTTCTCAACTGGGATGCTTCTTAAGCTG 138  
OY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
|||  
DB 137 AAAGACTGAGGAGCGCAACTCTGATGCCAG 105

## RESULT 9

LOCUS W60320 394 bp mRNA linear EST 15-OCT-1996  
DEFINITION zd29g01.s1 Soares fetal heart NBHL19W Homo sapiens CDNA clone  
IMAGE:342096 3', mRNA sequence.

ACCESSION W60320  
VERSION W60320.1 GI:1367079

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 394) Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished

COMMENT Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 476 Std Error: 0.00

Seq primer: mob.REGA+ET.

Location/Qualifiers

1. .394

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:1267471"

/db\_xref="taxon:9606"

/clone="IMAGE:342096"

/sex="unknown"

/dev\_stage="19 weeks"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_ltb="Soares\_fetal\_heart\_NBHL19W"

/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a

modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGGCCGATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M. Fatima Donald. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHL19W."

BASE COUNT 94 a 88 c 119 g 91 t 2 others

## Alignment Scores:

Pred. No.: 6.41e-68 Length: 394  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x W60320 (1-394)

OY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
|||  
DB 320 GAGGAAGAAAGCACCATTTGAGAAATATGCGTCACGACCCGAGGCTTTAAACACCCCGTTTC 261  
OY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTyrPheAla 40  
|||  
DB 260 CTGAACATCGACAAATTGCGATCTGCTTTAAGGCTGATGATGCTTGAAGTGGACGCC 201  
OY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTyrAspAlaPheProLysLeu 60  
|||  
DB 200 CTCCTTGAGTCTATCAAAAGAACTCTCTTCTCAACTGGGATGCTTCTTAAGCTG 141  
OY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
|||  
DB 140 AAAGACTGAGGAGCGCAACTCTGATGCCAG 108

## RESULT 10

LOCUS W60268 412 bp mRNA linear EST 15-OCT-1996  
DEFINITION zd29g01.r1 Soares fetal heart NBHL19W Homo sapiens CDNA clone  
IMAGE:342096 5', mRNA sequence.

ACCESSION W60268  
VERSION W60268.1 GI:1367169

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 412) Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished

COMMENT Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 476 Std Error: 0.00

Seq primer: mob.REGA+ET

High quality sequence stop: 385.

Location/Qualifiers

1. .412

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:1267471"

/db\_xref="taxon:9606"

/clone="IMAGE:342096"

/sex="unknown"

/dev\_stage="19 weeks"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_ltb="Soares\_fetal\_heart\_NBHL19W"

/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a



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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1267471"
/db_xref="taxon:9606"
/clone="IMAGE:342096"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NBHL19W"
/notes="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHL19W."
```

BASE COUNT 96 a 127 c 88 g 98 t 3 others  
ORIGIN

Alignment Scores:  
Pred. No.: 6.73e-68 Length: 412  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x W60268 (1-412)

```
QY 1 GUGUGUGUSeThrIleGluAsnTYrAlaSerArgProGluAlaPheAsnThrProPhe 20
Db 97 GAGGAGAGAAAGCACCATTGAGAAATTATCGCTCAGCAGCCGACCCCTTTAACACCCCGTTTC 156
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40
Db 157 CTGAACATCGACAATTCGATCTGCGTTTAAAGGCTGATGATGATTCCTGAACGGCAGCC 216
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60
Db 217 CTCTTTGAGTCTATCAAAAGAACTTCCTTCTCAACTGGATGCCCTTCCCTAAGCTG 276
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71
Db 277 AAAGGACTGAGGAGCGCACTCCTGATGCCAG 309
```

## RESULT 11

W69083/c 424 bp mRNA linear EST 16-OCT-1996  
LOCUS z44b06.s1 Soares fetal heart\_NbHL19W Homo sapiens cDNA clone  
DEFINITION IMAGE:343475 3', mRNA sequence.

ACCESSION W69083  
VERSION W69083.1 GI:1378383  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 424)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800

Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through INL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Insert length: 466 Std Error: 0.00  
Seq primer: mob.REGA+ET  
High quality sequence stop: 339.  
Location/Qualifiers  
1. 424

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1268850"
/db_xref="taxon:9606"
/clone="IMAGE:343475"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NBHL19W"
/notes="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHL19W."
```

BASE COUNT 98 a 100 c 129 g 97 t  
ORIGIN

Alignment Scores:  
Pred. No.: 6.94e-68 Length: 424  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x W69083 (1-424)

```
QY 1 GUGUGUGUSeThrIleGluAsnTYrAlaSerArgProGluAlaPheAsnThrProPhe 20
Db 317 GAGGAGAGAAAGCACCATTGAGAAATTATCGCTCAGCAGCCGACCCCTTTAACACCCCGTTTC 258
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40
Db 257 CTGAACATCGACAATTCGATCTGCGTTTAAAGGCTGATGATGATTCCTGAACGGCAGCC 198
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60
Db 197 CTCTTTGAGTCTATCAAAAGAACTTCCTTCTCAACTGGATGCCCTTCCCTAAGCTG 138
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71
Db 137 AAAGGACTGAGGAGCGCACTCCTGATGCCAG 105
```

## RESULT 12

BX112106 432 bp mRNA linear EST 07-FEB-2003  
LOCUS BX112106 Soares fetal heart\_NbHL19W Homo sapiens cDNA clone  
DEFINITION IMAGE:342096, mRNA sequence.

ACCESSION BX112106  
VERSION BX112106.1 GI:27878783  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 432)  
AUTHORS Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,



TITLE  
JOURNAL  
COMMENT  
Radelof, U., Schneider, D. and Korn, B.  
Human Unigeneset - RZPD3  
Unpublished  
Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD, IMAGP998D01781.  
RZPDLIB: I.M.A.G.B. CDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No.972)  
http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de  
This clone is available royalty-free from RZPD;  
contact RZPD (clone@rzpd.de) for further information. Seq primer:  
M13r, Primer sequence: TTTCACACAGGAACAGCTATGAC.  
Location/Qualifiers  
1. 432  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGP998D01781 ; IMAGE:342096"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal heart NBHL19W"  
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCGCATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHL19W."  
BASE COUNT 113 a 129 c 92 g 98 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 7.08e-68 Length: 432  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x BX112106 (1-432)  
QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 99 GAGGAAGAAAGCACCATTGAGATATATGCGTCACGACCCGAGGCTTTAACAACCCCGTTC 158  
QY 21 LeuAsnIleAspIleuArgSerAlaPheIleuAlaAspGluPheLeuAsnTyrPheIle 40  
DB 159 CTGAACATCGACAATGCGATCTGCGTTTAAGGCTGATGAGTTCTTGAAGTGGACGCC 218  
QY 41 LeupheGluSerIleIleuArgIleuProPheLeuAsnTyrPheAlaPheProIleu 60  
DB 219 CTCCTTGAAGTCTATCAAAAGAACTTCCTTCTCAACTGGGATGCGCTTCTTAAGCTG 278  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 279 AAAGGACTGAGAGCGCAACTCTGATGCCAG 311  
RESULT 13  
W69233  
LOCUS W69233 432 bp mRNA linear EST 16-OCT-1996

DEFINITION z44c04.r1 Soares fetal heart NBHL19W Homo sapiens cDNA clone  
IMAGE:343494 5', mRNA sequence.  
ACCESSION W69233  
VERSION W69233.1 GI:1378493  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 432)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maira, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
The Washu-Merck EST Project  
TITLE Unpublished  
JOURNAL  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.lbnl.gov) for further information.  
Insert Length: 442 Std Error: 0.00  
Seq primer: mob.REGA+ET  
High quality sequence stop: 341.  
Location/Qualifiers  
1. 432  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:1268869"  
/db\_xref="taxon:9606"  
/clone="IMAGE:343494"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal heart NBHL19W"  
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCGCATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHL19W."  
BASE COUNT 106 a 127 c 94 g 102 t 3 others  
ORIGIN  
Alignment Scores:  
Pred. No.: 7.08e-68 Length: 432  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x W69233 (1-432)  
QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 96 GAGGAAGAAAGCACCATTGAGATATATGCGTCACGACCCGAGGCTTTAACAACCCCGTTC 155  
QY 21 LeuAsnIleAspIleuArgSerAlaPheIleuAlaAspGluPheLeuAsnTyrPheIle 40  
DB 156 CTGAACATCGACAATGCGATCTGCGTTTAAGGCTGATGAGTTCTTGAAGTGGACGCC 215  
QY 41 LeupheGluSerIleIleuArgIleuProPheLeuAsnTyrPheAlaPheProIleu 60

Db 216 CTCTTTGAGTCTATCAAAAGAACTTCCTTCTCACTGGATGCCCTTCTTAAGCTG 275  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 276 AAAGACTGAGGAGCGCACTCTGATGCCCAA 308  
RESULT 14  
W69227 431 bp mRNA linear EST 16-OCT-1996  
LOCUS z44b06.r1 Soares\_fetal\_heart\_NbHH19W Homo sapiens cDNA clone  
DEFINITION IMAGE:343475 5', mRNA sequence.  
W69227  
ACCESSION W69227.1 GI:1378487  
VERSION EST.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 431)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,  
'M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,  
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston,  
'R., Williamson, A., Wohlmann, P. and Wilson, R.  
The Washu-Merck EST Project  
JOURNAL Unpublished  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Insert Length: 466 Std Error: 0.00  
Seq primer: mob.REGA+ET  
High quality sequence stop: 410.  
Location/Qualifiers  
1. .431  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:1268850"  
/db\_xref="taxon:9606"  
/clone="IMAGE:343475"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares\_fetal\_heart\_NbHH19W"  
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by  
M.Fatima Bonaldo. This library was constructed from the  
same fetus as the fetal lung library, Soares fetal lung  
NbHH19W."  
BASE COUNT 106 a 127 c 94 g 102 t 2 others  
ORIGIN  
Alignment Scores:  
Pred. No.: 1.07e-54 Length: 431  
Score: 59.00 Matches: 59  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 83.10% Indels: 0  
DB: 14 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x W69227 (1-431)  
QY 13 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 32

Db 134 CCGAGGCGCTTTACACCCCGTTCGTGACATCGACAATTCGATCTCGTTTAAGGCT 193  
QY 33 AspGluPheLeuAsnThrPheIleAlaLeuPheGlnSerIleLysArgLysLeuProPheLeu 52  
Db 194 GATGAGTTCCTGAACTGGACAGCCCTCTTTGAGTCTATCAAAAGAACTTCCTTCCTC 253  
QY 53 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 254 AACTGGAGTCTTCTTAAGCTGAAGAGTGAAGAGCGCAACTCTGTGATGCCAG 310  
RESULT 15  
AA393296 413 bp mRNA linear EST 16-MAY-1997  
LOCUS z74f05.r1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:728097  
DEFINITION 5', mRNA sequence.  
AA393296  
ACCESSION AA393296.1 GI:2046264  
VERSION EST.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 413)  
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,  
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,  
Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie,  
'T., Waterston, R. and Wilson, R.  
Washu-Merck EST Project 1997  
JOURNAL Unpublished  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Seq primer: -28m13 rev2 RT from Amersham  
High quality sequence stop: 386.  
Location/Qualifiers  
1. .413  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:5925010"  
/db\_xref="taxon:9606"  
/clone="IMAGE:728097"  
/sex="male"  
/lab\_host="DH10B"  
/clone\_lib="Soares testis NHT"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech Laboratories  
'Inc., and primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'].  
Double-stranded cDNA was ligated to Eco RI adapters  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 96 a 113 c 125 g 79 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 1.28e-53 Length: 413  
Score: 58.00 Matches: 71  
Percent Similarity: 98.61% Conservative: 0  
Best Local Similarity: 98.61% Mismatches: 0  
Query Match: 81.69% Indels: 1  
DB: 9 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AA393296 (1-413)

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Db      164 GAGGAGAAAGCACCATTTGAGATTATGCGTCACGACCGAGCCCTTTAACACCCCGATT 223
QY      20  eleuAsnIleAspLysleuArgSeraIaPheLysAlaAspGUlupheleuAsnTrpHisAl 40
Db      224 CCTGAACATCGACAAATTGCCGATCTGCCGTTAAGGCTGATGAGTTCCTGAACCTGGCACGC 283
QY      40  aleupheGUSeThrIleLysArgLysleuProPheleuAsnTrpAspAlaPheProLysle 60
Db      284 CCTCTTTGAGTCTATCAAAAGAACTTCCTTCTCAACTGGAGTGCCCTTCTTAAGCT 343
QY      60  uLysGUleuArgSeraIaThrProAspAlaGln 71
Db      344 GAAAGGACTGAGGAGCGCAACTCCTGATGCCCAAG 377
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Search completed: November 28, 2003, 13:33:49  
Job time : 1606 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 10:53:40 ; Search time 54 Seconds

(without alignments)  
580.337 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Perfect score: 71  
Sequence: 1 EEBSTIENYASRPEAFNTPF.....LWMDAFPKLGLRSATPDAQ 71

Scoring table:

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Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 563978 seqs, 220691566 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1135135

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO\_spool/US10059395/runat 25112003\_140845\_7689/app\_query.fasta\_1.263  
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=ol1.rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
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-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA: \*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq: \*  
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4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/2/ina/PTCUTS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	100.0	415	4	US-09-996-243-200
2	9	12.7	666	4	US-09-252-991A-5754
3	9	12.7	837	4	US-09-252-991A-5702
4	9	12.7	1035	4	US-09-252-991A-5715
5	9	12.7	1245	4	US-09-252-991A-5725
6	7	9.9	765	4	US-09-107-532A-1141
7	7	9.9	774	4	US-09-252-991A-9431
8	7	9.9	2397	4	US-09-221-017B-272
9	7	9.9	3964	4	US-09-620-312D-128
10	7	9.9	5804	4	US-09-369-364A-12
11	7	9.9	31208	4	US-09-852-067-3
12	7	9.9	34446	4	US-09-103-330-35

C 13	7	9.9	123025	4	US-09-198-452A-1	Sequence 1, Appli
C 14	7	9.9	1664976	4	US-08-916-421B-1	Sequence 1, Appli
C 15	6	8.5	20	1	US-08-335-583C-20	Sequence 20, Appl
C 16	6	8.5	20	4	US-08-668-313A-170	Sequence 170, Appl
C 17	6	8.5	31	1	US-08-383-743A-9	Sequence 9, Appli
C 18	6	8.5	31	3	US-08-808-881-9	Sequence 9, Appli
C 19	6	8.5	31	3	US-09-017-631-9	Sequence 9, Appli
C 20	6	8.5	31	4	US-09-520-118-9	Sequence 9, Appli
C 21	6	8.5	31	5	PCT-US93-07116-9	Sequence 9, Appli
C 22	6	8.5	38	6	5185431-28	Patent No. 5185431
C 23	6	8.5	46	3	US-09-252-292-22	Sequence 22, Appl
C 24	6	8.5	62	3	US-08-483-511-13	Sequence 13, Appl
C 25	6	8.5	62	5	PCT-US93-01009-13	Sequence 13, Appl
C 26	6	8.5	74	3	US-08-258-287B-11	Sequence 11, Appl
C 27	6	8.5	74	3	US-08-368-704C-11	Sequence 11, Appl
C 28	6	8.5	75	3	US-09-060-756-146	Sequence 146, App
C 29	6	8.5	75	4	US-09-670-314-146	Sequence 146, App
C 30	6	8.5	164	1	US-08-480-552-1	Sequence 1, Appli
C 31	6	8.5	164	1	US-08-039-385-1	Sequence 1, Appli
C 32	6	8.5	164	3	US-08-929-208-1	Sequence 1, Appli
C 33	6	8.5	164	3	US-09-158-469-1	Sequence 1, Appli
C 34	6	8.5	164	3	US-09-561-844-1	Sequence 1, Appli
C 35	6	8.5	164	4	US-09-568-315-1	Sequence 1, Appli
C 36	6	8.5	164	4	US-09-562-226-1	Sequence 1, Appli
C 37	6	8.5	164	5	PCT-US91-07492-1	Sequence 1, Appli
C 38	6	8.5	165	3	US-08-836-261A-95	Sequence 95, Appl
C 39	6	8.5	240	6	5177308-2	Patent No. 5177308
C 40	6	8.5	255	4	US-09-134-001C-82	Sequence 82, Appl
C 41	6	8.5	277	1	US-08-391-339-12	Sequence 12, Appl
C 42	6	8.5	277	1	US-08-484-274A-12	Sequence 12, Appl
C 43	6	8.5	277	3	US-08-746-111-54	Sequence 54, Appl
C 44	6	8.5	305	4	US-09-313-294A-7107	Sequence 7107, Ap
C 45	6	8.5	318	4	US-09-252-991A-10314	Sequence 10314, A

#### ALIGNMENTS

RESULT 1  
US-09-996-243-200  
Sequence 200, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996, 243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16





PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.:	1.46e-67	Length:	415
Score:	71.00	Matches:	71
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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-996-243-200 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAAGAAAGCACCATTGAGATTATGCGTCACGACCGAGCGCTTTACACCCCGTTC 156  
QY 21 LeuAsnIleAspIleuArgSerAlaPheIleuAlaAspGluPheLeuAsnTrpHisAla 40  
DB 157 CTGAACATCGACAATTCGATCTGCGTTTAAGGCTGATGATCTTCTGAAGTGGACGCC 216  
QY 41 LeuPheGluSerIleLeuArgIleuProPheLeuAsnTrpAspAlaPheProIleu 60  
DB 217 CTCTTGAGTCTATCAAGAAAGAACTTCTTCTCACTGGAGATGCCCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGGAGCGCACTCTGATGCCACG 309

## RESULT 2

US-09-252-991A-5754/c  
Sequence 5754, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 5754  
LENGTH: 666  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5754

Alignment Scores:  
Pred. No.: 0.508 Length: 666  
Score: 9.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 12.68% Indels: 0  
DB: 4 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-252-991A-5754 (1-666)

QY 62 GlyLeuArgSerAlaThrProAspAla 70  
DB 62 GGGCTCGGAGCGCCACCGCGGACGCT 36

## RESULT 3

US-09-252-991A-5702  
Sequence 5702, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 5702  
LENGTH: 837  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5702

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Pred. No.: 0.635 Length: 837  
Score: 9.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 12.68% Indels: 0  
DB: 4 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-252-991A-5702 (1-837)

QY 62 GlyLeuArgSerAlaThrProAspAla 70  
DB 218 GGGCTCGGAGCGCCACCGCGGACGCT 244

## RESULT 4

US-09-252-991A-5715  
Sequence 5715, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 5715  
LENGTH: 1035  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5715

Alignment Scores:  
Pred. No.: 0.781 Length: 1035  
Score: 9.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 12.68% Indels: 0  
DB: 4 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-252-991A-5715 (1-1035)  
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Db 628 GGGCTGCGAGCGCCACGCGCGGACGCT 654  
RESULT 5  
US-09-252-991A-5725/c  
; Sequence 5725, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 5725  
; LENGTH: 1245  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5725  
Alignment Scores:  
Pred. No.: 0.935 Length: 1245  
Score: 9.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 12.68% Indels: 0  
DB: 4 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-252-991A-5725 (1-1245)  
Qy 62 GlyLeuArgSerAlaThrProAspAla 70  
Db 631 GGGCTGCGAGCGCCACGCGCGGACGCT 605  
RESULT 6  
US-09-107-532A-1141  
; Sequence 1141, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781) 893-5007  
TELEFAX: (781) 893-8277  
INFORMATION FOR SEQ ID NO: 1141:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 765 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (B) LOCATION 1...765  
SEQUENCE DESCRIPTION: SEQ ID NO: 1141:  
US-09-107-532A-1141  
Alignment Scores:  
Pred. No.: 80.3 Length: 765  
Score: 7.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 9.86% Indels: 0  
DB: 4 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-107-532A-1141 (1-765)  
Qy 46 LysArgLysLeuProPheLeu 52  
Db 97 AAAAGAAATTACTTCTTG 117  
RESULT 7  
US-09-252-991A-9431  
; Sequence 9431, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 9431  
; LENGTH: 774  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9431  
Alignment Scores:  
Pred. No.: 81.2 Length: 774  
Score: 7.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 9.86% Indels: 0  
DB: 4 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-252-991A-9431 (1-774)  
Qy 60 LeuLysGlyLeuArgSerAla 66  
Db 60 LeuLysGlyLeuArgSerAla 66

Db 739 CTCAGGCGCTGCGTAGCGCT 759

## RESULT 8

US-09-221-017B-272/c  
; Sequence 272, Application US/09221017B  
; Patent No. 6444799  
; GENERAL INFORMATION:  
; APPLICANT: Ross, Bruce C.  
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
; NUMBER OF SEQUENCES: 1120  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/221,017B  
; FILING DATE: 23-DEC-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PP1182  
; FILING DATE: 31-DEC-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PP1546  
; FILING DATE: 30-JAN-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PP2911  
; FILING DATE: 09-APR-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/AU98/01023  
; FILING DATE: 10-DEC-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Montroy, Gladys H  
; REGISTRATION NUMBER: 32,430  
; REFERENCE/DOCKET NUMBER: 27340-20021.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 272:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2397 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: UNKNOWN  
; ORIGINAL SOURCE:  
; ORGANISM: PORYPHYROMONAS GINGIVALIS  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1...2397  
US-09-221-017B-272

## Alignment Scores:

Pred. No.:	244	Length:	2397
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	9.86%	Indels:	0
DB:	4	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-221-017B-272 (1-2397)

QY 20 PheleuA5n1leAsplysleu 26

Db 647 TTCCTAATATAGATAAATTA 627

## RESULT 9

US-09-620-312D-128  
; Sequence 128, Application US/09620312D  
; Patent No. 6569662  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yungqing  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: John, Tillinghast  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 784CIP2B  
; CURRENT APPLICATION NUMBER: US/09/620,312D  
; CURRENT FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1105  
; SOFTWARE: pt\_fl\_genes Version 1.0  
; SEQ ID NO 128  
; LENGTH: 3964  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (174)..(2540)  
US-09-620-312D-128

## Alignment Scores:

Pred. No.:	399	Length:	3964
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	9.86%	Indels:	0
DB:	4	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-620-312D-128 (1-3964)

QY 10 AlaserArgProGluAlaPhe 16

Db 2273 GCTTCAGGCCAGAGCCTTT 2293

## RESULT 10

US-09-369-364A-12  
; Sequence 12, Application US/09369364A  
; Patent No. 6391610  
; GENERAL INFORMATION:  
; APPLICANT: Apte, Suneel  
; APPLICANT: Hurskainen, Tiina L.  
; APPLICANT: Hirohata, Satoshi  
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
; FILE REFERENCE: 26473/4007/10-30-00  
; CURRENT APPLICATION NUMBER: US/09/369,364A  
; CURRENT FILING DATE: 1999-08-06  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 12
; LENGTH: 5804
; TYPE: DNA
; ORGANISM: Homo sapiens ADAMTS-9
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(5648)
; NAME/KEY: misc_feature
; LOCATION: (1406)
; OTHER INFORMATION: n=T
; NAME/KEY: misc_feature
; LOCATION: (1563)
; OTHER INFORMATION: n=T
US-09-369-364A-12
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```
Alignment Scores:
Pred. No.: 578          length: 5804
Score: 7.00           Matches: 7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 9.86%          Indels: 0
DB: 4                  Gaps: 0
```

```
US-10-059-395-142_COPY_29_99 (1-71) x US-09-369-364A-12 (1-5804)
```

```
OY 45 l1e1y5Arg1y5LeuProphe 51
DB 2959 ATCAAGAGAAAGTTACCAATTC 2979
```

## RESULT 11

```
US-09-852-067-3
; Sequence 3, Application US/09852067
; Patent No. 6531297
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL600897-CIP
; CURRENT APPLICATION NUMBER: US/09/852,067
; CURRENT FILING DATE: 2001-05-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 31208
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(31208)
; OTHER INFORMATION: n = A,T,C or G
US-09-852-067-3
```

```
Alignment Scores:
Pred. No.: 2.97e+03      length: 31208
Score: 7.00           Matches: 7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 9.86%          Indels: 0
DB: 4                  Gaps: 0
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```
US-10-059-395-142_COPY_29_99 (1-71) x US-09-852-067-3 (1-31208)
```

```
OY 46 lY5Arg1y5LeuProphe1eu 52
DB 24241 AAGAGGAACCTCCCTTCTTG 24261
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## RESULT 12

```
US-09-103-330-35
; Sequence 35, Application US/09103330A
; Patent No. 6319716
; GENERAL INFORMATION:
```

```
; APPLICANT: TIKOO, SURESH K.
; APPLICANT: BABIUX, LORNE A.
; APPLICANT: REDDY, POLICE S.
; TITLE OF INVENTION: ISOLATION OF MUTANTS IN THE E3 REGION OF THE
; TITLE OF INVENTION: BOVINE ADENOVIRUS GENOME AND THEIR USE IN VACCINES
; FILE REFERENCE: 293102002121
; CURRENT APPLICATION NUMBER: US/09/103,330A
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 08/880,234
; EARLIER FILING DATE: 1997-06-23
; EARLIER APPLICATION NUMBER: 08/164,292
; EARLIER FILING DATE: 1993-12-09
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 34446
; TYPE: DNA
; ORGANISM: Bovine adenovirus type 3
US-09-103-330-35
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Alignment Scores:
Pred. No.: 3.28e+03      length: 34446
Score: 7.00           Matches: 7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 9.86%          Indels: 0
DB: 4                  Gaps: 0
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```
US-10-059-395-142_COPY_29_99 (1-71) x US-09-103-330-35 (1-34446)
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```
OY 62 G1yLeuArgSera1aThrPro 68
DB 14923 GGCCCTACGGTCACCAACACCG 14943
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## RESULT 13

```
US-09-198-452A-1/c
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffaib, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev.
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(15000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (15001)..(30000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (30001)..(45000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (45001)..(60000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (60001)..(75000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (75001)..(90000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (90001)..(105000)
; OTHER INFORMATION: n=a or c or g or t
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; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (840001)..(855000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (855001)..(870000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (870001)..(885000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (885001)..(900000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (900001)..(915000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature

Alignment Scores:
Pred. No.: 1.02e+05      Length: 1230025
Score: 7.00             Matches: 7
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 9.86%              Indels: 0
DB: 4                       Gaps: 0

US-10-059-395-142_COPY_29_99 (1-71) x US-09-198-452A-1 (1-1230025)
Qy      16 PheasnThrProPheLeuasn 22
Db      391689 TTCACACACCATTTTGAAT 391669

RESULT 14
US-08-916-421B-1/c
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
; Patent No. 6503729
; TITLE OF INVENTION: jannaschi
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschi
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (28257)..(28258)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84773)..(84773)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84808)..(84808)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84812)..(84812)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98120)..(98120)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98159)..(98159)
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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98239)..(98239)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (103998)..(103998)
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; NAME/KEY: misc feature
; LOCATION: (148948)..(148948)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (163385)..(163385)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (191989)..(191989)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (191995)..(191995)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (231980)..(231980)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234187)..(234187)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234220)..(234220)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234814)..(234814)
; OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (309398)..(309398)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (309418)..(309418)
; OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (312837)..(312837)
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; NAME/KEY: misc feature
; LOCATION: (312993)..(312993)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (319226)..(319226)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559167)..(559167)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559241)..(559241)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (600992)..(600992)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (622708)..(622708)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (657081)..(657081)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (657203)..(657203)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (674435)..(674435)
; OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc\_feature  
LOCATION: (682442)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (713652)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (741684)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (779455)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (779676)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (855539)..  
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NAME/KEY: misc\_feature  
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OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1084830)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1096846)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1119881)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1130881)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1310988)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1313224)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1349473)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1349491)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1470091)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1569020)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1602912)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1603734)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1637998)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (1664855)..  
OTHER INFORMATION: n equals a, t, c, or g  
US-08-916-421B-1

## Alignment Scores:

Pred. No.:	1.34e+05	Length:	1664976
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	9.86%	Indels:	0
DB:	4	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-08-916-421B-1 (1-1664976)  
Oy 44 SerilelyArglySerleupro 50  
Db 1134223 AGCATAAAGAGAGTACT 1134203

## RESULT 15

US-08-335-583C-20  
Sequence 20, Application US/08335583C  
Patent No. 5693779  
GENERAL INFORMATION:  
APPLICANT: Moos Jr., Malcolm  
APPLICANT: Wang, Shouwan  
APPLICANT: Krinks, Marie  
TITLE OF INVENTION: PRODUCTION AND USE OF  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson and Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: USA  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/335,583C  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: NIH104.001A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-760-0404  
TELEFAX: 714-760-9502  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
IMMEDIATE SOURCE:  
LIBRARY: GENWORKS, X57234  
US-08-335-583C-20

## Alignment Scores:

Pred. No.:	27.1	Length:	20
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	8.45%	Indels:	0
DB:	1	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-08-335-583C-20 (1-20)

Oy 62 GylleuArgSerleupro 67  
Db 3 GGAAGTTCGAGTCAACC 20

Sat Nov 29 17:52:39 2003

us-10-059-395-142\_copy\_29\_99.014\_1.rn1

Page 10

Search completed: November 28, 2003, 12:18:00  
Job time : 309 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 10:52:35 ; Search time 1606 Seconds

(without alignments)  
1074.482 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99  
Perfect score: 71  
Sequence: 1 EESTIENTYASRPEAFNTPF.....LNMDFPKLKLRSATPDQ 71

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Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Word size: 1

Total number of hits satisfying chosen parameters: 45562437

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:  
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-Q=/cgn2\_1/USPTO\_spool/US10059395/runat\_25112003\_140844\_7677/app\_query.fasta\_1.263  
-DB=EST -QFMT=fastap -SUFFIX=oli.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10059395 @CGN 1 1 2810 @runat\_25112003\_140844\_7677 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : EST: \*  
1: em\_estba: \*  
2: em\_esthum: \*  
3: em\_estin: \*  
4: em\_estmu: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_htc: \*  
9: gb\_est1: \*  
10: gb\_est2: \*  
11: gb\_htc: \*  
12: gb\_est3: \*  
13: gb\_est4: \*  
14: gb\_est5: \*  
15: em\_estfun: \*  
16: em\_estom: \*  
17: em\_gss\_hum: \*  
18: em\_gss\_inv: \*  
19: em\_gss\_pln: \*  
20: em\_gss\_vrt: \*  
21: em\_gss\_fun: \*  
22: em\_gss\_mam: \*  
23: em\_gss\_mus: \*  
24: em\_gss\_pro: \*  
25: em\_gss\_rod: \*  
26: em\_gss\_phg: \*  
27: em\_gss\_vrl: \*  
28: gb\_gss1: \*

29: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	71	100.0	318	9	AA586846 nm67e11.s
C 2	71	100.0	334	9	AA297512 EST113061
C 3	71	100.0	339	9	AA778414 zf39e05.s
C 4	71	100.0	348	9	AW238758 xp03e08.x
C 5	71	100.0	359	10	BE466728 hz24g06.x
C 6	71	100.0	362	9	AI140605 ge05f03.x
C 7	71	100.0	373	9	AA722694 zg82b06.s
C 8	71	100.0	381	14	W69108 zd44c04.s1
C 9	71	100.0	394	14	W60320 zd29g01.s1
C 10	71	100.0	412	14	W60268 zd29g01.s1
C 11	71	100.0	424	14	W69083 zd44b06.s1
C 12	71	100.0	432	13	BX112106 BX112106
C 13	71	100.0	432	14	W69233 zd44c04.r1
C 14	59	83.1	431	14	W69227 zd44b06.r1
C 15	58	81.7	413	9	AA393296 zt74f05.r
C 16	57	80.3	345	9	AI217565 qd43d02.x
C 17	56	78.9	241	9	AA595989 nm64g08.s
C 18	53	74.6	359	10	BG150312 7j98g03.x
C 19	51	71.8	334	9	AI217587 qd43f04.x
C 20	43	60.6	345	9	AA583942 nm64f07.s
C 21	43	60.6	376	14	W95920 ze08d01.r1
C 22	39	54.9	221	9	AA584333 nm73a09.s
C 23	39	54.9	326	9	AA297513 EST113062
C 24	37	52.1	358	9	AW003825 wg83f12.x
C 25	37	52.1	377	9	AA583988 nm72h02.s
C 26	35	49.3	330	14	W95883 ze08d01.s1
C 27	33	46.5	218	9	AA398638 zc74f05.s
C 28	33	46.5	239	9	AA595930 nm66a07.s
C 29	27	38.0	339	14	W52030 zd13b01.s1
C 30	27	38.0	378	9	AI184682 qd68b02.x
C 31	24	33.8	368	9	AW260965 EQUK0243
C 32	24	33.8	436	9	AV597545 AV597545
C 33	18	25.4	163	9	AA776980 zf23d05.s
C 34	15	21.1	377	9	AW260982 EQUK0196
C 35	14	19.7	421	9	AV618771 AV618771
C 36	12	16.9	323	10	BE715771 MR2-HT075
C 37	8	11.3	271	10	BE701465 PM2-NN017
C 38	8	11.3	304	9	AI894297 ms66b04.x
C 39	8	11.3	310	14	CD036743 mgsu011xd
C 40	8	11.3	353	10	BF366304 CM1-NT008
C 41	8	11.3	365	10	BF735391 CM1-AN008
C 42	8	11.3	378	10	BF522420 UI-R-C3-t
C 43	8	11.3	382	12	BI81645 fm88g05.Y
C 44	8	11.3	399	12	BI81568 fm87c01.Y
C 45	8	11.3	404	14	R80137 y195c09.r1

ALIGNMENTS

RESULT 1  
AA586846/c 318 bp mRNA linear EST 26-SEP-1997  
LOCUS nm67e11.s1 NCI\_CGAP\_Lar1 Homo sapiens cDNA clone IMAGE:1088972 3',  
DEFINITION mRNA sequence.  
ACCESSION AA586846  
VERSION AA586846.1 GI:2397660  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 318)

**AUTHORS** NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
**JOURNAL** Unpublished  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: Stratagene, Inc.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
 Insert length: 465 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amersham.

**FEATURES**  
 Source  
 1. .318  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1088972"  
 /tissue\_type="larynx"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /clone\_lib="NCI\_CGAP\_Lar1"  
 /note="Organ: larynx; Vector: Bluescript SK-; Site\_1:  
 EcoRI; Site\_2: XhoI; Cloned unidirectionally. Primer:  
 Oligo dt. larynx. 5' adaptor sequence: 5' GAATTCGGCAGCAG  
 3' 3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'  
 Average insert size: 0.9 kb."  
 76 a 67 c 90 g 85 t

**BASE COUNT**  
 ORIGIN

**Alignment Scores:**  
 Pred. No.: 5.07e-68 Length: 318  
 Score: 71.00 Matches: 71  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AA586846 (1-318)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
 |||||  
 Db 316 GAGGAAGAAGCACCATTGAGATTATGCGTCACGACCCGAGGCTTTAACACCCCGCTTC 257

QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
 |||||  
 Db 256 CTGAACATCGACAATTGCGATCTGCGTTTAAGGCTGATGAGTTCCTGAACGACGCC 197

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
 |||||  
 Db 196 CTCTTGAGTCTATCAAAAGAACTTCCTTCTCACTGGGATGCCCTTCTTAAGCTG 137

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
 |||||  
 Db 136 AAAGACTGAGAGCGCACTCCTGATGCCAG 104

**RESULT 2**  
 AA297512 334 bp mRNA linear EST 18-APR-1997  
 LOCUS EST113061 Fetal skin Homo sapiens cDNA 5' end, mRNA sequence.  
 ACCESSION AA297512  
 VERSION AA297512.1 GI:1949866  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE**  
 1 (bases 1 to 334)  
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult  
 ,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White

,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,  
 Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald  
 ,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodek,A.,  
 Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,  
 Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,  
 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,  
 Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,  
 Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,  
 Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,  
 Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.,  
 Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,  
 Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,  
 Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon  
 ,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and  
 Venter,J.C.  
 Initial assessment of human gene diversity and expression patterns  
 based upon 83 million nucleotides of cDNA sequence  
 Nature 377 (6547 Suppl), 3-174 (1995)  
 96026280  
 7566098  
**JOURNAL**  
**MEDLINE**  
**PUBMED**  
**COMMENT** Other\_ESTs: THC151622  
 Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: [arkerlav@tigr.org](mailto:arkerlav@tigr.org)  
 For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/tcdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse.

**FEATURES**  
 Source  
 1. .334  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="ATCC (inhost):141532"  
 /db\_xref="taxon:9606"  
 /tissue\_type="epithelium"  
 /cell\_type="epithelial cell"  
 /dev\_stage="fetus"  
 /clone\_lib="Fetal skin"  
 /note="Organ: skin; Vector: pBluescript SK-; Site\_1: EcoRI  
 ; Site\_2: XhoI"

**BASE COUNT**  
 ORIGIN  
 77 a 100 c 78 g 78 t 1 others

**Alignment Scores:**  
 Pred. No.: 5.35e-68 Length: 334  
 Score: 71.00 Matches: 71  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AA297512 (1-334)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
 |||||  
 Db 98 GAGGAAGAAGCACCATTGAGATTATGCGTCACGACCCGAGGCTTTAACACCCCGCTTC 157

QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
 |||||  
 Db 158 CTGAACATCGACAATTGCGATCTGCGTTTAAGGCTGATGAGTTCCTGAACGACGCC 217

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
 |||||  
 Db 218 CTCTTGAGTCTATCAAAAGAACTTCCTTCTCACTGGGATGCCCTTCTTAAGCTG 277

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
 |||||  
 Db 278 AAAGACTNAGAGCGCAACTCCTGATGCCAG 310



```
RESULT 3
AA778414/c 339 bp mRNA linear EST 05-FEB-1998
LOCUS zf39e05.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
DEFINITION IMAGE:379328 3', mRNA sequence.
ACCESSION AA778414
VERSION AA778414.1 GI:2837745
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 339)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin,
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
JOURNAL Unpublished
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham.
FEATURES
Source location/Qualifiers
1..339
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1287584"
/db_xref="taxon:9606"
/clone="IMAGE:379328"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NbHH19W"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTACCAATCTGAGTGGAGCGCGCGCATCTTTTCTTTTCTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHH19W."
BASE COUNT 79 a 77 c 96 g 87 t
ORIGIN
Alignment Scores:
Pred. No.: 5.44e-68 Length: 339
Score: 71.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 9
DB: 9
US-10-059-395-142_COPY_29_99 (1-71) x AA778414 (1-339)
QY 1 GUGUGUGUSeThrIleGUASeNTYrAlaSeArGProGluAlaPheAsnThrProPhe 20
Db 316 GAGGAGAAAGACACCATGTGAGAAATATGCGTCACGACCCGAGGCGCTTTAACACCCCGTTC 257
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40
Db 256 CTGAACATCGACAAATTGCGATCTGCGTTTAAAGGCTGATGAGTTCCTGAACCTGGCAGCC 197
QY 41 LeupheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60
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Db 196 CTCTTTGAGTCTATCAAAAGAACTTCCTTCTCACTGGATGCTTCTTAAGCTG 137
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71
Db 136 AAGGACTGAGAGCGCAACTCTGATGCCAG 104
RESULT 4
AM238758 348 bp mRNA linear EST 13-DEC-1999
LOCUS xp03e08.x1 NCI_CGAP_HN8 Homo sapiens cDNA clone IMAGE:2739302 3',
DEFINITION mRNA sequence.
ACCESSION AM238758
VERSION AM238758.1 GI:6571147
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 348)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Edward Shillitoe Ph.D., Silvio Gutkind Ph.D.,
Chidchanok Leethanakul D.D.S., Michael Emmert-Buck M.D. Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bbrp/image/image.html
FEATURES
Source Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 331.
location/Qualifiers
1..348
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2739302"
/tissue_type="well-differentiated invasive carcinoma,
floor of mouth"
/lab_host="DH10B"
/clone_lib="NCI CGAP HN8"
/note="Vector: pAMP10; cDNA made by oligo-dT priming.
Non-directionally cloned into the UDG sites of pAMP10.
Size-selected on agarose gel, average insert size 500 bp.
Primary library; non-amplified. cDNA Library
Preparation: David B. Krizman, Ph.D (NCI). Reference:
Krizman et al. (1996) Cancer Research 56:5380-5383."
BASE COUNT 82 a 104 c 84 g 78 t
ORIGIN
Alignment Scores:
Pred. No.: 5.6e-68 Length: 348
Score: 71.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 9
DB: 9
US-10-059-395-142_COPY_29_99 (1-71) x AM238758 (1-348)
QY 1 GUGUGUGUSeThrIleGUASeNTYrAlaSeArGProGluAlaPheAsnThrProPhe 20
Db 81 GAGGAGAAAGACACCATGTGAGAAATATGATCAGACCCGAGGCGCTTTAACACCCGTTTC 140
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40
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Db 141 CTGAACATCGACAATTGCGATCTGCGTTAAGGCTGATGAGTTCCTGAACCTGGCAGGCC 200

QY 41 LeuphegluserilelysarqlyseuPropheluansTrpaspAlaphProlyseu 60  
|||||  
Db 201 CTCCTTGAGTCTATCAAAAGGAACTCTTCTCTCACTGGGATGCCCTTCTTAAGCTG 260

QY 61 LysgilyleuargseralathrProaspAlagin 71  
|||||  
Db 261 AAAGAGCTGAGAGCGCAACTCTGATGCCAG 293

RESULT 5  
BE466728/c 359 bp mRNA linear EST 27-JUL-2000  
LOCUS h224906.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:3208954 3',  
DEFINITION mRNA sequence.  
ACCESSION BE466728  
VERSION BE466728.1 GI:9512503  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 359)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
[info@image.llnl.gov](mailto:info@image.llnl.gov)  
Seq primer: -40UP from Gibco.  
FEATURES  
source  
1.359  
location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3208954"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_GC6"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA  
from the normalized library NCI\_CGAP\_GC4 was prepared, and  
ss circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (cloneIDs  
1257096-1258631, 1469064-1470983, and 1475592-1476743).  
Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 77 a 80 c 96 g 106 t

ORIGIN

Alignment Scores:  
Pred. No.: 5.79e-68 Length: 359  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0 \*

US-10-059-395-142\_COPY\_29\_99 (1-71) x BE466728 (1-359)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
|||||  
Db 332 GAGGAAGAAGACCATGTGAGATATGCGTCACGACCGAGGCGCTTTAACAACCCCGTTC 273

QY 21 LeuAnlleAspIlyseuArgSerAlaPheIlysaAlaSpGluPheLeuAnTrpHisAla 40  
|||||  
Db 272 CTGAACATCGACAATTGCGATCTGCGTTAAGGCTGATGAGTTCCTGAACCTGGCAGGCC 213

QY 41 LeuphegluserilelysarqlyseuPropheluansTrpaspAlaphProlyseu 60  
|||||  
Db 212 CTCCTTGAGTCTATCAAAAGGAACTCTTCTCTCACTGGGATGCCCTTCTTAAGCTG 153

QY 61 LysgilyleuargseralathrProaspAlagin 71  
|||||  
Db 152 AAAGAGCTGAGAGCGCAACTCTGATGCCAG 120

RESULT 6  
A1140605/c 362 bp mRNA linear EST 29-OCT-1998  
LOCUS ge05f03.x1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1738109  
DEFINITION 3', mRNA sequence.  
ACCESSION A1140605  
VERSION A1140605.1 GI:3648062  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 362)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Insert Length: 425 Std Error: 0.00  
Seq primer: -40m13 fwd. RT from Amersham.  
FEATURES  
source  
1.362  
location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1738109"  
/sex="male"  
/lab\_host="DH10B"  
/clone\_lib="Soares\_testis\_NHT"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech laboratories  
, Inc., and primed with a Not I - oligo(dT) primer [5',  
TGTTACCAATCTGAAGTGGAGCGCGCCCAATTCTTTTCTTTT 3'].  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 77 a 81 c 99 g 105 t

ORIGIN

Alignment Scores:  
Pred. No.: 5.84e-68 Length: 362  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x A1140605 (1-362)

QY 1 GIUGLUGLuserThrillegluAsnTYrAlaSerArgProGluAlaPheAsnThrProPhe 20  
 |||||  
 Db 331 GAGGAAGAAAGCACCATTGAGAAATTATGCGTCACGACCGAGCCCTTTAAACACCCCGCTTC 272

QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
 |||||  
 Db 271 CTGAACATCGACAATTTGCGATTCGCTTTAAGGCTGATGAGTTCCTGAAGTGGACGCC 212

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
 |||||  
 Db 211 CTCTTTGAGTCTATCAAAAGAACTTCCTTCTCACTGGAGATGCCTTCTTAAGCTG 152

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
 |||||  
 Db 151 AAAGACTGAGAGCGCACTCTGATGCCAG 119

RESULT 7  
 AA722694 373 bp mRNA linear EST 02-JAN-1998  
 LOCUS AA722694/c  
 DEFINITION z982b06.s1 Soares fetal\_heart\_NbHH19W Homo sapiens cDNA clone  
 IMAGE:399827 3', mRNA sequence.  
 AA722694  
 AA722694.1 GI:2740401  
 EST.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS  
 1 (bases 1 to 373)  
 Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,  
 Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin  
 'J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,  
 White,Y., Wylie,T., Waterston,R. and Wilson,R.  
 WashU-NCI human EST Project  
 Unpublished  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: -40m13 fwd. ET from Amersham.

FEATURES  
 Source  
 1..373  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:1307650"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:399827"  
 /sex="unknown"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares fetal\_heart\_NbHH19W"  
 /note="Organ: heart; Vector: pT73D (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dt) primer [5'  
 TGTACCAATCTGAAGTGGAGCGCGCGCATCTTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by  
 M.Fatima Bonaldo. This library was constructed from the  
 same fetus as the fetal lung library, Soares fetal lung  
 NbHL19W."

BASE COUNT 89 a 81 c 113 g 90 t

ORIGIN

Alignment Scores:  
 Pred. No.: 6.04e-68 length: 373  
 Score: 71.00 Matches: 71

Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AA722694 (1-373)

QY 1 GIUGLUGLuserThrillegluAsnTYrAlaSerArgProGluAlaPheAsnThrProPhe 20  
 |||||  
 Db 319 GAGGAAGAAAGCACCATTGAGAAATTATGCGTCACGACCGAGCCCTTTAAACACCCCGCTTC 260

QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
 |||||  
 Db 259 CTGAACATCGACAATTTGCGATTCGCTTTAAGGCTGATGAGTTCCTGAAGTGGACGCC 200

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
 |||||  
 Db 199 CTCTTTGAGTCTATCAAAAGAACTTCCTTCTCACTGGAGATGCCTTCTTAAGCTG 140

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
 |||||  
 Db 139 AAAGACTGAGAGCGCACTCTGATGCCAG 107

RESULT 8  
 W69108 381 bp mRNA linear EST 16-OCT-1996  
 LOCUS W69108/c  
 DEFINITION zd44c04.s1 Soares fetal\_heart\_NbHH19W Homo sapiens cDNA clone  
 IMAGE:343494 3', mRNA sequence.  
 W69108  
 W69108.1 GI:1378389  
 EST.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS  
 1 (bases 1 to 381)  
 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman  
 'M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,  
 Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaaskis,E., Waterston  
 'R., Williamson,A., Wohlmann,P. and Wilson,R.  
 The WashU-Merck EST Project  
 Unpublished  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert length: 442 Std Error: 0.00  
 Seq primer: mob.REGA+ET  
 High quality sequence stop: 347.

FEATURES  
 Source  
 1..381  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:1268869"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:343494"  
 /sex="unknown"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares fetal\_heart\_NbHH19W"  
 /note="Organ: heart; Vector: pT73D (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dt) primer [5'  
 TGTACCAATCTGAAGTGGAGCGCGCGCATCTTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was size selected, digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by

M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHL19W."

BASE COUNT 91 a 86 c 114 g 89 t 1 others

## Alignment Scores:

Pred. No.:	6.18e-68	Length:	381
Score:	71.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x W69108 (1-381)

QY 1 GUGUGUGUSeThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
|||||  
Db 317 GAGGAGAGAAAGCACCATTGAGAAATTATGCGTCACGACCGAGCCCTTTAACACCCCGTTTC 258  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrHisAla 40  
|||||  
Db 257 CTGAACATCGACAATGCGATCTGCGTTTAAAGGCTGATGAGTTCTGAACTGGACGCGCC 198  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
|||||  
Db 197 CTCCTTGAGTCTATCAAAAGGAACTTCCTTCTCACTGGGATGCCCTTCTTAAGCTG 138  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
|||||  
Db 137 AAAGAGCTGAGAGCGCAACTCCTGATGCCAG 105

## RESULT 9

W60320 394 bp mRNA linear EST 15-OCT-1996  
LOCUS zd29g01.s1 Soares fetal heart NBHL19W Homo sapiens cDNA clone  
DEFINITION IMAGE:342096 3', mRNA sequence.

W60320  
VERSION W60320.1 GI:1367079  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 394)

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

The WashU-Merck EST Project

## TITLE

## JOURNAL

## COMMENT

Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

Insert length: 476 Std Error: 0.00

Seq primer: mob.REGA+ET.

Location/Qualifiers

1. .394

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:1267471"

/db\_xref="taxon:9606"

/clone="IMAGE:342096"

/sex="unknown"

/dev\_stage="19 weeks"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares fetal heart NBHL19W"

/note="Organ: heart; Vector: pT773D (Pharmacia) with a

modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHL19W."

BASE COUNT 94 a 88 c 119 g 91 t 2 others

## Alignment Scores:

Pred. No.:	6.41e-68	Length:	394
Score:	71.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x W60320 (1-394)

QY 1 GUGUGUGUSeThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
|||||  
Db 320 GAGGAGAGAAAGCACCATTGAGAAATTATGCGTCACGACCGAGCCCTTTAACACCCCGTTTC 261  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrHisAla 40  
|||||  
Db 260 CTGAACATCGACAATGCGATCTGCGTTTAAAGGCTGATGAGTTCTGAACTGGACGCGCC 201  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
|||||  
Db 200 CTCCTTGAGTCTATCAAAAGGAACTTCCTTCTCACTGGGATGCCCTTCTTAAGCTG 141  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
|||||  
Db 140 AAAAGACTGAGAGCGCAACTCCTGATGCCAG 108

## RESULT 10

W60268 412 bp mRNA linear EST 15-OCT-1996  
LOCUS zd29g01.r1 Soares fetal heart NBHL19W Homo sapiens cDNA clone  
DEFINITION IMAGE:342096 5', mRNA sequence.

W60268  
VERSION W60268.1 GI:1367169  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 412)

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

The WashU-Merck EST Project

## TITLE

## JOURNAL

## COMMENT

Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

Putative full length read

Insert length: 476 Std Error: 0.00

Seq primer: mob.REGA+ET

High quality sequence stop: 385.

Location/Qualifiers

1. .412

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:1267471"

/db\_xref="taxon:9606"

/clone="IMAGE:342096"

/sex="unknown"

/dev\_stage="19 weeks"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares fetal heart NBHL19W"

/note="Organ: heart; Vector: pT773D (Pharmacia) with a



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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1267471"
/db_xref="taxon:9606"
/clone="IMAGE:342096"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NBHL19W"
/note="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M. Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHL19W."
BASE COUNT      96 a      127 c      88 g      98 t      3 others
ORIGIN
```

```
Alignment Scores:
Pred. No.:      6.73e-68      Length:      412
Score:          71.00      Matches:      71
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:              14      Gaps:          0
```

US-10-059-395-142\_COPY\_29\_99 (1-71) x W60268 (1-412)

```
QY      1  GUGUGUUserThrileGUASnTYrAlaSerArgProGUAlaPheAsnThrProPhe 20
          |||||
Db      97  GAGGAAGAAGCACCATTTGAGAAATTATGCGTCACGACCGAGCCCTTAAACACCCCGTTT 156
          |||||
QY      21  LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40
          |||||
Db      157 CTGAACATCGACCAATTGCGATCTGCGTTAAGGTGATGAGTTCCTGAACTCGACACGCC 216
          |||||
QY      41  LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60
          |||||
Db      217 CTCTTTGAGTCTATCAAAAGAACTTCCTTCCTCAACTGGGATGCTTCTTAAGCTG 276
          |||||
QY      61  LysGlyLeuArgSerAlaThrProAspAlaGln 71
          |||||
Db      277 AAAGACTGAGGAGCGCACTCTGATGCCAG 309
          |||||
```

#### RESULT 11

W69083/c 424 bp mRNA linear EST 16-OCT-1996  
LOCUS zd44b06.s1 Soares fetal heart NBHL19W Homo sapiens cDNA clone  
DEFINITION IMAGE:343475 3', mRNA sequence.

ACCESSION W69083  
VERSION W69083.1 GI:1378383  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 424)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished

COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800

Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Insert Length: 466 Std Error: 0.00  
Seq primer: mob.REGA+ET  
High quality sequence stop: 339.

#### FEATURES

```
Source
1. 424
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1268850"
/db_xref="taxon:9606"
/clone="IMAGE:343475"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NBHL19W"
/note="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M. Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHL19W."
BASE COUNT      98 a      100 c      129 g      97 t
ORIGIN
```

```
Alignment Scores:
Pred. No.:      6.94e-68      Length:      424
Score:          71.00      Matches:      71
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:              14      Gaps:          0
```

US-10-059-395-142\_COPY\_29\_99 (1-71) x W69083 (1-424)

```
QY      1  GUGUGUUserThrileGUASnTYrAlaSerArgProGUAlaPheAsnThrProPhe 20
          |||||
Db      317 GAGGAAGAAGCACCATTTGAGAAATTATGCGTCACGACCGAGCCCTTAAACACCCCGTTT 258
          |||||
QY      21  LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40
          |||||
Db      257 CTGAACATCGACCAATTGCGATCTGCGTTAAGGTGATGAGTTCCTGAACTCGACACGCC 198
          |||||
QY      41  LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60
          |||||
Db      197 CTCTTTGAGTCTATCAAAAGAACTTCCTTCCTCAACTGGGATGCTTCTTAAGCTG 138
          |||||
QY      61  LysGlyLeuArgSerAlaThrProAspAlaGln 71
          |||||
Db      137 AAAGACTGAGGAGCGCAACTCTGATGCCAG 105
          |||||
```

#### RESULT 12

BX112106 432 bp mRNA linear EST 07-FEB-2003  
LOCUS BX112106 Soares fetal heart NBHL19W Homo sapiens cDNA clone  
DEFINITION IMAGE:998D01781 ; IMAGE:342096, mRNA sequence.

ACCESSION BX112106  
VERSION BX112106.1 GI:27878783  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 432)  
AUTHORS Ebert, L., Heil, O., Hennig, S., Neubert, P., Patsch, E., Peters, M.,



TITLE Radelof, U., Schneider, D. and Korn, B.  
JOURNAL Human Unigeneset - RZPD3  
COMMENT Unpublished  
Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD, IMAGp998D01781.  
RZPDLIB, I.M.A.G.E. cDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No. 972)  
[http://www.rzpd.de/CloneCards/cgi-  
bin/showlib.pl.cgi?responseLibNo=972](http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi?responseLibNo=972) Contact: Ina Rofls  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
[www.rzpd.de](http://www.rzpd.de)

This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCAACACAGAAACAGCTATGAC.

## FEATURES

**BOURCE**

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE998D01781 ; IMAGE:342096"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_1b="Soares_fetal_heart_NbH19W"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5
TGTTCACCATCTGCAAGTGGAGCGGCCGCATCTTTTTTTTTTTTTTT
3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung

```

BASE COUNT	113 a	129 c	92 g	98 t
ORIGIN				

**Alignment Scores:**

Pred. No.:	7.08e-68	Length:	432
Score:	71.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) X BX112106 (1-432)

QY	1	GIluGIuGIuSerThrIleGIuAsnTYrAlaSerArgProGLuAlaPheAsnThrProPhe	20
Db	99	GAGGAAGAAGCACCATTGAGAATTATGCGTCACGACCCGAGGCCCTTAAACACCCCGTTC	158
QY	21	LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla	40
Db	159	CTGAACATCGACAAATTGCGATCTGCGTTTAAGGCTGATGAGTTCCCTGAACCTGGCACGCC	218
QY	41	LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu	60
Db	219	CTCTTTGAGTCTATCAAAAAGGAACCTCTTCTCTCAACTGGATGCCTTCTCTAAGCTG	278
QY	61	LysGlyLeuArgSerAlaThrProAspAlaGln	71
Db	279	AAAGGACTGAGGAGCGCAACTCCTGATGCCCGAC	311

RESULT 13	
W69233	
LOCUS	W69233
	432 bp
	mRNA
	linear
	EST 16-OCT-1996

DEFINITION	z444c04.r1 Soares fetal heart NBHH19W Homo sapiens cDNA clone	
IMAGE	IMAGE:343494 5', mRNA sequence.	
ACCESSION	W69233	
VERSION	W69233.1	GI:1378493
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

## REFERENCE AUTHORS

**TITLE**

**JOURNAL  
COMMENT**

**COMMENT**

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

**Tel: 314 286 1800**  
**Fax: 314 286 1810**

Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)

This clone is available royalty-free through LBNL ; contact the IMAGE Consortium ([info@image.lbnl.gov](mailto:info@image.lbnl.gov)) for further information.

Insert Length: 442    Std Error: 0.00

Seq primer: mob.REGA+ET  
High quality sequence stop: 341.

**Location/Qualifiers**

**SOURCES**

**Source**

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1268869"
/db_xref="Xaxon:9606"
/clone="IMAGE:343494"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NBHL19W"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGGCCGCATCTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library was through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHL19W."

```

BASE COUNT	106 a	127 c	94 g	102 t	3 others
ORIGIN					

**Alignment Scores:**

Pred. No:	7,086-68	length:	432
Score:	71.00	Matches:	71
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Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) X W69233 (1-432)

Qy	1	GIUGIUGIUSerThrIleGIUAsnTyrrAlaSerArgProGIUAlaphAAsnThrProPhe	20
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Qy	21	IeuAsnIleAspLyIysLeuArgSerAlaphelysAlaAspGIUphLeuAsnTrpHisAla	40
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41 LeuPheGluSerIleLysValArgLysLeuProPheLeuValNTrpAspAlaPheProLysLeu 60

Db 216 CTCTTGAGTCTATCAAAAGGAACCTTCTTCTCAACTGGATGCTTCTTAAGCTG 275

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
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Db 276 AAAGACTGAGGAGCGCAACTCTGATGCCCA 308

RESULT 14

W69227 431 bp mRNA linear EST 16-OCT-1996  
LOCUS zd44b06.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone  
DEFINITION IMAGE:343475 5', mRNA sequence.

W69227  
W69227.1 GI:1378487

ACCESSION  
VERSION W69227.1 GI:1378487  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
The WashU-Merck EST Project

TITLE Unpublished  
JOURNAL  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
Insert Length: 466 Std Error: 0.00  
Seq primer: mob.REGA+ET  
High quality sequence stop: 410.

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source  
location/Qualifiers  
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/clone="IMAGE:343475"  
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/note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' GTTACCAATCTGAAGTGGAGCGCGCCGATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."

BASE COUNT 106 a 127 c 94 g 102 t 2 others

ORIGIN

Alignment Scores:  
Pred. No.: 1.07e-54 Length: 431  
Score: 59.00 Matches: 59  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 83.10% Indels: 0  
DB: 14 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x W69227 (1-431)

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Db 134 CCCGAGGCTTTAACACCCCGTTCTCGAACATCGACAAATTGCGATCGCTTAAGCT 193

QY 33 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 52  
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Db 194 GATGAGTTCCTGAAGTGGACGCGCCCTCTTGAGTCTATCAAAAGGAACCTCTTCCTC 253

QY 53 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 71  
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Db 254 AACTGGATGCTTCTTCTTAAGCTGAAGACTGAGAGCGCACTCTGATGCCCA 310

RESULT 15

AA393296 413 bp mRNA linear EST 16-MAY-1997  
LOCUS zc74f05.r1 Soares testis\_NHT Homo sapiens cDNA clone IMAGE:728097  
DEFINITION 5', mRNA sequence.

AA393296  
AA393296.1 GI:2046264

ACCESSION  
VERSION AA393296  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Scheilenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.  
WashU-Merck EST Project 1997

TITLE Unpublished  
JOURNAL  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
Seq primer: -28m3 rev2 ET from Amersham  
High quality sequence stop: 386.

FEATURES  
source  
location/Qualifiers  
1.413  
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/lab\_host="DH10B"  
/clone\_lib="Soares testis\_NHT"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5' GTTACCAATCTGAAGTGGAGCGCGCCCAATTTTCTTTTCTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 96 a 113 c 125 g 79 t

ORIGIN

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Pred. No.: 1.28e-53 Length: 413  
Score: 58.00 Matches: 71  
Percent Similarity: 98.61% Conservative: 0  
Best Local Similarity: 98.61% Mismatches: 0  
Query Match: 81.69% Indels: 1  
DB: 9 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AA393296 (1-413)

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Db      164  GAGGAGAGAAAGCACCAATTCAGAAATTATGCGTCACGACCCGAGGCCCTTTAACACCCCGAATT 223
QY      20  eLeuAsnIleAspIleLeuArgSerAlaPheIleAlaAspGluPheLeuAsnTrpHisAla 40
Db      224  CCTGAACATCGACAAATTGGATCTGCGTTTAAAGGCTGATGAGTTCCTGAACCTGGCACGC 283
QY      40  aLeuPheGluSerIleIleValArgLysLeuProPheLeuAsnTrpAspAlaPheProLysIle 60
Db      284  CCTCTTTGAGTCTATCAAAAGAAACTTCCCTTCCTCAACTGGGATGCGCTTCTTAAGCT 343
QY      60  uLysGlyLeuArgSerAlaThrProAspAlaGln 71
Db      344  GAAAGGACTGAGGAGCGCACTCCTGATGCCCAAG 377
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Search completed: November 28, 2003, 12:12:46  
Job time : 1608 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2003, 13:38:12 ; Search time 21 Seconds  
(without alignments)  
143.051 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99  
Perfect score: 375  
Sequence: 1 EBESTIENYASRPEAFNTPF.....LNWDAPFKLGLRSATPDAQ 71

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
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4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep: \*  
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6: /cgn2\_6/ptodata/2/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	375	100.0	99	4	US-09-996-243-201 Sequence 201, App
2	59.5	15.9	233	4	US-09-328-352-6059 Sequence 6059, App
3	59	15.7	324	4	US-08-311-731A-262 Sequence 262, App
4	56.5	15.1	518	3	US-08-999-723-2 Sequence 2, Appli
5	56.5	15.1	518	3	US-09-434-427-2 Sequence 2, Appli
6	56.5	15.1	518	4	US-09-548-372D-2 Sequence 2, Appli
7	56.5	15.1	518	4	US-09-548-367D-2 Sequence 2, Appli
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9	56	14.9	400	4	US-09-150-347-1 Sequence 1, Appli
10	56	14.9	400	4	US-09-665-313-1 Sequence 1, Appli
11	55	14.7	513	4	US-09-595-857B-30 Sequence 30, Appli
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13	54	14.4	285	4	US-09-328-352-6996 Sequence 6996, App
14	54	14.4	1098	1	US-08-290-301-82 Sequence 82, Appli
15	54	14.4	1098	4	US-09-013-598-82 Sequence 82, Appli
16	53.5	14.3	634	4	US-09-295-744A-2 Sequence 2, Appli
17	53.5	14.3	649	4	US-09-134-001C-3891 Sequence 3891, App
18	53.5	14.3	853	5	PCT-US92-09326-2 Sequence 2, Appli
19	53	14.1	187	3	US-08-981-392-46 Sequence 46, Appli
20	53	14.1	192	4	US-09-134-001C-5386 Sequence 5386, App
21	53	14.1	373	4	US-09-328-352-7009 Sequence 7009, App
22	53	14.1	401	4	US-09-252-991A-19274 Sequence 19274, A
23	53	14.1	693	4	US-08-705-477E-101 Sequence 101, App
24	53	14.1	707	1	US-08-528-122-18 Sequence 18, Appli
25	53	14.1	707	5	PCT-US95-11720-18 Sequence 2, Appli
26	53	14.1	750	1	US-08-325-553-2 Sequence 2, Appli
27	53	14.1	750	2	US-08-394-152A-2 Sequence 2, Appli

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35	52.5	14.0	382	4	US-09-252-991A-32165	Sequence 32165, A
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44	51.5	13.7	396	3	US-08-961-083-16	Sequence 16, Appli
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ALIGNMENTS

RESULT 1  
US-09-996-243-201  
; Sequence 201, Application US/09996243  
; Patent No. 6478825  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerltsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C13  
; CURRENT APPLICATION NUMBER: US/09/996, 243  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
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; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28

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6	PRIOR APPLICATION NUMBER: 60/089907
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61	PRIOR FILING DATE: 1998-07-01
62	PRIOR APPLICATION NUMBER: 60/091478
63	PRIOR FILING DATE: 1998-07-02
64	PRIOR APPLICATION NUMBER: 60/091544
65	PRIOR FILING DATE: 1998-07-01
66	PRIOR APPLICATION NUMBER: 60/091519
67	PRIOR FILING DATE: 1998-07-02
68	PRIOR APPLICATION NUMBER: 60/091626
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70	PRIOR APPLICATION NUMBER: 60/091633
71	PRIOR FILING DATE: 1998-07-02



; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 375; DB 4; Length 99;  
Best Local Similarity 100.0%; Pred. No. 2e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPPKL 60  
Db 29 EESTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPPKL 88

QY 61 KGLRSATPDAQ 71  
Db 89 KGLRSATPDAQ 99

## RESULT 2

US-09-328-352-6059  
; Sequence 6059, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 6059  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-6059

Query Match 15.9%; Score 59.5; DB 4; Length 233;  
Best Local Similarity 31.0%; Pred. No. 5.6;  
Matches 18; Conservative 12; Mismatches 21; Indels 7; Gaps 3;

QY 3 ESTIENYASRPEAFNTPLN----IDKLSAFKADFLNWHALFESIKRKLPLNWDAPPKL 56  
Db 166 QAWIDTYAG--EEFHTAVRNVLATVDKVAARCADDTLEKWHAAAY-TMGAKLEWLFNDS 220

## RESULT 3

US-08-311-731A-262  
; Sequence 262, Application US/08311731A  
; Patent No. 6583266  
; GENERAL INFORMATION:

; APPLICANT: SMITH, DOUGLAS  
; APPLICANT: MAO, JEN-I  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES  
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 411  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
; STREET: 600 ATLANTIC AVENUE  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/311,731A  
; FILING DATE:

; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GATES, EDWARD R.  
; REGISTRATION NUMBER: 31,616  
; REFERENCE/DOCKET NUMBER: C0044/7125  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/720-3500  
; TELEFAX: 617/720-2441  
; INFORMATION FOR SEQ ID NO: 262:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 324 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Mycobacterium leprae  
US-08-311-731A-262

Query Match 15.7%; Score 59; DB 4; Length 324;  
Best Local Similarity 30.8%; Pred. No. 9.7;  
Matches 20; Conservative 11; Mismatches 26; Indels 8; Gaps 3;

QY 11 SRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPPKL 64  
Db 62 SNLDSANIVFEVDEDTSTYDGDHAGAIKLDWRADLDPIKR--DFIDTQGFSLGDR 119

QY 65 SATPD 69  
Db 120 GISND 124

## RESULT 4

US-08-999-723-2  
; Sequence 2, Application US/08999723A  
; Patent No. 6025180  
; GENERAL INFORMATION:

; APPLICANT: Powell, David J.  
; APPLICANT: Southan, Christopher  
; APPLICANT: Chapman, Conrad G.  
; APPLICANT: Evans, Joanne R.  
; TITLE OF INVENTION: ASPI  
; FILE REFERENCE: GH70262  
; CURRENT APPLICATION NUMBER: US/08/999,723A  
; CURRENT FILING DATE: 1997-10-06  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 518  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-999-723-2

Query Match 15.1%; Score 56.5; DB 3; Length 518;  
Best Local Similarity 29.5%; Pred. No. 3.7;  
Matches 18; Conservative 8; Mismatches 18; Indels 17; Gaps 2;

QY 7 ENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPPKL 66  
Db 160 EDLVTIPKGFNTSPL-----VNIAIFESSENFPLPGIKWNG---ILGLAYA 202

QY 67 T 67  
Db 203 T 203

## RESULT 5

US-09-434-427-2  
; Sequence 2, Application US/09434427  
; Patent No. 6162630  
; GENERAL INFORMATION:

; APPLICANT: POWELL, DAVID J.  
; APPLICANT: SOUTHAN, CHRISTOPHER

```

; APPLICANT: CHAPMAN, CONRAD G.
; APPLICANT: EVANS, JOANNE R.
; TITLE OF INVENTION: ASP1
; FILE REFERENCE: GH-70262-D1
; CURRENT APPLICATION NUMBER: US/09/434,427
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: US 08/999,723
; EARLIER FILING DATE: 1997-10-06
; EARLIER APPLICATION NUMBER: UK 9626022.9
; EARLIER FILING DATE: 1996-12-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-434-427-2

```

Query Match	15.1%	Score 56.5;	DB 3;	Length 518;
Best Local Similarity	29.5%;	Pred. No. 37;		
Matches	18; Conservative	8; Mismatches	18;	Indels 17; Gaps 2;

QY       7 ENYASRPEAFNTPLNIDKRSFAKADEFNLWHALESISKRLPLFNWDAPFKLKGRSA 66  
         | : : | | | : | : | : | :  
Db      160 EDLVLPKGFTNSFL-----VNIATIFESENFLLPGIKWNG--ILGLAYA 2022

QY 67 T 67  
Db 203 T 203

RESULT 6  
US-09-548-372D-2  
; Sequence 2, Application US/09548372D

```

: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: 29915/62801
: CURRENT APPLICATION NUMBER: US/09/548,372D
: PRIOR FILING DATE: 2000-04-12
: PRIOR APPLICATION NUMBER: US 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 2
: LENGTH: 518
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-548-372D-2

```

Query Match	15.1%	Score 56.5;	DB 4;	Length 518;
Best Local Similarity	29.5%;	Pred. No. 37;		
Matches	18; Conservative	8; Mismatches	18;	Indels 17; Gaps 2

```

Oy      7  ENASRPEAFNTPLNIDKLSAFKADEFLNWHALESIRKRLPLFNWDAFPKLKGLRSA 66
      | : : | | | : | : | | : : |
Db     160 EDLVTIPIKGFNTSFL-----VNATIFESENFPLPGIKWNG---ILGLAYA 202

```

QY	67	T	67
Db	203	T	203

RESULT 7  
US-09-548-367D-2

```

; Sequence 2, application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-2

```

Query Match	15.1%;	Score 56.5;	DB 4;	Length 518;
Best Local Similarity	29.5%;	Pred. No. 37;		
Matches 18; Conservative	8;	Mismatches 18;	Indels 17;	Gaps 2;

```

QY      7  ENYASRPEAFNTPFNLINIDKLSAFKADFLNWHALFESIKRKLPLFNWDAFPKUKGARS 66
      | : : | | | | : | | | : | : |
Db     160 EDLVTPKGFNTSPL-----VNIAITFESBNFLLPGIKWNG---ITGLAYA 2022

```

QY 67 T 67  
Db 203 T 203

RESULT 8  
US-09-551-853D-2  
; Sequence 2, Application US/09551853D

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: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: 29915/6280L
: CURRENT APPLICATION NUMBER: US/09/551,853D
: CURRENT FILING DATE: 2000-04-18
: PRIOR APPLICATION NUMBER: US 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 2
: LENGTH: 518
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-551-853D-2

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Query Match	15.1%	Score 56.5;	DB 4;	length 518;
Best Local Similarity	29.5%;	Pred. No. 37;		
Matches	18;	Conservative	8;	Mismatches 18;
				Indels 17;
				Gaps 2;

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Qy      7  ENYASRPEAFNTPFPLNIDKLSAFKDEFLNWHALFESIKRKLPLFNWDFAFKLKGLSRA 66
      | : : | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db     160 EDLVTI PKGFNTSFL-----VNIAITFESENFLLPGIKWNG--ILGLAVA 202

```

OY 67 T 67  
Db 203 T 203

## RESULT 9

US-09-150-347-1  
; Sequence 1, Application US/09150347  
; Patent No. 6372269  
; GENERAL INFORMATION:  
; APPLICANT: Rangel-Aldao, Rafael  
; APPLICANT: Bravo, Adriana  
; APPLICANT: Sanchez, Beatriz  
; APPLICANT: Galindo-Castro, Ivan  
; TITLE OF INVENTION: Malt Beverage Having Stabilized Flavor and Methods of Production  
; FILE REFERENCE: 1390.0070004  
; CURRENT APPLICATION NUMBER: US/09/150,347  
; PRIOR FILING DATE: 1998-09-09  
; EARLIER APPLICATION NUMBER: 60/058,398  
; EARLIER FILING DATE: 1997-09-09  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 400  
; TYPE: PRT  
; ORGANISM: Saccharomyces carlsbergensis  
US-09-150-347-1

Query Match 14.9%; Score 56; DB 4; Length 400;  
Best Local Similarity 23.9%; Pred. No. 31;  
Matches 17; Conservative 9; Mismatches 27; Indels 18; Gaps 3;

OY 6 IENYASRPE-----AFNTPEL-NIDKLSAFKADFLNWHALFESIKRKLPP--- 51  
Db 55 VEYTYQRAQRPGTMITTEGAFISPOAGGYDNAPGVWSEQWVETWKIFNAIHEKKSFTWV 114  
OY 52 ----LWMDAFP 58  
Db 115 QLMVLGWMAFP 125

## RESULT 10

US-09-665-313-1  
; Sequence 1, Application US/09665313  
; Patent No. 6468567  
; GENERAL INFORMATION:  
; APPLICANT: Rangel-Aldao, Rafael  
; APPLICANT: Bravo, Adriana  
; APPLICANT: Sanchez, Beatriz  
; APPLICANT: Galindo-Castro, Ivan  
; TITLE OF INVENTION: Malt Beverage Having Stabilized Flavor and Methods of Production  
; FILE REFERENCE: 1390.0070004  
; CURRENT APPLICATION NUMBER: US/09/665,313  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: 09/150,347  
; PRIOR FILING DATE: 1998-09-09  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 400  
; TYPE: PRT  
; ORGANISM: Saccharomyces carlsbergensis  
US-09-665-313-1

Query Match 14.9%; Score 56; DB 4; Length 400;  
Best Local Similarity 23.9%; Pred. No. 31;  
Matches 17; Conservative 9; Mismatches 27; Indels 18; Gaps 3;

OY 6 IENYASRPE-----AFNTPEL-NIDKLSAFKADFLNWHALFESIKRKLPP--- 51  
Db 55 VEYTYQRAQRPGTMITTEGAFISPOAGGYDNAPGVWSEQWVETWKIFNAIHEKKSFTWV 114

OY 52 ----LWMDAFP 58  
Db 115 QLMVLGWMAFP 125

## RESULT 11

US-09-595-857B-30  
; Sequence 30, Application US/09595857B  
; Patent No. 6495743  
; GENERAL INFORMATION:  
; APPLICANT: Pauli, Robert E.  
; APPLICANT: Chen, Nancy J.  
; TITLE OF INVENTION: PLANT XYLANASES  
; FILE REFERENCE: 234612001800  
; CURRENT APPLICATION NUMBER: US/09/595,857B  
; PRIOR FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/141,543  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 513  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-595-857B-30

Query Match 14.7%; Score 55; DB 4; Length 513;  
Best Local Similarity 21.2%; Pred. No. 57;  
Matches 14; Conservative 14; Mismatches 30; Indels 8; Gaps 2;

OY 2 EESTIENYASRPEAFNTPEL-NIDKLSAFKADFLNWHALFESIKRKLPPFNWDAFPK 61  
Db 268 QPSWVKNIKDPNDVNMVTLNRINSVMKRYKG-KLTGWDVNNEN-----LHWDFEKG 319  
OY 62 GLRSAT 67  
Db 320 GANAST 325

## RESULT 12

US-08-117-083-22  
; Sequence 22, Application US/08117083  
; Patent No. 5719054  
; GENERAL INFORMATION:  
; APPLICANT: Boursnell, Michael E.  
; APPLICANT: Inglis, Stephen C.  
; APPLICANT: Munro, Alan J.  
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human  
; NUMBER OF SEQUENCES: 70  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Walter H. Dregger  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/117,083  
; FILING DATE: 10-SEP-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dregger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-58783  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989

TELEFAX: 415-398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 186 amino acids  
TYPE: amino acid  
STRANDEDNESS: double-  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-117-083-22

Query Match 14.5%; Score 54.5; DB 1; Length 186;  
Best Local Similarity 24.5%; Pred. No. 19;  
Matches 12; Conservative 10; Mismatches 8; Indels 19; Gaps 2;

OY 9 YASRPEAF-----NTP-----FLNIDKLSAFKADFLNW 38  
DB 22 FAEYPSRGSVSTTRTPRAGEVNGKDYNFVSVDKSKMKNNEFIEM 70

RESULT 13  
US-09-328-352-6996  
Sequence 6996, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 6996  
LENGTH: 285  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-6996

Query Match 14.4%; Score 54; DB 4; Length 285;  
Best Local Similarity 27.6%; Pred. No. 37;  
Matches 16; Conservative 10; Mismatches 26; Indels 6; Gaps 1;

OY 16 FNTPLNIDKLSAF-----KADEPLNHALFESIKRKLPLNWDAPFKLKGLSAT 67  
DB 4 FNDYVVICMNSAFIKNGIKLSPLFASTLSLTPVMAQATFLIWIPIYKIEANEKAT 61

RESULT 14  
US-08-290-301-82  
Sequence 82, Application US/08290301  
Patent No. 5792921  
GENERAL INFORMATION:  
APPLICANT: Londeborough, John  
APPLICANT: Tunnela, Outi  
APPLICANT: Palva, Tupio  
APPLICANT: Holmstrom, Kjell-Ove  
APPLICANT: Welin, Bjorn  
APPLICANT: Mandel, Abul  
TITLE OF INVENTION: Increasing the trehalose content  
TITLE OF INVENTION: of organisms by transforming them with combinations of  
TITLE OF INVENTION: the structural genes for trehalose synthase.  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Alko Ltd.  
STREET: PO Box 350  
CITY: Helsinki  
STATE: -  
COUNTRY: Finland  
ZIP: SF-00101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb  
COMPUTER: IBM PC/XT/AT  
OPERATING SYSTEM: PC-DOS

SOFTWARE: WP5.1 file exported as DOS text file  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/290,301  
FILING DATE: 15 August 1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FI 943133  
FILING DATE: 29 June 1994  
APPLICATION NUMBER: PCT/FI93/00049  
FILING DATE: 15 February 1993  
APPLICATION NUMBER: 07/841,997  
FILING DATE: 28 February 1992  
APPLICATION NUMBER: 07/836,021  
FILING DATE: 14 February 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Kubovcik, Ronald J.  
NAME: Lydon, James C.  
REGISTRATION NUMBER: 25,401  
REGISTRATION NUMBER: 30,082  
REFERENCE/DOCKET NUMBER: LAIN-001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 467-6300  
TELEFAX: (202) 466-2006  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1098 amino acids  
TYPE: Amino acid  
TOPOLOGY: Linear  
MOLECULE TYPE: Polypeptide  
HYPOTHETICAL: yes  
US-08-290-301-82

Query Match 14.4%; Score 54; DB 1; Length 1098;  
Best Local Similarity 23.5%; Pred. No. 2e+02;  
Matches 16; Conservative 11; Mismatches 33; Indels 8; Gaps 1;

OY 3 ESTIENYASRPEAFNTPLNIDKLSAFKADFLNHALFESIKRKLPLNWDAPFKLKG 54  
DB 287 ESDPDDLTPADEEYVSDLEMDAKQDYKVPKFGYSNKSLLKYYALLRSSQELFSRLPW 346

OY 55 DAFPKLG 62  
DB 347 SIVPSIKG 354

RESULT 15  
US-09-013-598-82  
Sequence 82, Application US/09013598  
Patent No. 6323001  
GENERAL INFORMATION:  
APPLICANT: Londeborough, John  
APPLICANT: Tunnela, Outi  
APPLICANT: Palva, Tupio  
APPLICANT: Holmstrom, Kjell-Ove  
APPLICANT: Welin, Bjorn  
APPLICANT: Mandel, Abul  
TITLE OF INVENTION: Increasing the trehalose content  
TITLE OF INVENTION: of organisms by transforming them with combinations of  
TITLE OF INVENTION: the structural genes for trehalose synthase.  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Alko Ltd.  
STREET: PO Box 350  
CITY: Helsinki  
STATE: -  
COUNTRY: Finland  
ZIP: SF-00101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb  
COMPUTER: IBM PC/XT/AT  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WP5.1 file exported as DOS text file

APPLICATION NUMBER: US/09/013,598  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/290,301  
FILING DATE:  
APPLICATION NUMBER: PCT/FI93/00049  
FILING DATE: 15 February 1993  
APPLICATION NUMBER: 07/841,997  
FILING DATE: 28 February 1992  
APPLICATION NUMBER: 07/836,021  
FILING DATE: 14 February 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Kubovcik, Ronald J.  
NAME: Lydon, James C.  
REGISTRATION NUMBER: 25,401  
REGISTRATION NUMBER: 30,082  
REFERENCE/DOCKET NUMBER: LAIN-001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 467-6300  
TELEFAX: (202) 466-2006  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1098 amino acids  
TYPE: Amino acid  
TOPOLOGY: Linear  
MOLECULE TYPE: Polypeptide  
HYPOTHETICAL: Yes  
US-09-013-598-82

Query Match 14.4%; Score 54; DB 4; Length 1098;  
Best Local Similarity 23.5%; Pred. No. 2e+02;  
Matches 16; Conservative 11; Mismatches 33; Indels 8; Gaps 1;  
QY 3 ESTIENYASRPEAFNTPLNIDKLSAFKADF-----LNWHLFESIKRKLPLNW 54  
Db 287 ESDPDDLTTAPDEEYVSDLEMDAKQDYKVPKFGYSNKSRLKRYALLRSSQELFSRLPW 346  
QY 55 DAFPKLKG 62  
Db 347 SIVPSIKG 354

Search completed: November 28, 2003, 13:41:30  
Job time : 24 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 13:43:24 ; Search time 2638 Seconds

(without alignments)  
1101.055 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99  
Perfect score: 375

Sequence: 1 EESTIENYASRPEAFNTPP.....LNWDAFPKLGKLSATPDAQ 71

Scoring table: BLOSUM62

Xgapop 10.0 ,	Xgapext 0.5
Ygapop 10.0 ,	Ygapext 0.5
Fgapop 6.0 ,	Fgapext 7.0
Delop 6.0 ,	Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO\_spool/US10059395/runat\_25112003\_141912\_11679/app\_query.fasta\_1.263  
-DB=GenEmbl -QFMT=fastap -SUFFIX=rgc -MINMATCH=0.1 -IOOPT=0 -LOOPEXT=0  
-UNITS=bite -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10059395 @CGN 1 1 3508 @runat\_25112003\_141912\_11679 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_hcg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*  
15: gb\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
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19: em\_mu: \*  
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22: em\_ov: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*

29: em\_vi: \*  
30: em\_htg\_hum: \*  
31: em\_htg\_inv: \*  
32: em\_htg\_other: \*  
33: em\_htg\_mus: \*  
34: em\_htg\_pjn: \*  
35: em\_htg\_rod: \*  
36: em\_htg\_mam: \*  
37: em\_htg\_vtc: \*  
38: em\_sy: \*  
39: em\_htgo\_hum: \*  
40: em\_htgo\_mus: \*  
41: em\_htgo\_other: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	375	100.0	414	6	AX055438	AX055438 Sequence
2	375	100.0	415	6	AR252517	AR252517 Sequence
3	375	100.0	415	6	AX077031	AX077031 Sequence
4	375	100.0	415	6	AX358892	AX358892 Sequence
5	375	100.0	415	6	AX362385	AX362385 Sequence
6	375	100.0	415	6	AX403313	AX403313 Sequence
7	375	100.0	415	6	AX454546	AX454546 Sequence
8	375	100.0	415	6	AX491024	AX491024 Sequence
9	375	100.0	432	6	AX080815	AX080815 Sequence
10	375	100.0	432	6	AX080818	AX080818 Sequence
11	375	100.0	456	6	BD082389	BD082389 87 human
12	375	100.0	490	6	AX080817	AX080817 Sequence
13	375	100.0	529	9	HS4293408	AJ293408 Homo sapi
14	368	98.1	435	6	AX080816	AX080816 Sequence
15	362	96.5	435	6	AX041085	AX041085 Sequence
16	308	82.1	278	6	AB011028	AB011028 Rattus no
17	219.5	58.5	449	10	AR248775	AR248775 Sequence
18	210.5	56.1	288	6	CH19F21246	AD001502 Homo sapi
19	109	29.1	44679	9	BD01921246	BD01921246 Sequence
20	82.5	22.0	590	6	BD025234	AC120613 Rattus no
21	80	21.3	244944	2	AC120613	AC099301 Rattus no
22	80	21.3	263584	2	AC099301	AX135555 Sequence
23	78.5	20.9	700	6	AX135555	BC011886 Homo sapi
24	78.5	20.9	1000	9	BC011886	AK096215 Homo sapi
25	78.5	20.9	1579	9	AK096215	BC035311 Homo sapi
26	78.5	20.9	1982	9	BC035311	AC007581 Drosophila
27	78	20.8	156508	3	AC007581	AC007574 Drosophila
28	78	20.8	171151	3	AC007574	AE003464 Drosophila
29	78	20.8	310958	3	AE003464	AX602111 Sequence
30	74	19.7	680	6	AX602111	X65871 H. vulgare m
31	74	19.7	2667	8	HVSSYNMR	AC096645 Homo sapi
32	74	19.7	167878	9	AC096645	AE012868 Chlorobiu
33	73.5	19.6	9216	1	AE012868	AC097151 Rattus no
34	73	19.5	243387	2	AC097151	AC111694 Rattus no
35	73	19.5	267104	2	AC111694	AC105854 Rattus no
36	73	19.5	303894	2	AC105854	Continuation (4 of
37	72.5	19.3	55568	2	AC015850_3	AC087611 Homo sapi
38	72.5	19.3	104869	9	AC087611	Continuation (3 of
39	72.5	19.3	110000	2	AC015850_2	AE009124 Agrobacte
40	72	19.2	11533	1	AE009124	AE008089 Agrobacte
41	72	19.2	12074	1	AE008089	AC121065 Gallus ga
42	72	19.2	140667	2	AC121065	AX607240 Sequence
43	71	18.9	1155	6	AX607240	AX602209 Sequence
44	71	18.9	97666	6	AX602209	AC100808 Homo sapi
45	71	18.9	148801	9	AC100808	

RESULT 1

#### ALIGNMENTS

AX055438  
LOCUS AX055438 414 bp DNA linear PAT 13-JAN-2001  
DEFINITION Sequence 68 from Patent WO0073452.  
ACCESSION AX055438  
VERSION AX055438.1 GI:12228711  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE  
AUTHORS 1 Ashkenazi, A.J., Baker, K.P., Chan, B., Goddard, A., Godowski, P.J.,  
Gurney, A.L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D.L.,  
Tumas, D., Watanabe, C.K. and Wood, W.I.  
TITLE Compositions and methods for the treatment of immune related  
diseases  
JOURNAL Patent: WO 0073452-A 68 07-DEC-2000;  
Genentech, Inc. (US)

FEATURES  
source location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 98 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 8.02e-44 Length: 414  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX055438 (1-414)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
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QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrPheHisAla 40  
Db 157 CTGAACATCGACAATGCGATCTGCGTTAAGGCTGATGAGTTCTCTGAACCTGGCAGCC 216

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnThrPaspAlaPheProLysLeu 60  
Db 217 CTCTTGAGTCTATCAAAAGGAACTTCCTTCTCACTGGGATGCCCTTCTTAAGCTG 276

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGACTGAGAGCGCAACTCCTGATGCCAG 309

RESULT 2  
AR252517  
LOCUS AR252517 415 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 200 from patent US 6478825.  
ACCESSION AR252517  
VERSION AR252517.1 GI:27300425  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 415)  
AUTHORS Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.  
TITLE Implant, method of making same and use of the implant for the  
treatment of bone defects  
JOURNAL Patent: US 6478825-A 200 12-NOV-2002;  
location/Qualifiers  
1..415  
/organism="unknown"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 8.05e-44 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AR252517 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 97 GAGGAAGAAGCACCATTGAGATTATGCGTCACGACCGAGCCCTTAAACCCCGTTTC 156

QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrPheHisAla 40  
Db 157 CTGAACATCGACAATGCGATCTGCGTTAAGGCTGATGAGTTCTCTGAACCTGGCAGCC 216

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnThrPaspAlaPheProLysLeu 60  
Db 277 AAAGACTGAGAGCGCAACTCCTGATGCCAG 309

RESULT 3  
AX077031  
LOCUS AX077031 415 bp DNA linear PAT 22-FEB-2001  
DEFINITION Sequence 19 from Patent WO0105972.  
ACCESSION AX077031  
VERSION AX077031.1 GI:13121661  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE  
AUTHORS 1 Ashkenazi, A.J., Baker, K.P., Fong, S., Goddard, A., Godowski, P.J.,  
Gurney, A.L., Hillan, K.J., Mark, M.R., Marsters, S.A., Pitti, R.M.,  
Tumas, D., Watanabe, C.K. and Wood, W.I.  
TITLE Compositions and methods for the treatment of immune related  
diseases  
JOURNAL Patent: WO 0105972-A 19 25-JAN-2001;  
Genentech, Inc. (US)

FEATURES  
source location/Qualifiers  
1..415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 8.05e-44 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX077031 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 97 GAGGAAGAAGCACCATTGAGATTATGCGTCACGACCGAGCCCTTAAACCCCGTTTC 156

QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrPheHisAla 40  
Db 157 CTGAACATCGACAATGCGATCTGCGTTAAGGCTGATGAGTTCTCTGAACCTGGCAGCC 216

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnThrPaspAlaPheProLysLeu 60  
Db 277 AAAGACTGAGAGCGCAACTCCTGATGCCAG 309

Db 217 CTCTTGAGTCTATCAAGAAGAACTTCCTTCTCACTGGGATGCCCTTCTTAAGCTG 276

Qy 61 LygGlyLeuArgSerAlaThrProAspAlaGln 71  
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Db 277 AAAGGACTGAGGAGCGCAACTCCTGATGCCAG 309

RESULT 4  
AX358892 415 bp DNA linear PAT 13-FEB-2002  
LOCUS AX358892  
DEFINITION Sequence 145 from Patent WO0193983.  
ACCESSION AX358892  
VERSION AX358892.1 GI:18675347  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,  
Watanabe, C.K. and Wood, W.I.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0193983-A 145 13-DEC-2001;  
Genentech Inc. (US)  
FEATURES  
source 1. .415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 8.05e-44 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX358892 (1-415)

Qy 1 GIUGLUGLuserThriIleGluAsnTYrAlaSerArgProGluAlaPheAsnThrProPhe 20  
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Db 97 GAGGAAGAAAGCACCATTTAGAAATTATGCGTCACGACCCGAGGCTTTAAACACCCCGTTTC 156

Qy 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
|||||  
Db 157 CTGAACATCGACAATTCGATTCGCTTAAAGCTGATGAGTTCTTGAAGTGGCAGCC 216

Qy 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
|||||  
Db 217 CTCTTGAGTCTATCAAGAAGAACTTCCTTCTCACTGGGATGCCCTTCTTAAGCTG 276

Qy 61 LygGlyLeuArgSerAlaThrProAspAlaGln 71  
|||||  
Db 277 AAAGGACTGAGGAGCGCAACTCCTGATGCCAG 309

RESULT 5  
AX362385 415 bp DNA linear PAT 15-FEB-2002  
LOCUS AX362385  
DEFINITION Sequence 145 from Patent WO0208288.  
ACCESSION AX362385  
VERSION AX362385.1 GI:18694650  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,

Watanabe, C.K. and Wood, W.I.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0208288-A 145 31-JAN-2002;  
Genentech, Inc. (US)  
FEATURES  
source 1. .415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 8.05e-44 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX362385 (1-415)

Qy 1 GIUGLUGLuserThriIleGluAsnTYrAlaSerArgProGluAlaPheAsnThrProPhe 20  
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Db 97 GAGGAAGAAAGCACCATTTAGAAATTATGCGTCACGACCCGAGGCTTTAAACACCCCGTTTC 156

Qy 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
|||||  
Db 157 CTGAACATCGACAATTCGATTCGCTTAAAGCTGATGAGTTCTTGAAGTGGCAGCC 216

Qy 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
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Db 217 CTCTTGAGTCTATCAAGAAGAACTTCCTTCTCACTGGGATGCCCTTCTTAAGCTG 276

Qy 61 LygGlyLeuArgSerAlaThrProAspAlaGln 71  
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Db 277 AAAGGACTGAGGAGCGCAACTCCTGATGCCAG 309

RESULT 6  
AX403313 415 bp DNA linear PAT 14-JUN-2002  
LOCUS AX403313  
DEFINITION Sequence 200 from Patent WO0073454.  
ACCESSION AX403313  
VERSION AX403313.1 GI:21436871  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Aehkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Eaton, D.,  
Ferrara, N., Gerder, H., Gerritsen, M., Goddard, A., Godowski, P.,  
Grimaldi, C.J., Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J.,  
Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,  
Williams, P., Wood, W.I. and Zhang, Z.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0073454-A 200 07-DEC-2000;  
Genentech Inc. (US)  
FEATURES  
source 1. .415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 8.05e-44 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AX403313 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAAGAAGCACCATTTGAGAATTATGCGTCACGACCCGAGGCGCTTTAACAACCCCGTTC 156

QY 21 LeuAsnIleAspIleuArgSerAlaThrProAspAlaGln 40  
DB 157 CTGAACATCGACAAATTCGATCTGCGTTAAGGCTGATGAGTTCCTGAAGTGGACGCGC 216

QY 41 LeuPheGluSerIleIleuArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
DB 217 CTCCTTGAGTCTATCAAAAGGAACTTCCTTCTCAACTGGATGCTTCTTAAGCTG 276

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGGAGCGCACTCTGATGCCAG 309

RESULT 7  
AX454546 415 bp DNA linear PAT 06-JUL-2002  
LOCUS Sequence 131 from Patent WO0208284.  
ACCESSION AX454546  
VERSION AX454546.1 GI:21713897  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
and Ye, W.  
Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
Patent: WO 0208284-A 131 31-JAN-2002;  
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone  
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,  
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;  
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)  
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;  
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William  
I. (US)

TITLE Location/Qualifiers  
JOURNAL 1. .415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

FEATURES  
source  
Location/Qualifiers  
1. .415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Alignment Scores:  
Pred. No.: 8.05e-44 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AX454546 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAAGAAGCACCATTTGAGAATTATGCGTCACGACCCGAGGCGCTTTAACAACCCCGTTC 156

QY 21 LeuAsnIleAspIleuArgSerAlaThrProAspAlaGln 40  
DB 157 CTGAACATCGACAAATTCGATCTGCGTTAAGGCTGATGAGTTCCTGAAGTGGACGCGC 216

QY 41 LeuPheGluSerIleIleuArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
DB 217 CTCCTTGAGTCTATCAAAAGGAACTTCCTTCTCAACTGGATGCTTCTTAAGCTG 276

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGGAGCGCACTCTGATGCCAG 309

RESULT 8  
AX491024 415 bp DNA linear PAT 16-AUG-2002  
LOCUS Sequence 131 from Patent WO0200690.  
ACCESSION AX491024  
VERSION AX491024.1 GI:22323849  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
and Ye, W.  
Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
Patent: WO 0200690-A 131 03-JAN-2002;  
Genentech, Inc. (US)

TITLE Location/Qualifiers  
JOURNAL 1. .415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

FEATURES  
source  
Location/Qualifiers  
1. .415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Alignment Scores:  
Pred. No.: 8.05e-44 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AX491024 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAAGAAGCACCATTTGAGAATTATGCGTCACGACCCGAGGCGCTTTAACAACCCCGTTC 156

QY 21 LeuAsnIleAspIleuArgSerAlaThrProAspAlaGln 40  
DB 157 CTGAACATCGACAAATTCGATCTGCGTTAAGGCTGATGAGTTCCTGAAGTGGACGCGC 216

QY 41 LeuPheGluSerIleIleuArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
DB 217 CTCCTTGAGTCTATCAAAAGGAACTTCCTTCTCAACTGGATGCTTCTTAAGCTG 276

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGGAGCGCACTCTGATGCCAG 309

RESULT 9  
AX574494 415 bp DNA linear PAT 07-JAN-2003  
LOCUS Sequence 21 from Patent WO0224888.  
ACCESSION AX574494  
VERSION AX574494.1 GI:27551800  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Baker, K.P., Eaton, D.L., Filvaroff, E., Goddard, A., Grimaldi, J.C.,  
Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K., Wood, W.I.,  
Zhang, Z. and Fong, S.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0224888-A 21 28-MAR-2002;  
GENENTECH, INC. (US)  
FEATURES Location/Qualifiers  
source 1. 415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 8.05e-44 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX574494 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
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DB 97 GAGGAAGAAAGCACCATTGAGATTATGCGTACGACCGAGGCCCTTAACACCCCGTTC 156

QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
|||||  
DB 157 CTGAACATCGACAATTGCGATCTGCGTTTAAGGCTGATGAGTTCCTGAAGTGGACAGCC 216

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
|||||  
DB 217 CTCTTGAGTCTATCAAAAGAACTCTTCTCTCAACTGGAGTGCCTTCTTAAGCTG 276

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
|||||  
DB 277 AAAGGACTGAGAGCGCAACTCTGATGCCAG 309

RESULT 10  
AX080815 432 bp DNA linear PAT 27-FEB-2001  
LOCUS Sequence 61 from Patent WO0109327.  
AX080815  
VERSION AX080815.1 GI:13169784  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE artificial sequences.  
AUTHORS 1  
Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Kljasin, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Pitti, R.M.,  
Watanabe, C.K. and Wood, W.I.  
TITLE Method of preventing the injury or death of retinal cells and  
treating ocular diseases  
JOURNAL Patent: WO 0109327-A 61 08-FEB-2001;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
source 1. 432  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Virtual DNA fragment used in the isolation of  
DN557694."  
BASE COUNT 106 a 127 c 94 g 102 t 3 others  
ORIGIN

Alignment Scores:  
Pred. No.: 8.45e-44 Length: 432  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

Percent Similarity: 100.00% Conservative: 0  
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Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

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QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
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QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
|||||  
DB 156 CTGAACATCGACAATTGCGATCTGCGTTTAAGGCTGATGAGTTCCTGAAGTGGACAGCC 215

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
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DB 216 CTCTTGAGTCTATCAAAAGAACTCTTCTCTCAACTGGAGTGCCTTCTTAAGCTG 275

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
|||||  
DB 276 AAAGGACTGAGAGCGCAACTCTGATGCCCAA 308

RESULT 11  
AX080818 432 bp DNA linear PAT 27-FEB-2001  
LOCUS Sequence 64 from Patent WO0109327.  
AX080818  
VERSION AX080818.1 GI:13169787  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1  
Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Kljasin, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Pitti, R.M.,  
Watanabe, C.K. and Wood, W.I.  
TITLE Method of preventing the injury or death of retinal cells and  
treating ocular diseases  
JOURNAL Patent: WO 0109327-A 64 08-FEB-2001;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
source 1. 432  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 106 a 127 c 94 g 102 t 3 others  
ORIGIN

Alignment Scores:  
Pred. No.: 8.45e-44 Length: 432  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

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DB 96 GAGGAAGAAAGCACCATTGAGATTATGCGTACGACCGAGGCCCTTAACACCCCGTTC 155

QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
|||||  
DB 156 CTGAACATCGACAATTGCGATCTGCGTTTAAGGCTGATGAGTTCCTGAAGTGGACAGCC 215

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
|||||  
DB 216 CTCTTGAGTCTATCAAAAGAACTCTTCTCTCAACTGGAGTGCCTTCTTAAGCTG 275

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71



|||||  
Db 276 AAAGACTGAGAGCGCACTCCTGATGCCCA 308  
RESULT 12  
BD082389  
LOCUS BD082389 456 bp DNA linear PAT 27-AUG-2002  
DEFINITION 87 human secreted proteins.  
ACCESSION BD082389  
VERSION BD082389.1 GI:22627999  
KEYWORDS JP 2001522239-A/31.  
SOURCE Mastadenovirus  
ORGANISM Mastadenovirus  
REFERENCE Viruses; dsDNA viruses, no RNA stage; Adenoviridae.  
1 (bases 1 to 456)  
AUTHORS Young,P., Greene,J.M., Ferrie,A.M., Ruben,S.M., Rosen,C.A.,  
Duan,R.D., Hu,J.S., Florence,K.A., Olsen,H.S., Ebner,R.,  
Brewer,L.A., Moore,P.A., Shi,Y., Lafleur,D.W. and Ni,J.  
TITLE 87 human secreted proteins  
JOURNAL Patent: JP 2001522239-A 31 13-NOV-2001;  
HUMAN GENOME SCIENCES INC SECRETARY OF THE DEPARTMENT OF HEALTH  
HUMAN SERVICES  
COMMENT PN JP 2001522239-A/31  
PD 13-NOV-2001  
PF 19-MAR-1998 JP 1998542119  
PR 21-MAR-1997 US 60/041281,21-MAR-1997 US 60/041276 PR  
21-MAR-1997 US 60/042344,21-MAR-1997 US 60/041277 PR  
30-MAY-1997 US 60/048355,30-MAY-1997 US 60/048096 PR  
30-MAY-1997 US 60/048351,30-MAY-1997 US 60/048154 PR  
30-MAY-1997 US 60/048160,30-MAY-1997 US 60/048069 PR  
30-MAY-1997 US 60/048131,30-MAY-1997 US 60/048186 PR  
30-MAY-1997 US 60/048095,30-MAY-1997 US 60/048187 PR  
30-MAY-1997 US 60/048099,30-MAY-1997 US 60/050937 PR  
30-MAY-1997 US 60/048352,30-MAY-1997 US 60/048135 PR  
30-MAY-1997 US 60/048188,30-MAY-1997 US 60/048094 PR  
30-MAY-1997 US 60/048350,05-AUG-1997 US 60/054804 PR  
19-AUG-1997 US 60/056370,02-OCT-1997 US 60/060862 PI  
YOUNG,JOHN M GREENE,ANN M FERRIE,STEVEN M RUBEN,CRAIG A PI  
ROSEN,  
PI ROXANNE D DUAN,JING SHAN HU,KIMBERLY A FLORENCE,HENRIK S  
OLSEN,  
PI REINHARD EBNER,LAURIE A BREWER,PAUL A MOORE,YANGGU SHI,DAVID W  
PI LAFLEUR,  
PI JIAN NI  
PC C07K14/00  
CC Strandedness: Double;  
CC Topology: Linear;  
FH Key Location/Qualifiers.  
FEATURES  
source 1..456  
/organism="Mastadenovirus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10509"  
BASE COUNT 117 a 136 c 104 g 98 t 1 others  
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Alignment Scores:  
Pred. No.: 9.02e-44 length: 456  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
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QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 105 GAGGAGAAGACCATGTGAGAAATTATGCGTCACGACCGAGGCTTTAACACCCCGTTC 164  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 165 CTGAACATCGACAATTCGATCTGCGTTTAAGGCTGATGATTCCTGAAGTGCACGCC 224

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 225 CTCTTGAGTCTATCAAAAGGAACCTTCCTTCTCACTGGGATGCTTCTTAAGCTG 284  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 285 AAAGACTGAGAGCGCAACTCCTGATGCCAG 317  
RESULT 13  
AX080817 490 bp DNA linear PAT 27-FEB-2001  
LOCUS AX080817  
DEFINITION Sequence 63 from Patent WO0109327.  
ACCESSION AX080817  
VERSION AX080817.1 GI:13169786  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Ashkenazi,A.J., Baker,K.P., Goddard,A., Godowski,P.J., Gurney,A.L.,  
Kljavin,I.J., Lafleur,M., Mark,M.R., Masters,S.A., Pitti,R.M.,  
Watanabe,C.K. and Wood,W.I.  
TITLE Method of preventing the injury or death of retinal cells and  
JOURNAL Patent: WO 0109327-A 63 08-FEB-2001;  
Genentech, Inc. (US)  
FEATURES  
source 1..490  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Virtual DNA fragment used in the isolation of  
DNAs7694."  
BASE COUNT 118 a 149 c 116 g 107 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 9.84e-44 length: 490  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
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QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 164 GAGGAGAAGACCATGTGAGAAATTATGCGTCACGACCGAGGCTTTAACACCCCGTTC 223  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 224 CTGAACATCGACAATTCGATCTGCGTTTAAGGCTGATGATTCCTGAAGTGCACGCC 283  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 284 CTCTTGAGTCTATCAAAAGGAACCTTCCTTCTCACTGGGATGCTTCTTAAGCTG 343  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 344 AAAGACTGAGAGCGCAACTCCTGATGCCAG 376  
RESULT 14  
HSA293408 529 bp mRNA linear PRI 06-JAN-2003  
LOCUS HSA293408  
DEFINITION Homo sapiens mRNA differentially expressed in malignant melanoma,  
clone NM 15.  
ACCESSION AJ293408  
VERSION AJ293408.1 GI:27526545  
KEYWORDS differential expression; malignant; melanoma.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Deichmann, M., Thome, M., Wacker, J. and Naeher, H.  
TITLE Genes differentially expressed in malignant melanoma  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 529)  
AUTHORS Deichmann, M.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Deichmann M., Dermatology, University Of Heidelberg, Vossstrasse 2, 69115 Heidelberg, GERMANY

FEATURES  
source 1. 529  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="NN 15"

mRNA 1. 529  
/note="differentially expressed in malignant melanoma"

BASE COUNT 133 a 157 c 126 g 113 t

ORIGIN

Alignment Scores:  
Pred. No.: 1.06e-42 Length: 529  
Score: 368.00 Matches: 70  
Percent Similarity: 98.59% Conservative: 0  
Best Local Similarity: 98.59% Mismatches: 1  
Query Match: 98.13% Indels: 0  
DB: 9 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x HSA293408 (1-529)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
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QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
|||||  
DB 195 CTGAACATCGACAATTGCGATTCGCTTTAAGGCTGATGAGTTCCTGAACCTGGCAGCC 254

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
|||||  
DB 255 CTCTTGAGTCTATCAAAAGGAACTTCCTTCTCAACTGGGATGCTTCTCTAAGCTG 314

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
|||||  
DB 315 AAGGACTGAGGAGCGCACTCCTGATGCCAG 347

RESULT 15  
AX080816 435 bp DNA linear PAT 27-FEB-2001  
LOCUS Sequence 62 from Patent WO0109327.  
ACCESSION AX080816  
VERSION AX080816.1 GI:13169785  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L., Kljavin, I.J., Lafleur, M., Mark, M.R., Masters, S.A., Pitti, R.M., Watanabe, C.K. and Wood, W.I.  
TITLE Method of preventing the injury or death of retinal cells and treating ocular diseases  
JOURNAL Patent: WO 0109327-A 62 08-FEB-2001;  
Genentech, Inc. (US)  
FEATURES  
source 1. 435  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Virtual DNA fragment used in the isolation fo DNA57694."

BASE COUNT 108 a 130 c 96 g 101 t  
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Pred. No.: 5.95e-42 Length: 435  
Score: 362.00 Matches: 71  
Percent Similarity: 98.61% Conservative: 0  
Best Local Similarity: 98.61% Mismatches: 0  
Query Match: 96.53% Indels: 1  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX080816 (1-435)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
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DB 99 GAGGAAGAAAGCACCATTGAGAAATTATGCGTCACGACCCGAGGCGCTTTAACACCCCGTT 158

QY 20 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
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DB 159 CCGAATCGACAATTGCGATCTGCGTTTAAAGGCTGATGAGTTCTGAACCTGGCAGCC 218

QY 40 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLe 60  
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DB 219 CTCTTGAGTCTATCAAAAGGAACTTCCTTCTCAACTGGGATGCTTCTCTAAGCT 278

QY 60 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
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DB 279 GAAAGACTGAGAGCGCACTCCTGATGCCAG 312

Search completed: November 28, 2003, 14:29:23  
Job time : 2641 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 13:44:54 ; Search time 53 Seconds

(without alignments)  
591.287 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Perfect score: 375

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Fgapop 6.0			7.0
Delop 6.0			7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	375	100.0	415	4	US-09-996-243-200 Sequence 200, App
2	210.5	56.1	288	4	US-09-313-294A-4134 Sequence 4134, Ap
3	78.5	20.9	686	3	US-09-328-111-364 Sequence 364, App
4	67.5	18.0	1830121	4	US-09-557-884-1 Sequence 1, Appli
5	67.5	18.0	1830121	4	US-09-643-990A-1 Sequence 1, Appli
6	62.5	16.7	4084	3	US-08-866-340-1 Sequence 1, Appli
7	62.5	16.7	4460	3	US-09-103-875-4 Sequence 4, Appli
8	62	16.5	1845	4	US-09-328-352-1350 Sequence 1350, Ap
9	62	16.5	71989	4	US-09-443-501A-2 Sequence 2, Appli
10	60.5	16.1	1664976	4	US-08-916-421B-1 Sequence 1, Appli
11	60	16.0	1542	1	US-08-328-962-1 Sequence 1, Appli
12	59.5	15.9	702	4	US-09-328-352-1933 Sequence 1933, Ap

13	59.5	15.9	2253	4	US-09-107-532A-2214	Sequence 2214, Ap
14	59	15.7	40123	4	US-08-311-731A-137	Sequence 137, App
15	58	15.5	1062	4	US-08-961-527-197	Sequence 197, App
16	57	15.2	340	3	US-08-836-075A-61	Sequence 61, Appl
17	57	15.2	2095	1	US-08-405-230-8	Sequence 8, Appli
18	57	15.2	2095	2	US-08-910-990-8	Sequence 8, Appli
19	57	15.2	2564	3	US-08-276-968A-19	Sequence 19, Appl
20	57	15.2	4655	4	US-09-643-597-151	Sequence 151, App
21	57	15.2	4655	4	US-09-480-884A-151	Sequence 151, App
22	57	15.2	4655	4	US-09-542-615A-151	Sequence 151, App
23	57	15.2	4655	4	US-09-606-421B-151	Sequence 151, App
24	57	15.2	4849	4	US-09-542-597-335	Sequence 335, App
25	57	15.2	4849	4	US-09-542-615A-335	Sequence 335, App
26	57	15.2	4849	4	US-09-606-421B-335	Sequence 335, App
27	57	15.2	1830121	4	US-09-557-884-1	Sequence 1, Appli
28	57	15.2	1830121	4	US-09-643-990A-1	Sequence 1, Appli
29	56.5	15.1	1021	4	US-09-280-116-85	Sequence 85, Appl
30	56.5	15.1	1804	4	US-09-548-372D-1	Sequence 1, Appli
31	56.5	15.1	1804	4	US-09-548-367D-1	Sequence 1, Appli
32	56.5	15.1	1804	4	US-09-551-853D-1	Sequence 1, Appli
33	56.5	15.1	1862	3	US-08-999-723-1	Sequence 1, Appli
34	56.5	15.1	1862	3	US-09-434-427-1	Sequence 1, Appli
35	56.5	15.1	18596	3	US-09-318-448-11	Sequence 11, Appl
36	56.5	15.1	61663	4	US-09-453-702B-62	Sequence 62, Appl
37	56	14.9	1005	4	US-08-961-527-354	Sequence 354, App
38	56	14.9	2022	1	US-08-803-972-6	Sequence 6, Appli
39	56	14.9	2022	1	US-08-803-972-6	Sequence 6, Appli
40	56	14.9	2058	1	US-08-358-117-1	Sequence 1, Appli
41	56	14.9	2058	3	US-08-470-588-1	Sequence 1, Appli
42	56	14.9	2124	1	US-08-803-973-11	Sequence 11, Appl
43	56	14.9	2124	1	US-08-803-972-11	Sequence 11, Appl
44	56	14.9	3089	4	US-09-016-434-1330	Sequence 1330, Ap
45	56	14.9	4371	1	US-08-803-973-1	Sequence 1, Appli

#### ALIGNMENTS

RESULT 1  
US-09-996-243-200  
Sequence 200, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhong, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996,243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16



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; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
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## Alignment Scores:

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Score:	375.00	Matches:	71
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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-996-243-200 (1-415)

```
QY      1  GluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20
      |||
      97  GAGGAGAAAGCACCATGAGATTATGCGTCACGACCGAGCGCTTTACACCCCGTTC 156
QY      21  LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40
      |||
      157  CTGAACATCGACAATATGCGATCGCGTTTAAGCTGATGATGCTTCTGAAGTGGCAGCC 216
QY      41  LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60
      |||
      217  CTCTTGAGTCTATCAAAAGAACTTCTTCTCACTGGAGATGCCCTTCTTAAGCTG 276
Db      61  LySGlyLeuArgSerAlaThrProAspAlaGln 71
      |||
      277  AAAGACTGAGGAGCGCACTCTGATGCCAG 309
```

## RESULT 2

```
US-09-313-294A-4134
; Sequence 4134, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalugudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 4134
; LENGTH: 288
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700347768H1
; NAME/KEY: unsure
; LOCATION: 57, 71, 98, 240
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-4134
```

Alignment Scores:

Pred. No.:	5.85e-24	Length:	288
Score:	210.50	Matches:	39
Percent Similarity:	72.86%	Conservative:	12
Best Local Similarity:	55.71%	Mismatches:	18
Query Match:	56.13%	Indels:	1
DB:	4	Gaps:	1

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-313-294A-4134 (1-288)

```
QY      2  GluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPheLeu 21
      |||
      66  GAAGANACCACCTCCAGTAATTACCTTCGGNACAGAGGCGCTT--AGTGAATTCTG 122
QY      22  AsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAlaLeu 41
      |||
      123  AACTTTAACAAGTTACAGTCTGCCCTTTAAGTCGATGACTTCTGAACTGGCAGTCTC 182
QY      42  PheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeuLys 61
      |||
      183  ACTGATATGTTCAAAAAGCGCTTCTTCACTTAAGTGAATTTCTCCCTAAGTGNA 242
Db      62  GlyLeuArgSerAlaThrProAspAlaGln 71
      |||
      243  GGAAGTGAAGCGCAGTTCCTGATTCACAG 272
```

## RESULT 3

```
US-09-328-111-364
; Sequence 364, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dertl, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 364
; LENGTH: 686
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(686)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-364
```

Alignment Scores:

Pred. No.:	0.0065	Length:	686
Score:	78.50	Matches:	23
Percent Similarity:	39.19%	Conservative:	6
Best Local Similarity:	31.08%	Mismatches:	20
Query Match:	20.93%	Indels:	25
DB:	3	Gaps:	3

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-328-111-364 (1-686)

QY 3 GluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPheLeuAsn 22



Db 164 GAATCTGGATTGAGAACTCTGAGCGTCTCTGGATGTT-----AAC 208  
Qy 23 IleaapLysleuArgSerAlaPheLysAlaAsp---GluPheLeuAsnTrpHisAla--- 40  
Db 209 TTTGACACTTTCTGGAAGAATTTTAAATCCAGCTGGTTTCATCACTGGATGCCATA 268  
Qy 41 -----LeuPhe 42  
Db 269 AACAGAACCAGTCCCGCCCCCAGACACCCGAGCCCTCTCTACTTCAGCCGACTCTGG 328  
Qy 43 GluSerIleLysArgLysLeuProPheLeuAsnTrpAspAla 56  
Db 329 GAGGATTTCAACAGACACTCTTCTCTCACTGGAAGCA 370

RESULT 4  
US-09-557-884-1  
; Sequence 1, Application US/09557884  
; Patent No. 6506581  
; GENERAL INFORMATION:  
; APPLICANT: Fleischmann et al.  
; TITLE OF INVENTION: The Nucleotide sequence of  
; the Haemophilus influenzae Rd Genome, Fragments  
; thereof, and Uses Thereof  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3 1/2 inch diskette  
; COMPUTER: Dell Pentium  
; OPERATING SYSTEM: MS DOS v6.22  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/557,884  
; FILING DATE: 25-Apr-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/476,102  
; FILING DATE: JUN-5-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michelle S. Marks  
; REGISTRATION NUMBER: 41,971  
; REFERENCE/DOCKET NUMBER: PB186P3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8439  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1830121 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-557-884-1

Alignment Scores:  
Pred. No.: 3.09e+04 Length: 1830121  
Score: 67.50 Matches: 13  
Percent Similarity: 66.67% Conservative: 7  
Best Local Similarity: 43.33% Mismatches: 9  
Query Match: 18.00% Indels: 1  
DB: 4 Gaps: 1

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-557-884-1 (1-1830121)

Qy 26 LeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAlaLeuPheGluSerIle 45  
Db 1299803 CTCAAAAGTCCGTAATAAAGAAACGTTTATGATTGGCAATTCTATCAATAAAAAATAG 1299862

Qy 46 Lys---ArgLysLeuProPheLeuAsnTrp 54  
Db 1299863 AAAGAGAGAAAATAAATCCCAATTGG 1299892

RESULT 5  
US-09-643-990A-1  
; Sequence 1, Application US/09643990A  
; Patent No. 6528289  
; GENERAL INFORMATION:  
; APPLICANT: Robert D. Fleischmann  
; Mark D. Adams  
; Owen White  
; Hamilton O. Smith  
; J. Craig Venter  
; TITLE OF INVENTION: The Nucleotide sequence of  
; the Haemophilus influenzae Rd Genome, Fragments  
; thereof, and Uses Thereof  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville,  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3 1/2 inch diskette  
; COMPUTER: Dell Pentium  
; OPERATING SYSTEM: MS DOS v6.22  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/643,990A  
; FILING DATE: 23-Aug-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/487,429  
; FILING DATE: 1995-06-07  
; APPLICATION NUMBER: 08/426,787  
; FILING DATE: 1995-04-21  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kenley K. Hoover  
; REGISTRATION NUMBER: 40,302  
; REFERENCE/DOCKET NUMBER: PB186P1C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-610-5790  
; TELEFAX: 301-309-8439  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1830121 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-643-990A-1

Alignment Scores:  
Pred. No.: 3.09e+04 Length: 1830121  
Score: 67.50 Matches: 13  
Percent Similarity: 66.67% Conservative: 7  
Best Local Similarity: 43.33% Mismatches: 9  
Query Match: 18.00% Indels: 1  
DB: 4 Gaps: 1

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-643-990A-1 (1-1830121)

Qy 26 LeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAlaLeuPheGluSerIle 45  
Db 1299803 CTCAAAAGTCCGTAATAAAGAAACGTTTATGATTGGCAATTCTATCAATAAAAAATAG 1299862

Qy 46 Lys---ArgLysLeuProPheLeuAsnTrp 54  
Db 1299863 AAAGAGAGAAAATAAATCCCAATTGG 1299892

```

RESULT 6
US-08-866-340-1/c
; Sequence 1, Application US/08866340
; Patent No. 6020318
; GENERAL INFORMATION:
; APPLICANT: Szyf, Moshe
; APPLICANT: Bigey, Pascal
; APPLICANT: Ramchandani, Shyam
; TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC
; TITLE OF INVENTION: SEQUENCES AND ANTISENSE OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DOR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States of America
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,340
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Keown, Wayne A.
; REGISTRATION NUMBER: 33,923
; REFERENCE/DOCKET NUMBER: 106.101.187
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4084 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; US-08-866-340-1

Alignment Scores:
Pred. No.:          26.5          Length:          4084
Score:              62.50         Matches:          18
Percent Similarity: 56.60%       Conservative:     12
Best Local Similarity: 33.96%    Mismatches:      12
Query Match:       16.67%        Indels:          11
DB:                 3            Gaps:               3

US-10-059-395-142_COPY_29_99 (1-71) x US-08-866-340-1 (1-4084)

QY      16  PheAsnThrProPheLeuAsnIleAspIleuArgSerAlaPheIysAlaAspGluPhe 35
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      2745 TTTGAAACTCCATGG-----GAAAAATGCAAAATCCATTTAAGAAACAATTT 2695

QY      36  LeuAsnTrp--HisAlaLeuPheGluSer-----IleIysArg 47
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      2694 CTTTATATGAGCCACCAAGTGTGTCAATGATTTGGTAATAAGAAAAATTTTAAGAGG 2635

QY      48  LysLeuProPheLeuAsnTrpAspAlaPheProIysLeu 60
      ::|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      2634 AGATTACCTTTCTGTGTTAAGCTGTCTCTTCCAATCTT 2596

RESULT 7
US-09-103-875-4/c
; Sequence 4, Application US/09103875A
; Patent No. 6221849
; GENERAL INFORMATION:

```

```

; APPLICANT: Szyf, Moshe
; APPLICANT: Bigey, Pascal
; APPLICANT: Ramchandani, Shyam
; TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC SEQUENCES AND ANTISENSE
; FILE REFERENCE: OLIGONUCLEOTIDES
; FILE REFERENCE: 106101.194
; CURRENT APPLICATION NUMBER: US/09/103,875A
; CURRENT FILING DATE: 1998-06-24
; EARLIER APPLICATION NUMBER: 60/069,865
; EARLIER FILING DATE: 1997-12-17
; EARLIER APPLICATION NUMBER: 08/866,340
; EARLIER FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 4460
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-103-875-4

Alignment Scores:
Pred. No.: 30.1          length: 4460
Score: 62.50           Matches: 18
Percent Similarity: 56.60%      Conservative: 12
Best Local Similarity: 33.96%   Mismatches: 12
Query Match: 16.67%           Indels: 11
DB: 3                      Gaps: 3

US-10-059-395-142_COPY_29_99 (1-71) x US-09-103-875-4 (1-4460)

QY 16 PheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPhe 35
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2743 TTGGAACCTCCATGG-----GAAAAAATGCAAAATCCATTAAAGAAAAACAATTT 2693

QY 36 LeuAsnTrp--HisAlaLeuPheGluSer-----IleLysArg 47
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2692 CTTTATGAGCCACAAAGTGTCTCAGTCAGATTGGTAATAGAAAAATTTTAAGAGG 2633

QY 48 LysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60
   ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2632 AGATTACCTTTCTGTGTTAAGCTGTCTCTTCCAAATCTT 2594

RESULT 8
US-09-328-352-1350
; Sequence 1350, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1350
; LENGTH: 1845
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1350

Alignment Scores:
Pred. No.: 9.99          length: 1845
Score: 62.00           Matches: 18
Percent Similarity: 47.89%      Conservative: 16
Best Local Similarity: 25.35%   Mismatches: 30
Query Match: 16.53%           Indels: 7
DB: 4                      Gaps: 2

US-10-059-395-142_COPY_29_99 (1-71) x US-09-328-352-1350 (1-1845)

QY 4 SerThrIleGluAsnTrpAlaSerArgProGluAlaPheAsnThrProPheLeuAsnIle 23
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 966 AGCACCTGCTACAATATACCAAACTAAACCCGAAGTATGGC-----AACTCT 1013

```

QY 24 AsplyleuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAlaLeu-PheG1 43  
Db 1014 TCACAAAGACGTTATCTATCAAAACGTAGCAGTACGATGATGTCAGTATGCTGGGA 1073  
QY 43 userileysArgLysLeuPro-----PheLeuAsnTrpAspAlaPheProLysLeuL 61  
Db 1074 AGCTCTTCTTAAGAAGTTCCAGCAAACTTAACCACTGGAAGGTCAACCTCAGCTAAA 1133  
QY 61 sGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 1134 CGCGGAAAAAGCAGACATCCAAATGCTCGT 1164

## RESULT 9

US-09-443-501A-2/c  
; Sequence 2, Application US/09443501A  
; Patent No. 6303342  
; GENERAL INFORMATION:  
; APPLICANT: Kosan Biosciences, Inc.  
; APPLICANT: Julien, Bryan  
; APPLICANT: Katz, Leonard  
; APPLICANT: Khosla, Chaitan  
; APPLICANT: Tang, Li  
; APPLICANT: Ziermann, Rainer  
; TITLE OF INVENTION: Recombinant Methods and Materials for Producing  
; TITLE OF INVENTION: Epothilone and Epothilone Derivatives  
; FILE REFERENCE: 30062-20031.00  
; CURRENT APPLICATION NUMBER: US/09/443,501A  
; CURRENT FILING DATE: 1999-11-19  
; PRIOR APPLICATION NUMBER: US 60/130,560  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: US 60/122,620  
; PRIOR FILING DATE: 1999-03-03  
; PRIOR APPLICATION NUMBER: US 60/119,386  
; PRIOR FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: US 60/109,401  
; PRIOR FILING DATE: 1998-11-20  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 71989  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-09-443-501A-2

## Alignment Scores:

Pred. No.:	2.04e+03	Length:	71989
Score:	62.00	Matches:	21
Percent Similarity:	49.21%	Conservative:	10
Best Local Similarity:	33.33%	Mismatches:	22
Query Match:	16.53%	Indels:	10
DB:	4	Gaps:	5

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-443-501A-2 (1-71989)

QY 12 ArgProGluAlaPheAsnTrpProPheLeuAsnIleAspLysLeuArgSerAlaPheLys 31  
Db 64404 CGGCCGAGCGCTTCTAGCCACATTCCTTCAT-----CTCATCTGCGTCTTTTAC 64354  
QY 32 AlaAspGluPheLeu-----AsnTrpHisAlaLeuPheGluSerIleLysArgLys 48  
Db 64353 GGAATCCCTGTTTCATGTCATGATGACGACGCTGTG---CAGTGCGTAGCCGCGG 64297  
QY 49 LeuProPheLeuAsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrPro 68  
Db 64296 ACCCGGTAC--TCCTTCGCGAGCTTCGCCCGAGCTCGTCCCTCCGTTCC-----CCC 64246  
QY 69 AspAlaGln 71  
Db 64245 GGGTCCAG 64237

## RESULT 10

US-08-916-421B-1/c  
; Sequence 1, Application US/08916421B  
; Patent No. 6503729  
; GENERAL INFORMATION:  
; APPLICANT: Buit et al.  
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco  
; Patent No. 6503729  
; TITLE OF INVENTION: jannaschii  
; FILE REFERENCE: PB275  
; CURRENT APPLICATION NUMBER: US/08/916,421B  
; CURRENT FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: US 60/024,428  
; PRIOR FILING DATE: 1996-08-22  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1664976  
; TYPE: DNA  
; ORGANISM: Methanococcus jannaschii  
; FEATURE:  
; NAME/KEY: misc feature  
LOCATION: (28222)..(28222)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
LOCATION: (28257)..(28258)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
LOCATION: (84773)..(84773)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
LOCATION: (84808)..(84808)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
LOCATION: (84812)..(84812)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
LOCATION: (98120)..(98120)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
LOCATION: (98159)..(98159)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
LOCATION: (98239)..(98239)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
LOCATION: (98266)..(98266)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
LOCATION: (98343)..(98343)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
LOCATION: (103998)..(103998)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
LOCATION: (148948)..(148948)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
LOCATION: (163385)..(163385)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
LOCATION: (191989)..(191989)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
LOCATION: (191995)..(191995)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
LOCATION: (231980)..(231980)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
LOCATION: (234187)..(234187)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature

```
LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (312837)..(312837)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1130881)..(1130881)
```

```
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1470091)..(1470091)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1569020)..(1569020)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1664854)..(1664854)
OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1
```

```
Alignment Scores:
Pred. No.: 2.89e+05 Length: 1664976
Score: 60.50 Matches: 17
Percent Similarity: 53.85% Conservative: 11
Best Local Similarity: 32.69% Mismatches: 21
Query Match: 16.13% Indels: 3
DB: 4 Gaps: 3
```

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-08-916-421B-1 (1-1664976)

```
QY 8 AsnTyralaserArgProglualaphasnThrProPhelEuAsnIleAspLySLeuArg 27
Db 634055 AACTATGCCACAATGATTAAGAGATTCTTAAGAGATG--ATAAAAAAGCAGTT 633999
QY 28 SerAlaphelysAlaAspGluPhelEuAsnTrp---HisAlaLeuPhcGluSerIleLys 46
Db 633998 GGAAGAGTAAAAAGAAAGATTACGAGAAGTGTTAACTCTGTCTGAAGGTTAAG 633939
QY 47 ArgLySLeuProPhelEuAsnTrpAspAlaPhedro 58
Db 633938 CAAGAGCTA--ATAAAAAATTGGGAGGCACTTCT 633906
```

```
RESULT 11
US-08-328-962-1/C
; Sequence 1, Application US/08328962
; Patent No. 5536637
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; TITLE OF INVENTION: A NOVEL METHOD FOR ISOLATING CYTOKINES
; TITLE OF INVENTION: AND OTHER SECRETED PROTEINS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,962
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/045,267
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcdaniels, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: GI 5200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae
; IMMEDIATE SOURCE:
; CLONE: SUC2
; US-08-328-962-1

Alignment Scores:
Pred. No.: 15.7 length: 1542
Score: 60.00 Matches: 17
Percent Similarity: 57.78% Conservative: 9
Best Local Similarity: 37.78% Mismatches: 11
Query Match: 16.00% Indels: 9
DB: 1 Gaps: 1

US-10-059-395-142_COPY_29_99 (1-71) x US-08-328-962-1 (1-1542)

QY 19 ProPheleuAsnIleAspLysLeuAArgSerAlaPheLysAlaAspGluPheleuAsnTrp 38
Db 1025 CCAGCATTAATAATGTTCAATATGTTGCGCTTCAAAAT-GATCAATTCAGTCTCTGG 967

QY 39 HisAlaLeuPheGluSerIleLysArgLysLeu-----Pro 50
Db 966 ATTAGCTTGATATTCAAGTGTCAAGAAACTTGGCGCAAGACATGATGATCTCTCA 907

QY 51 PheleuAsnTrpAsp 55
Db 906 TGGGTAGTTGGAC 892

RESULT 12
US-09-328-352-1933
; Sequence 1933, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1933
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1933

Alignment Scores:
Pred. No.: 6 length: 702
Score: 59.50 Matches: 18
```

```

Percent Similarity: 51.72% Conservative: 12
Best Local Similarity: 31.03% Mismatches: 21
Query Match: 15.87% Indels: 7
DB: 4 Gaps: 3

US-10-059-395-142_COPY_29_99 (1-71) x US-09-328-352-1933 (1-702)

QY 3 GluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPheleuAsn 22
Db 496 CAGCATGATCGATCACTACGACAGT-----GAAGAGTTCATACAGCGTTCGTAAT 549

QY 23 -----IleAspLysLeuAArgSerAlaPheLysAlaAspGluPheleuAsnTrp 38
Db 550 GTGATTCGACGCGTAGATAAAGTTGCCGACGTTGTGATGCAGATACTTAGAGAAATG 609

QY 39 HisAlaLeuPheGluSerIleLysArgLysLeuProPheleuAsnTrpAspAla 56
Db 610 CATGACAGCTAT---ACCATGGGTGCAAACTGAATGTTATTTGGATAGT 660

RESULT 13
US-09-107-532A-2214
; Sequence 2214, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 2214:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2253 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...2253
; SEQUENCE DESCRIPTION: SEQ ID NO: 2214:
US-09-107-532A-2214

Alignment Scores:
Pred. No.: 6 length: 702
Score: 59.50 Matches: 18
```



Pred. No.: 32.6 Length: 2253  
Score: 59.50 Matches: 12  
Percent Similarity: 64.29% Conservative: 6  
Best Local Similarity: 42.86% Mismatches: 9  
Query Match: 15.87% Indels: 1  
DB: 4 Gaps: 1

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-107-532A-2214 (1-2253)

QY 38 TrpHisAlaLeuPheGluSerIleLeuArgLysLeuProPheLeuAsnTrpAspAlaPhe 57  
Db 1490 TGGATGCAGGTGTACCAATCA--AAGCGCAGTCGCCGGTATTGCGATGGGACTTGT 1546

QY 58 ProLysLeuLysGlyLeuArgSer 65  
Db 1547 CTGATGGTGAATACTATACGATCC 1570

## RESULT 14

US-08-311-731A-137/C

; Sequence 137, Application US/08311731A  
; Patent No. 6583266

; GENERAL INFORMATION:

; APPLICANT: SMITH, DOUGLAS

; APPLICANT: MAO, JEN-I

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR

; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 411

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.

; STREET: 600 ATLANTIC AVENUE

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: USA

; ZIP: 02210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/311,731A

; FILING DATE:

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: GATES, EDWARD R.

; REGISTRATION NUMBER: 31,616

; REFERENCE/DOCKET NUMBER: C0044/7125

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/720-3500

; TELEFAX: 617/720-2441

; INFORMATION FOR SEQ ID NO: 137:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 40123 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: circular

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Mycobacterium leprae

US-08-311-731A-137

Alignment Scores:

Pred. No.: 2.55e+03 Length: 40123

Score: 59.00 Matches: 20

Percent Similarity: 47.69% Conservative: 11

Best Local Similarity: 30.77% Mismatches: 26

Query Match: 15.73% Indels: 8

DB: 4 Gaps: 3

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-08-311-731A-137 (1-40123)

QY 11 SerArgProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPhe 30  
Db 19981 AGCAACCTCGACAGCGGAGACATCGTCTTCGTCAAGTGACGAGACACACCACTAC 19922

QY 31 LysAlaAspGluPhe-----LeuAsnTrpHisAla---LeuPheGluSer 44  
Db 19921 GACGGCGATCACATCGCGCGCCCATCAAGTTGGATTGGCGTGGGATTGCAAGACCCG 19862

QY 45 IleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeuLysGlyLeuArg 64  
Db 19861 ATCAAGCGC-----GACTTCATCGACACCCAGCAATTCCTCAAAATTGTTGGGTGACCGA 19808

QY 65 SerAlaThrProAsp 69  
Db 19807 GGCATTTCCAATGAC 19793

## RESULT 15

US-08-961-527-197

; Sequence 197, Application US/08961527  
; Patent No. 6420135

; GENERAL INFORMATION:

; APPLICANT: Charles Kunsch

; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 391

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/961,527

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Brookes, A. Anders

; REGISTRATION NUMBER: 36,373

; REFERENCE/DOCKET NUMBER: PB340P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 309-8504

; TELEFAX: (301) 309-8512

; INFORMATION FOR SEQ ID NO: 197:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1062 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

US-08-961-527-197

Alignment Scores:

Pred. No.: 18.7 Length: 1062

Score: 58.00 Matches: 18

Percent Similarity: 50.00% Conservative: 16

Best Local Similarity: 26.47% Mismatches: 23

Query Match: 15.47% Indels: 11

DB: 4 Gaps: 2

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-08-961-527-197 (1-1062)

QY 3 GluSerThrIleGluAsnTyrAlaSerArgProGluAla----- 15  
Db 355 CAAGCAAGATTCAAGCCTATCTAGACAGACCTGTAGCTGTTTACGATTGCCAAGGA 414

```

QY 16 ---PheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAlaaspGlu 34
Db 415 ATTTTAATCCTATTTCTTTAGTCGTGAGAACTTGAAAGCTTTTAGAGGCAGATGGC 474
QY 35 PheLeuAsnTrpHisAlaLeuPheGluSerIle-LysArgLysLeuProPheLeuAsnTr 54
Db 475 TTGGCTCAGTTTGAAGCGCGTGTGCGTGGCGTTCAAGAGACAGATGCCCTACTTTGCCA-- 532
QY 54 PAspAlaPheProLysLeuLys 61
Db 533 ----GAGTTTCCTCTATCAGG 550

```

Search completed: November 28, 2003, 15:11:03  
 Job time : 658 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2003, 13:33:57 ; Search time 25 Seconds  
(without alignments)  
273.119 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99  
Perfect score: 375  
Sequence: 1 EESTIENYASRPEAFNTPF.....LNWDAPPKLGLRSATPDAQ 71

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	19.7	807	2	S29242 sucrose synthase (
2	72	19.2	390	2	G97561 para-aminobenzoate
3	65.5	17.5	521	2	S55318 cytochrome P450 1A
4	65.5	17.5	521	2	S34184 cytochrome P450 1A
5	65.5	17.5	522	2	A28789 cytochrome P450 1A
6	65.5	17.5	522	2	S51557 cytochrome P450, 3
7	65.5	17.5	2434	2	S44861 DNA topoisomerase
8	65	17.3	368	2	A71727 hypothetical prote
9	65	17.3	459	2	A75097 hypothetical prote
10	64.5	17.2	506	2	S63181 hypothetical prote
11	64.5	17.2	583	2	JT0395 DNA-binding prote
12	64.5	17.2	871	2	E97035 DNA polymerase I,
13	63.5	16.9	129	2	A98038 hypothetical prote
14	63	16.8	1213	2	T19835 hypothetical prote
15	62.5	16.7	522	2	D81900 hypothetical prote
16	62.5	16.7	522	2	A81124 conserved hypothet
17	62	16.5	253	1	PMRTYM phosphoglycerate m
18	61.5	16.4	506	2	T12819 hypothetical prote
19	61	16.3	234	2	D81342 tRNA (guanine-N1-)
20	61	16.3	254	2	B84071 hypothetical prote
21	61	16.3	736	2	D90574 hypothetical prote
22	61	16.3	2344	2	T41590 probable sensor-li
23	60.5	16.1	276	2	C72298 hypothetical prote
24	60.5	16.1	384	2	B43592 outer membran pro
25	60.5	16.1	1232	2	D64413 cobalam biosynth
26	60.5	16.1	4589	2	T14914 dynein beta heavy
27	60	16.0	207	2	D64009 hypothetical prote
28	60	16.0	321	2	C89823 hypothetical prote
29	60	16.0	736	2	S69074 hypothetical prote

30	60	16.0	1044	2	T43800 protein kinase bub
31	59.5	15.9	325	2	F71283 outer membrane ant
32	59.5	15.9	481	2	T37505 hypothetical prote
33	59	15.7	161	2	T28413 ORF MSV252 tryptop
34	59	15.7	277	2	A87184 thiosulfate sulfur
35	59	15.7	441	2	D83555 hypothetical prote
36	59	15.7	480	2	T18905 hypothetical prote
37	58.5	15.6	197	2	E84606 probable WRKY-type
38	58.5	15.6	332	2	F82140 C4-dicarboxylate-b
39	58	15.5	128	2	PH0094 Ig heavy chain V r
40	58	15.5	128	2	PH0095 Ig kappa chain V r
41	58	15.5	379	2	T52405 hypothetical prote
42	58	15.5	412	2	A30605 acyl-CoA dehydroge
43	58	15.5	412	2	B30605 acyl-CoA dehydroge
44	58	15.5	529	2	S18453 variant surface gl
45	58	15.5	665	1	H97093 fructose-bisphosph

## ALIGNMENTS

```
RESULT 1
S29242
sucrose synthase (EC 2.4.1.13) Srl - barley
N:Alternate names: sucrose-UDP glucosyltransferase; UDPglucose-fructose glucosyltransfer
C:Species: Hordeum vulgare (barley)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Jun-1999
C:Accession: S29242; S21494
R:de la Hoz, P.S.; Vicente-Carabajosa, J.; Mena, M.; Carbonero, P.
FEBS Lett. 310, 46-50, 1992
A:Title: Homologous sucrose synthase genes in barley (Hordeum vulgare) are located in ch
A:Reference number: S29242; MUID:92405741; PMID:1388123
A:Accession: S29242
A:Molecule type: mRNA
A:Residues: 1-807 <HOZ>
A:Cross-references: EMBL:X65871; NID:G19105; PIDN:CMA46701.1; PID:G19106
C:Genetics:
A:Map position: 7H
C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C:Keywords: glycosyltransferase; hexosyltransferase
F:276-749/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

Query Match      19.7%; Score 74; DB 2; Length 807;
Best Local Similarity 27.7%; Pred. No. 1.9;
Matches 26; Conservative 12; Mismatches 32; Indels 24; Gaps 3;

QY      2 EESTIENYASRP-----EATNTPFLNIDKLSAFKADFLNMH--ALFESIKRLPF 51
      :|:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      116 KEQLVDEHASRKFLVLEDFEPFNASFPSPMSKSYGKGVFLNRHLSSKLFQDKESLYPL 175
QY      52 LNW-----DAFPKLGKLSATPDAQ 71
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      176 LNFKAHNYKGTMTILNDRIGSLRGLQSLARKAE 209

RESULT 2
para-aminobenzoate synthase, component I VC1303 [imported] - Agrobacterium tumefaciens (
C:Species: Agrobacterium tumefaciens
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C:Accession: G97561
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: G97561
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-390 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK87448.1; PID:G15156766; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C_3082
```







Query Match 17.2%; Score 64.5; DB 2; Length 506;  
Best Local Similarity 28.4%; Pred. No. 14;  
Matches 19; Conservative 9; Mismatches 16; Indels 23; Gaps 2;

OY 4 STIENYASRBEAFTNTPF-----LNIDKLSAFKADFLNWHALFESIKR 47  
DB 139 STIEDYLANPDCFNTDIGWCMIRGTGSLGNALQILHLGRDFRVNG-----NESLER 191

OY 48 KLPFLNW 54  
DB 192 ESKFVNW 198

RESULT 11  
JT0395  
DNA-binding protein homolog - fruit fly (Drosophila melanogaster) transposon jockey  
C/Species: Drosophila melanogaster  
C/Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 20-Mar-1998  
C/Accession: JT0395  
R;Primaegi, A.F.; Mizrokh, L.J.; Ilyin, Y.V.  
Gene 70, 253-262, 1988  
A/Title: The Drosophila mobile element jockey belongs to LINEs and contains coding sequence  
A/Reference number: JT0395; MUID:89108009; PMID:2463954  
A/Accession: JT0395  
A/Molecule type: DNA  
A/Residues: 1-583 <PRI>  
A/Cross-references: GB:M22874; NID:g157823; PID:g157824  
C/Genetics:  
A/Gene: FlyBase:jockey  
A/Cross-references: FlyBase:FBgn0001283  
C/Keywords: DNA binding; zinc finger

Query Match 17.2%; Score 64.5; DB 2; Length 583;  
Best Local Similarity 27.0%; Pred. No. 17;  
Matches 17; Conservative 10; Mismatches 21; Indels 15; Gaps 3;

OY 9 YASRPEAFNTPFLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPPKLGKLSATP 68  
DB 274 YTANPDARFRAVKEINKLNCQF-----WH---HQLKEKPYR-----VVLKGIHANVP 318

OY 69 DAQ 71  
DB 319 SSQ 321

RESULT 12  
E97035  
DNA polymerase I, polA [imported] - Clostridium acetobutylicum  
C/Species: Clostridium acetobutylicum  
C/Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 30-Sep-2001  
C/Accession: E97035  
R;Nolling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum  
A/Reference number: A96900; MUID:21359325; PMID:21359325  
A/Accession: E97035  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-871 <KUR>  
A/Cross-references: GB:AB001437; PIDN:AAK79072.1; PID:g15024015; GSPDB:GN00168  
A/Experimental source: Clostridium acetobutylicum ATCC824  
C/Genetics:  
A/Gene: CAC1098  
C/Superfamily: DNA-directed DNA polymerase I

Query Match 17.2%; Score 64.5; DB 2; Length 871;  
Best Local Similarity 28.1%; Pred. No. 27;  
Matches 27; Conservative 12; Mismatches 30; Indels 27; Gaps 4;

OY 3 ESTIENYASRPE-----AFNTPF-LNIDKLSAFKADFLNWHAL-----FESIKRKL 49  
DB 226 KENLENYAEQAVFSKGLATIMTNVPIEIDIEIRSKESPDVEGARHLRLRLQFKSLIEKI 285

OY 50 PFLNWD-----FPKLGKLSATPDAQ 71  
DB 286 PSLNVEAEKSDFVEVYNLIDFPKHELFSAIKOTE 321

RESULT 13  
A98038  
hypothetical protein spr1330 [imported] - Streptococcus pneumoniae (strain R6)  
C/Species: Streptococcus pneumoniae  
C/Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 22-Oct-2001  
C/Accession: A98038  
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; e, R.; LeBlanc, D.J.; Lee, L.N.; Letkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.  
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A/Reference number: A97872; MUID:21429245; PMID:11544234  
A/Accession: A98038  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-129 <KUR>  
A/Cross-references: GB:AE007317; PIDN:AAL00134.1; PID:g15458975; GSPDB:GN00174  
C/Genetics:  
A/Gene: spr1330

Query Match 16.9%; Score 63.5; DB 2; Length 129;  
Best Local Similarity 32.7%; Pred. No. 3.8;  
Matches 18; Conservative 10; Mismatches 26; Indels 1; Gaps 1;

OY 7 ENYASRBEAFTNTPFLNIDKL-RSAFKADFLNWHALFESIKRKLPLNWDAPPKL 60  
DB 70 KNVASFYEYWRSLFTVDKLVENLGSVQAVLDSYHLWANTIEKTLPLNWFVQKXL 124

RESULT 14  
T19835  
hypothetical protein C38D9.5 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 29-Oct-1999  
C/Accession: T19835; T27344  
R;Almscough, R.  
Submitted to the EMBL Data Library, November 1996  
A/Reference number: Z19184  
A/Accession: T19835  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1213 <WIL>  
A/Cross-references: EMBL:Z81481; PIDN:CAB03951.1; GSPDB:GN00023; CESP:C38D9.5  
A/Experimental source: clone C38D9  
R;Lloyd, C.  
Submitted to the EMBL Data Library, March 1997  
A/Reference number: Z20348  
A/Accession: T27344  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1213 <W12>  
A/Cross-references: EMBL:Z92973; PIDN:CAB07494.1; GSPDB:GN00023; CESP:C38D9.5  
A/Experimental source: clone Y6G8  
C/Genetics:  
A/Gene: CESP:C38D9.5  
A/Map position: 5  
A/Introns: 32/1; 490/3; 672/1; 770/2; 804/1; 863/1; 967/3; 1000/2; 1072/1

Query Match 16.8%; Score 63; DB 2; Length 1213;  
Best Local Similarity 30.9%; Pred. No. 58;  
Matches 21; Conservative 6; Mismatches 13; Indels 28; Gaps 4;

OY 23 IDKLSARF-----ADEFLNWHALFESIKRKLPLNWDAPPK-----LKG 62  
DB 465 VQSLRSALSGAQLTVAD-----IFERVKTT--YNWDSIASVHNSLSDTGLVDALKS 516



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 13:06:01 ; Search time 17 Seconds  
(without alignments)

196.406 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99  
Perfect score: 375

Sequence: 1 EESSTIENYASRPEAFNTPF.....LWDAFPKLGKRSATPDAQ 71

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	19.7	807	1 SUS1_HORVU	P31922 hordeum vul
2	68.5	18.3	413	1 ACDS_PIG	P79273 sus scrofa
3	67.5	18.0	521	1 CP11_PLAFA	Q9yh64 platichthys
4	65.5	17.5	521	1 CP11_PLEPL	Q92100 pleurocneste
5	65.5	17.5	521	1 CP11_SPAU	O42457 sparus aura
6	65.5	17.5	522	1 CP11_ONCMY	Q92110 oncorhynch
7	65.5	17.5	1053	1 TP2M_CABEL	P34534 caenorhabdi
8	65	17.3	368	1 Y165_RICPR	Q9zdz8 rickettsia
9	64.5	17.2	506	1 YMW3_YEAST	P53867 saccharomyc
10	64.5	17.2	568	1 GAGJ_DROME	P21330 drosophila
11	63.5	16.9	521	1 CP11_LIMLI	O42430 limanda lim
12	63.5	16.9	521	1 CP11_STECH	Q92116 stentomus
13	62.5	16.7	520	1 CP11_DICIA	P79716 dicentrarch
14	62	16.5	252	1 PMG2_MOUSE	O70250 mus musculu
15	62	16.5	252	1 PMG2_RAT	P16290 rattus norv
16	61	16.3	234	1 TRMD_CAMJE	Q9PJ4 campylobact
17	60.5	16.1	384	1 TMPB_TREBP	P29720 treponema p
18	60	16.0	207	1 Y552_HAEIN	P44013 haemophilus
19	60	16.0	1044	1 BUB1_SCHPO	O94751 schizosacch
20	59.5	15.9	325	1 TMPB_TREPA	P19649 treponema p
21	59	15.7	277	1 THTR_MYCLE	Q50036 mycobacteri
22	58.5	15.6	202	1 WR59_ARATH	Q9S109 arabidopsis
23	58.5	15.6	248	1 GPM4_METAC	Q8tn93 methanosarc
24	58.5	15.6	380	1 VINT_BBP21	P27077 bacterioph
25	58.5	15.6	521	1 CP11_LIZAU	O42231 liza aurata
26	58.5	15.6	521	1 CP11_LIZSA	Q9w683 liza salien
27	58	15.5	273	1 AROE_BUCAP	P46240 buchnera ap
28	58	15.5	412	1 ACDS_HUMAN	P16219 homo sapien
29	58	15.5	529	1 VSM6_TRYBB	P26334 trypanosoma
30	58	15.5	992	1 VP41_YEAST	P38959 saccharomyc
31	57.5	15.3	315	1 VN35_ROTAL	Q03244 avian rotav
32	57.5	15.3	522	1 CP13_ONCMY	Q92109 oncorhynch
33	57.5	15.3	669	1 CYK2_YEAST	Q05080 saccharomyc

34	57.5	15.3	1055	1 UBPP_MOUSE	P57080 mus musculu
35	57	15.2	252	1 TRT3_COTJA	P06398 coturnix co
36	57	15.2	262	1 TRT3_CHICK	P12620 gallus gall
37	57	15.2	353	1 YG98_HAEIN	O05083 haemophilus
38	57	15.2	490	1 Y035_CLOPE	Q06373 clostridium
39	57	15.2	1709	1 CHD1_HUMAN	O14646 homo sapien
40	57	15.2	1711	1 CHD1_MOUSE	P40201 mus musculu
41	57	15.2	2206	1 POLG_POL32	P06209 poliovirus
42	56.5	15.1	168	1 DUT_ARCFU	O29157 archaeoglob
43	56.5	15.1	460	1 PGMU_NEIGO	P40390 neisseria g
44	56.5	15.1	487	1 MALQ_CLOBU	Q59266 clostridium
45	56.5	15.1	515	1 CP11_PAGMA	P98181 pagrus majo

#### ALIGNMENTS

RESULT 1  
ID SUS1\_HORVU STANDARD; PRT; 807 AA.  
AC P31922;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Sucrose synthase 1 (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase 1).  
GN SS1.  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Abyssinian 2231; TISSUE=Endosperm;  
RX MEDLINE=92405741; PubMed=1388123;  
RA Sanchez de la Hoz P., Vicente-Carabajosa J., Mena M., Carbonero P.;  
RT "Homologous sucrose synthase genes in barley (Hordeum vulgare) are  
RT located in chromosomes 7H (syn. 1) and 2H. Evidence for a gene  
RT translocation?";  
RL FEBS Lett. 310:46-50 (1992).  
RN [2]  
RP SEQUENCE OF 223-807 FROM N.A.  
RC STRAIN=cv. Pallas;  
RA Brandt J., Thordal-Christensen H., Collinge D.B.;  
RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: SUCROSE-CLEAVING ENZYME THAT PROVIDES UDP-GLUCOSE AND  
CC FRUCTOSE FOR VARIOUS METABOLIC PATHWAYS.  
CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.  
CC -!- TISSUE-SPECIFICITY: HIGHLY EXPRESSED IN DEVELOPING ENDOSPERM AND  
CC IN ROOTS AND, AT LOWER LEVELS, IN COLEOPTILES AND ALEURONE.  
CC -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1. PLANT  
CC SUCROSE SYNTHASE SUBFAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; X65871; CAA46701.1; -.  
CC EMBL; X66728; CAA47264.1; -.  
CC PIR; S29242; S29242.  
CC InterPro; IPR001296; Glyco\_trans\_1.  
CC InterPro; IPR000368; Sucrose\_synth.  
CC Pfam; PF00534; Glycos\_transf\_1; 1.  
CC Pfam; PF00862; Sucrose\_synth; 1.  
CC Transferase; Glycosyltransferase; Multigene family.  
KW TRANSFERASE; 370 370 I -> IL (IN REF. 2).  
FT CONFLICT 374 374 I -> Y (IN RSP. 2).  
FT CONFLICT 392 393 NE -> KQ (IN REF. 2).  
SQ SEQUENCE 807 AA; 92211 MW; A863A8C876A060C8 CRC64;

Query Match 19.7%; Score 74; DB 1; Length 807;  
Best Local Similarity 27.7%; Pred. No. 0.7;  
Matches 26; Conservative 12; Mismatches 32; Indels 24; Gaps 3;

QY 2 EESTIENYASRP-----EAFNPPLNIDKLSAFKADEFILNWH---ALFESIKRKLDP 51  
Db 116 KEQGVDEHASRKFVLELDFEPFNASFPSPMSKSYGKGVGLNRHLSSKLFQDKESLYPL 175

QY 52 LNW-----DAFPKLGKLSATPDQAQ 71  
Db 176 LNFKAHNYKGTMTILNDRIQSLRGIQSALRKAE 209

RESULT 2  
ACDS\_PIG STANDARD; PRT; 413 AA.  
ID ACDS\_PIG STANDARD; PRT; 413 AA.  
AC P79273;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Acyl-CoA dehydrogenase, short-chain specific, mitochondrial precursor  
(EC 1.3.99.2) (SCAD) (Butyryl-CoA dehydrogenase).  
GN ACADS.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Suzuki H., Itoh T., Kimura M., Murakami Y., Hamasima N., Yasue H.;  
RT "Isolation of the pig short-chain acyl-CoA dehydrogenase gene and  
assignment to chromosome 14q16.2-q23.2."  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: Butanoyl-CoA + ETP = 2-butanoyl-CoA + reduced  
ETP.  
CC -1- COFACTOR: FAD.  
CC -1- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first  
step.  
CC -1- SUBUNIT: Homotetramer.  
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
CC -1- MISCELLANEOUS: A NUMBER OF STRAIGHT-CHAIN ACYL-CoA DEHYDROGENASES  
OF DIFFERENT SUBSTRATE SPECIFICITIES ARE PRESENT IN MAMMALIAN  
TISSUES.  
CC -1- SIMILARITY: BELONGS TO THE ACYL-CoA DEHYDROGENASE FAMILY.  
CC -----  
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CC -----  
DR EMBL; D89477; BAA13964.1; -.  
DR HSSP; Q06319; 1BUC.  
DR InterPro; IPR006089; Acyl-CoA dh.  
DR InterPro; IPR006090; Acyl-CoA dh\_C.  
DR InterPro; IPR006091; Acyl-CoA dh\_M.  
DR InterPro; IPR006092; Acyl-CoA dh\_N.  
DR Pfam; PF00441; Acyl-CoA dh; 1.  
DR Pfam; PF02770; Acyl-CoA dh\_M; 1.  
DR Pfam; PF02771; Acyl-CoA dh\_N; 1.  
DR PROSITE; PS00072; ACYL\_COA\_DH\_1; 1.  
DR PROSITE; PS00073; ACYL\_COA\_DH\_2; 1.  
KW Oxidoreductase; Flavoprotein; FAD; Fatty acid metabolism;  
KW Mitochondrion; Transit peptide.  
FT TRANSIT 1 24 MITOCHONDRION (BY SIMILARITY).  
FT CHAIN 25 413 SPECIFIC.  
FT ACT\_SITE 393 393 BASE (BY SIMILARITY).  
SQ SEQUENCE 413 AA; 44850 MW; B8C480ADEDF7E98 CRC64;

Query Match 18.3%; Score 68.5; DB 1; Length 413;  
Best Local Similarity 26.9%; Pred. No. 1.5;  
Matches 18; Conservative 8; Mismatches 34; Indels 7; Gaps 1;

QY 8 NYASRPEAFNTPFLNIDKLR-----SAFKADEFLNWHALFESIKRKLPLNWDAPPKL 60  
Db 292 NYAENRRAFGVPLTKGIGFKLADMALALAESARLLTWRAAMLKDNKNPFIKEPAMAKL 351

QY 61 KGLRSAT 67  
Db 352 AASEAAT 358

RESULT 3  
CP11\_PLAFA STANDARD; PRT; 521 AA.  
ID CP11\_PLAFA STANDARD; PRT; 521 AA.  
AC O9YH64;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1).  
GN CYP1A1 OR CYP1A.  
OS Platichthys flesus (European flounder).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthopterygii; Acanthopterygii; Percomorpha; Pleuronectiformes;  
OC Pleuronectoidae; Pleuronectidae; Platichthys.  
OX NCBI\_TaxID=8260;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=North Sea population; TISSUE=Liver;  
RX MEDLINE=21353730; PubMed=11460673;  
RA Williams T.D., Lee J.S., Shearer D.L., Chipman J.K.;  
RT "The cytochrome P450 1A gene (CYP1A) from European flounder  
(Platichthys flesus), analysis of regulatory regions and development  
of a dual luciferase reporter gene system."  
RL Mar. Environ. Res. 50:1-6(2000).  
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE  
MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED  
COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.  
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +  
oxidized flavoprotein + H(2)O.  
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.  
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.  
CC -----  
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CC -----  
DR EMBL; AJ132353; CAA10645.1; -.  
DR HSSP; P00179; 1DT6.  
DR InterPro; IPR001128; Cytochrome\_P450.  
DR Pfam; PF00067; P450; 1.  
DR PRINTS; PR00385; P450.  
DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;  
KW Microsome; Endoplasmic reticulum.  
FT METAL 463 463 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
SQ SEQUENCE 521 AA; 59009 MW; 58BA7DC3913C9091 CRC64;

Query Match 18.0%; Score 67.5; DB 1; Length 521;  
Best Local Similarity 30.2%; Pred. No. 2.5;  
Matches 19; Conservative 13; Mismatches 22; Indels 9; Gaps 3;

QY 7 ENYASRPEAFNTPFLNIDKLSAFKADEFILNWHALFESIKRKLPLNWDAPPKLGLRSA 66  
Db 106 DDFAGRPDLYSFRFINAGK-SLAFSTDQAGVWRA-----RRKLAYSALRSFSNLGG--T 156





DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1) (CYP1A2).  
 GN CYP1A1.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=94213487; PubMed=8161204;  
 RA Berndtson A.K., Chen T.T.;  
 RT "Two unique CYP1 genes are expressed in response to 3-  
 RT methylcholanthrene treatment in rainbow trout.";  
 RL Arch. Biochem. Biophys. 310:187-195(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Bailey G., You L., Harttig U.;  
 RT "Cloning, sequencing and functional expression of two trout CYP1A  
 RT cDNAs in yeast.";  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Bailey G., You L., Harttig U.;  
 RT "Cloning, sequencing and functional expression of two trout CYP1A  
 RT cDNAs in yeast.";  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Heilmann L.J., Sheen Y.-Y., Bigelow S.W., Nebert D.W.;  
 RT "Trout P4501A1: cDNA and deduced protein sequence, expression in  
 RT liver, and evolutionary significance.";  
 RL DNA 7:379-387(1988).  
 CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE  
 CC MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED  
 CC COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.  
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +  
 CC oxidized flavoprotein + H(2)O.  
 CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.  
 CC -1- TISSUE SPECIFICITY: Liver.  
 CC -1- INDUCTION: By 3-methylcholanthrene (3MC).  
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.  
 CC -1- CAUTION: THE SEQUENCE FROM REF.4 WAS A CHIMERA: ITS N-TERMINAL  
 CC PART HAS BEEN SHOWN TO BE DERIVED FROM WHAT IS NOW KNOWN AS THE  
 CC CYP1A3. CYP1A1 HAS ALSO BEEN CALLED CYP1A2.  
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 CC -----  
 DR EMBL; S69278; AAD14036.1; -;  
 DR EMBL; U62797; AAB40627.1; -;  
 DR EMBL; AF015660; AAB69383.1; -;  
 DR EMBL; M21310; AAA49550.1; ALT\_SEQ.  
 DR PIR; A28789; A28789.  
 DR PIR; S51557; S51557.  
 DR HSSP; P00179; 1DT6.  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR Pfam; PF00067; P450; 1.  
 DR PRINTS; PR00385; P450.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
 KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;  
 KW Microsome; Endoplasmic reticulum.  
 FT METAL 463 463 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
 FT CONFLICT 51 51 L -> P (IN REF. 3).  
 FT CONFLICT 97 97 V -> D (IN REF. 3).

FT CONFLICT 124 124 K -> N (IN REF. 3).  
 FT CONFLICT 306 306 Q -> H (IN REF. 3).  
 FT CONFLICT 390 390 T -> I (IN REF. 3).  
 FT CONFLICT 459 459 D -> G (IN REF. 2).  
 FT CONFLICT 470 470 R -> H (IN REF. 3).  
 FT CONFLICT 474 474 Y -> F (IN REF. 1).  
 FT CONFLICT 483 483 R -> K (IN REF. 2).  
 SQ SEQUENCE 522 AA; 59344 MW; 9D063B5891102CE9 CRC64;  
 Query Match 17.5%; Score 65.5; DB 1; Length 522;  
 Best Local Similarity 31.7%; Pred. No. 4.2;  
 Matches 20; Conservative 11; Mismatches 23; Indels 9; Gaps 3;  
 QY 7 ENYASRPEAFNTPTLNDKLSAFKADFLNWHALFESIKRLPLNWDAPFKLGRSA 66  
 Db 106 EDFAGRPDLVSFKFTN-DGKSLAFSTDKAGVRA-----RRKLAMSALRSFATLEG--T 156  
 QY 67 TPD 69  
 Db 157 TPE 159  
 RESULT 7  
 TP2M CAEEL STANDARD; PRT; 1053 AA.  
 ID TP2M CAEEL  
 AC P34534;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Putative DNA topoisomerase II, mitochondrial precursor (EC 5.99.1.3).  
 GN R05D3.1.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,  
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,  
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,  
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,  
 RA Sims M., Smaildon N., Smith A., Smith M., Sonhammer E., Staden R.,  
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,  
 RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,  
 RA Wohldman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans.";  
 RL Nature 368:32-38(1994).  
 RN [2]  
 RP REVISIONS.  
 RA Waterston R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT  
 CC BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II  
 CC MAKES DOUBLE-STRAND BREAKS (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining  
 CC of double-stranded DNA.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).  
 CC -1- SIMILARITY: Belongs to the type II topoisomerase family.  
 CC -----  
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```
CC -----
DR EMBL; L07144; AAM54162.1; -.
DR HSSP; P06786; 1BGW.
DR WormPep; R05D3.1; CE31047.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR001241; DNA_topoisom.
DR InterPro; IPR002205; DNA_topoisom.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF00521; DNA_topoisomIV; 1.
DR Pfam; PF02518; HATase_c; 1.
DR PRINTS; PR01158; TOPISMRASEII.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD000742; DNA_topoisomIV; 1.
DR SMART; SM00433; TOP2c; 1.
DR SMART; SM00434; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
DR Hypothetical protein; Isomerase; Topoisomerase; DNA-binding;
KW ATP-binding; Mitochondrion; Translt peptide.
FT TRANSIT 1 ? MITOCHONDRION (POTENTIAL).
FT CHAIN ? 1053 PUTATIVE DNA TOPOISOMERASE II.
FT NP_BIND 60 65 ATP (POTENTIAL).
FT ACT_SITE 697 697 DNA_CLEAVAGE (BY SIMILARITY).
SQ SEQUENCE 1053 AA; 120285 MW; BB167F2E01BFEA45 CRC64;
```

Query Match 17.5%; Score 65.5; DB 1; Length 1053;  
Best Local Similarity 31.6%; Pred. No. 9.1;  
Matches 18; Conservative 10; Mismatches 18; Indels 11; Gaps 2;

```
OY 14 EAFNTPFLNI---DKLSAFKADFLNWHALFESIKRLPFLNWDAPFKLXGLRSAT 67
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 474 QSFRTPLAKKKGDKVRSFSPMNEYRKADVEEGGKWKIKY-----YKGLGTST 522
```

```
RESULT 8
ID Y165_RICPR STANDARD; PRT; 368 AA.
AC Q9ZDZ8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein RP165.
GN RP165.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_Taxid=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sichertitz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria."
RL Nature 396:133-140(1998).
```

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```
CC -----
DR EMBL; AJ235270; CA14632.1; -.
DR PIR; A71727; A71727.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 368 AA; 41009 MW; 0410168F891F489C CRC64;
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Query Match 17.3%; Score 65; DB 1; Length 368;  
Best Local Similarity 20.9%; Pred. No. 3.3;  
Matches 19; Conservative 13; Mismatches 17; Indels 42; Gaps 3;

```
OY 7 ENYASRPEAFNT-----PFLNIDKLSA-----FKADEFLN 37
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 206 EVYNAKENIINTNOHVGINLVLPKINNEKSSSEAVGWFKLYLNISGSAVYKVAEYLN 265

OY 38 WHALFESIKRK-----LPFLNWD 55
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 266 FNMKFEGINNHKLKYFADLDPSAVIPIANWE 296
```

```
RESULT 9
ID YNM3_YEAST STANDARD; PRT; 506 AA.
AC P53867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 56.6 kDa protein in URE2-SSU72 intergenic region.
GN YNL223W OR N1274.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_Taxid=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97051596; PubMed=8896273;
RA Pandolfo D., de Antoni A., Lanfranchi G., Valle G.;
RT "The DNA sequence of cosmid 14-5 from chromosome XIV reveals 21 open
RT reading frames including a novel gene encoding a globin-like
RT domain."
RL Yeast 12:1071-1076(1996).
```

```
RN [2]
RP SEQUENCE FROM N.A.
RA Duesterhoeft A., Floeth M., Fritze C., Heuss-Netzel D., Hilbert H.,
RA Moestl D.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 13-506 FROM N.A.
RA Sun Z., Hampsey M.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
```

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```
CC -----
DR EMBL; Z69381; CAA93375.1; -.
DR EMBL; Z71499; CAA96126.1; -.
DR EMBL; U20390; AAA86498.1; -.
DR PIR; S63181; S63181.
DR MEROPS; C54.001; -.
DR SGD; S0005167; AUT2.
DR GO; GO:0005875; C:microtubule associated complex; IPI.
DR GO; GO:0008017; F:microtubule binding activity; IPI.
DR GO; GO:0006914; P:autophagy; IMP.
DR GO; GO:0006623; P:protein-vacuolar targeting; IMP.
DR InterPro; IPR005078; Peptidase C54.
DR Pfam; PF03416; Peptidase_C54; 2.
KW Hypothetical protein.
SQ SEQUENCE 506 AA; 56553 MW; 95EB599D6CDBB6F9 CRC64;
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Query Match 17.2%; Score 64.5; DB 1; Length 506;  
Best Local Similarity 28.4%; Pred. No. 5.4;  
Matches 19; Conservative 9; Mismatches 16; Indels 23; Gaps 2;

```
OY 4 STIENYASRPEAFNTPF-----LNIDKLSAFKADFLNWHALFESIKR 47
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 139 STIEDYIANPDCFNFDIGWGCMI RTGSLGNALQIHLGRDFRVNG-----NESLER 191

OY 48 KLPLFLNW 54
```

Db : |||  
192 ESKFVNW 198

## RESULT 10

AC GAGJ\_DROME STANDARD; PRT; 568 AA.  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Nucleic-acid-binding protein (Mobile element jockey) (ORF1).  
GN GAG.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_Taxid=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89108009; PubMed=2463954;  
RA Prismaegi A.F., Mizrokh L.J., Ilyin Y.V.;  
RT "The Drosophila mobile element jockey belongs to LINES and contains  
RT coding sequences homologous to some retroviral proteins.";  
RT Gene 70:253-262(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87303653; PubMed=3040362;  
RA Mizrokh L.J., Prismaegi A.F., Ilyin Y.V.;  
RT "Drosophila mobile element jockey is a retroposon and encodes the  
RT GAG-specific protein sequence characteristic for retroviruses.";  
RT Dokl. Akad. Nauk SSSR 294:1235-1239(1987).  
CC -1- FUNCTION: STRONGLY BASIC PROTEIN THAT BINDS DIRECTLY TO  
CC RETROVIRAL RNA AND MAY BE INVOLVED IN ITS PACKAGING AND  
CC IN THE REVERSE TRANSCRIPTION PROCESS.  
CC -1- SIMILARITY: STRONG TO THE EQUIVALENT PROTEIN OF DROSOPHILA  
CC FUNEBRIS.

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CC -----  
CC DR EMBL; M22874; AAA28674.1; ALT INIT.  
CC EMBL; M38643; AAA28939.1; ALT INIT.  
CC FlyBase; FBgn0020297; jockey\gag.  
CC InterPro; IPR006579; Pre\_C2HC.  
CC InterPro; IPR001878; Znf\_CCHC.  
CC SMART; SM00596; PRE\_C2HC; 1.  
CC DR SMART; SM00343; Znf\_C2HC; 1.  
CC KW Transposable element; Zinc-finger.  
CC FT DOMAIN 390 444 THREE ZINC-FINGER-LIKE REGIONS.  
CC FT ZN\_FING 390 403 POTENTIAL.  
CC FT ZN\_FING 403 423 POTENTIAL.  
CC FT ZN\_FING 430 444 POTENTIAL.  
CC SQ SEQUENCE 568 AA; 62878 MW; DE0E4834A24C759A CRC64;

Query Match 17.2%; Score 64.5; DB 1; Length 568;  
Best Local Similarity 27.0%; Pred. No. 6.1;  
Matches 17; Conservative 10; Mismatches 21; Indels 15; Gaps 3;

QY 9 YASRPEAFNTPLNIDKLSAFKADEFNLWHALFESIKRKLPLNWDAPPKLGLRSATP 68  
DB 259 YTNADDAFRTAVKELNLCNQF-----WH--HQLKEKPYR-----VTLKGIMANVP 303  
QY 69 DAQ 71  
DB 304 SSQ 306

RESULT 11  
CP11\_LIMLI STANDARD; PRT; 521 AA.  
ID CP11\_LIMLI  
AC 042430;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1).  
GN CYP1A1.  
OS Limanda limanda (Dab).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
OC Pleuronectoidae; Pleuronectidae; Limanda.  
OX NCBI\_Taxid=27771;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=21315588; PubMed=11423384;  
RA Craft J.A., Robertson P.E., McPhail M.E., Brown E., Stagg R.M.;

RT "Measurement of cytochrome P4501A induction in dab (Limanda limanda)  
RT and other teleosts with species-specific cDNA probes: isolation and  
RT characterisation of dab cDNA and its use in expression studies with  
RT beta-naphthoflavone-treated fish.";  
RT Comp. Biochem. Physiol. 129C:115-127(2001).  
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE  
CC MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED  
CC COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.  
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +  
CC oxidized flavoprotein + H(2)O.  
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.  
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.  
CC -----  
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CC -----  
CC DR EMBL; AJ001724; CAA04953.1; -.  
CC HSSP; P00179; 1DT6.  
CC InterPro; IPR001128; Cytochrome\_P450.  
CC Pfam; PF00067; P450; 1.  
CC DR PRINTS; PR00385; P450.  
CC DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
CC KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;  
CC Microsome; Endoplasmic reticulum.  
CC FT METAL 463 463 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
CC SQ SEQUENCE 521 AA; 59063 MW; 11DE326C8A7FBD9 CRC64;

Query Match 16.9%; Score 63.5; DB 1; Length 521;  
Best Local Similarity 30.2%; Pred. No. 7.2;  
Matches 19; Conservative 13; Mismatches 22; Indels 9; Gaps 3;

QY 7 ENYASRPEAFNTPLNIDKLSAFKADEFNLWHALFESIKRKLPLNWDAPPKLGLRSA 66  
DB 106 DDFAGRPDLYSFRFINBGK-SLAFSTDKAGIWR-----RRKLAYSALRSFATLEG---T 156  
QY 67 TPD 69  
DB 157 TPE 159

RESULT 12  
CP11\_STECH STANDARD; PRT; 521 AA.  
ID CP11\_STECH  
AC Q92116;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1).

```
GN CYP1A1.
OS Stenotomus chrysops (Scup).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Stenotomus.
OX NCBI_TaxID=35579;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95275266; PubMed=7755595;
RA Morrison H.G., Oleksiak M.F., Cornell N.W., Sogin M.L., Stegeman J.J.;
RT "Identification of cytochrome P-450 1A (CYP1A) genes from two teleost
RT fish, toadfish (Opsanus tau) and scup (Stenotomus chrysops), and
RT phylogenetic analysis of CYP1A genes.";
RL Biochem. J. 308:97-104(1995).
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
CC COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
CC -----
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CC -----
DR EMBL; U14162; AAA74969.1; -.
DR HSSP; P00179; 1DT6.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KM Microsome; Endoplasmic reticulum.
FT METAL 463 463 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 521 AA; 59019 MW; 8BDC4312074025D4 CRC64;
Query Match 16.9%; Score 63.5; DB 1; Length 521;
Best Local Similarity 30.2%; Pred. No. 7.2;
Matches 19; Conservative 12; Mismatches 23; Indels 9; Gaps 3;
QY 7 ENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRLPLNWDAPPKLGLRSA 66
DB 106 DXFAGRPDLYSFRFIN-DGKSLAFSTDQAGVWRA-----RKLAYSALRSFATLEG--T 156
QY 67 TPD 69
DB 157 TPE 159
RESULT 13
CPI1_DIC1A STANDARD; PRT; 520 AA.
ID CPI1_DIC1A
AC P79716;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1).
GN CYP1A1.
OS Dicotylarchus labrax (European sea bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Moronidae; Dicotylarchus.
OX NCBI_TaxID=13489;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC TISSUE=Liver;
RX MEDLINE=99138413; PubMed=9972466;
RA Stien X., Amichot M., Borge J.B., Lafaurie M.;
RT "Molecular cloning of a CYP1A cDNA from the teleost fish
RT Dicotylarchus labrax.";
RL Comp. Biochem. Physiol. 121C:241-248(1998).
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
CC OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
CC ACIDS, AND XENOBIOTICS.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U78316; AAB36951.1; -.
DR HSSP; P00179; 1DT6.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KM Microsome; Endoplasmic reticulum.
FT METAL 464 464 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 520 AA; 58743 MW; 86761584B28E57FB CRC64;
Query Match 16.7%; Score 62.5; DB 1; Length 520;
Best Local Similarity 30.6%; Pred. No. 9.4;
Matches 19; Conservative 9; Mismatches 25; Indels 9; Gaps 3;
QY 7 ENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRLPLNWDAPPKLGLRSA 66
DB 106 DEFAGRPDLYSFRFIN-DGKSLAFSTDQAGVWRA-----RKLAY---SALRSFSSLEES 156
QY 67 TP 68
DB 157 TP 158
RESULT 14
PMG2_MOUSE STANDARD; PRT; 252 AA.
ID PMG2_MOUSE
AC O70250;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Phosphoglycerate mutase 2 (EC 5.4.2.1) (EC 5.4.2.4) (EC 3.1.3.13)
DE (Phosphoglycerate mutase isozyme M) (PGAM-M) (BPG-dependent PGAM 2)
DE (Muscle-specific phosphoglycerate mutase).
GN PGAM2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu G., Yu L., Tu Q., Jiang Y., Fan Y., Zhao S.;
RT "Cloning and expression analysis of a mouse gene coding
RT phosphoglycerate mutase muscle-specific subunit.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21147938; PubMed=11250083;
RA Zhang J., Yu L., Fu Q., Gao J., Xie Y., Chen J., Zhang P., Liu Q.,
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RA Zhao S.;  
 RT "Mouse phosphoglycerate mutase M and B isozymes: cDNA cloning, enzyme  
 RT activity assay and mapping.";  
 RL Gene 264:273-279(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Interconversion of 3- and 2-phosphoglycerate with  
 CC 2,3-bisphosphoglycerate as the primer of the reaction. Can also  
 CC catalyze the reaction of EC 5.4.2.4 (synthase) and EC 3.1.3.13  
 CC (phosphatase), but with a reduced activity.  
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate + 2,3-diphosphoglycerate  
 CC = 3-phospho-D-glycerate + 2,3-diphosphoglycerate.  
 CC -1- CATALYTIC ACTIVITY: 3-phospho-D-glyceroyl phosphate = 2,3-  
 CC bisphospho-D-glycerate.  
 CC -1- CATALYTIC ACTIVITY: 2,3-diphosphoglycerate + H(2)O = 3-  
 CC phosphoglycerate + phosphate.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- TISSUE SPECIFICITY: In mammalian tissues there are two types of  
 CC phosphoglycerate mutase isozymes: type-M in muscles and type-B in  
 CC other tissues.  
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE MUTASE FAMILY. BPG-  
 CC DEPENDENT PGAM SUBFAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF029843; AAC13263.1; -;  
 DR EMBL; AF317587; AAK06662.1; -;  
 DR EMBL; BC010750; AAH10750.1; -;  
 DR HSSP; P00950; 5PGM.  
 DR MGD; MGI:1933118; Pgam2.  
 DR SWISS-2DPAGE; O70250; MOUSE.  
 DR InterPro; IPR001345; PG/BPGM\_mutase.  
 DR InterPro; IPR005952; Phosphogly\_mut1.  
 DR Pfam; PF00300; PGAM; 1.  
 DR TIGRFAMs; TIGR01258; pgm\_1; 1.  
 DR PROSITE; PS00175; PG\_MUTASE; 1.  
 KW isomerase; Hydrolase; Glycolysis.  
 FT INIT MET 0 0 BY SIMILARITY.  
 FT ACT\_SITE 10 10 PHOSPHOHISTIDINE INTERMEDIATE  
 FT ACT\_SITE 61 61 (BY SIMILARITY).  
 FT ACT\_SITE 61 61 REQUIRED FOR BINDING CARBOXYL GROUP OF  
 FT ACT\_SITE 185 185 PHOSPHOGLYCERATES (BY SIMILARITY).  
 SQ SEQUENCE 252 AA; 28696 MW; 7EB3F9EC4B985B86 CRC64;

Query Match 16.5%; Score 62; DB 1; Length 252;  
 Best Local Similarity 30.5%; Pred. No. 4.9;  
 Matches 18; Conservative 11; Mismatches 18; Indels 12; Gaps 2;  
 Qy 15 AFNTP-----FLNIDKLR--SAFKADEFLNWHALFESIKRKLPLNWDAPPKLK 61  
 Db 117 SFDTPPPMDEKNNYTSISKDRYAGLKPEELPTCESLKDTIARALPFWNIEIAPKIK 175  
 RESULT 15  
 ID PMG2 RAT STANDARD; PRT; 252 AA.  
 AC P16290;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Phosphoglycerate mutase 2 (EC 5.4.2.1) (EC 5.4.2.4) (EC 3.1.3.13)  
 DE (Phosphoglycerate mutase isozyme M) (PGAM-M) (BPG-dependent PGAM 2)  
 DE (Muscle-specific phosphoglycerate mutase).  
 GN PGAM2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=90121247; PubMed=2558656;  
 RA Castella-Escola J., Montoliu L., Pons G., Puigdomenech P.,  
 RA Cohen-Solal M., Carreras J., Rigau J., Climent F.;  
 RT "Sequence of rat skeletal muscle phosphoglycerate mutase cDNA.";  
 RL Biochem. Biophys. Res. Commun. 165:1345-1351(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95011622; PubMed=7926808;  
 RA Ruiz-Lozano P., de Lecea L., Buesa C., Perez de la Osa P.,  
 RA Lepage D., Gualberto A., Walsh K., Pons G.;  
 RT "The gene encoding rat phosphoglycerate mutase subunit M: cloning and  
 RT promoter analysis in skeletal muscle cells.";  
 RL Gene 147:243-248(1994).  
 CC -1- FUNCTION: Interconversion of 3- and 2-phosphoglycerate with  
 CC 2,3-bisphosphoglycerate as the primer of the reaction. Can also  
 CC catalyze the reaction of EC 5.4.2.4 (synthase) and EC 3.1.3.13  
 CC (phosphatase), but with a reduced activity.  
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate + 2,3-diphosphoglycerate  
 CC = 3-phospho-D-glycerate + 2,3-diphosphoglycerate.  
 CC -1- CATALYTIC ACTIVITY: 3-phospho-D-glyceroyl phosphate = 2,3-  
 CC bisphospho-D-glycerate.  
 CC -1- CATALYTIC ACTIVITY: 2,3-diphosphoglycerate + H(2)O = 3-  
 CC phosphoglycerate + phosphate.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- TISSUE SPECIFICITY: In mammalian tissues there are two types of  
 CC phosphoglycerate mutase isozymes: type-M in muscles and type-B in  
 CC other tissues.  
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE MUTASE FAMILY. BPG-  
 CC DEPENDENT PGAM SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL; M31835; AAA41835.1; -;  
 DR EMBL; Z17319; CAA78967.1; -;  
 DR PIR; A33793; PMRTM.  
 DR HSSP; P00950; 5PGM.  
 DR InterPro; IPR001345; PG/BPGM\_mutase.  
 DR InterPro; IPR005952; Phosphogly\_mut1.  
 DR Pfam; PF00300; PGAM; 1.  
 DR TIGRFAMs; TIGR01258; pgm\_1; 1.



DR PROSITE; PS00175; PG\_MUTASE; 1.  
KW Isomerase; Hydrolase; Glycolysis.  
FT INIT MET 0  
FT ACT\_SITE 10 10 PHOSPHOHISTIDINE INTERMEDIATE.  
FT ACT\_SITE 61 61 REQUIRED FOR BINDING CARBOXYL GROUP OF  
FT ACT\_SITE PHOSPHOGLYCERATES.  
FT ACT\_SITE 185 185  
SQ SEQUENCE 252 AA; 28624 MW; 4A3F118A0E4AD545 CRC64;

Query Match 16.5%; Score 62; DB 1; length 252;  
Best Local Similarity 30.5%; Pred. No. 4.9;  
Matches 18; Conservative 11; Mismatches 18; Indels 12; Gaps 2;

OY 15 AFNTP-----FLNIDKLK--SAFKADEFLNWHALFESIKRKLPLNWDAPPKLK 61  
Db 117 SFDTPPPPMDEKHNYYASISKDRRYAGLKPPEELPTCESISKDTIARALPFWNEELAPKIK 175

Search completed: November 28, 2003, 13:39:28  
Job time : 21 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 13:11:21 ; Search time 55 Seconds

(without alignments)  
333.122 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Perfect score: 375

Sequence: 1 EBESTIENYASRPEAFNTPF.....LNWDAPFKLGLRSATPDAQ 71

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	19.2	390	16 Q8UES9	Q8UES9 agrobacteri
2	70	18.7	251	16 Q935B8	Q935B8 salmonella
3	69.5	18.5	407	11 Q8C4L6	Q8C4L6 mus musculu
4	67.5	18.0	439	13 Q98SG4	Q98SG4 scophthalmu
5	67.5	18.0	439	13 Q98SG7	Q98SG7 platichthys
6	67.5	18.0	521	13 Q90WD4	Q90WD4 lithognathu
7	67	17.9	203	4 Q9BSY6	Q9BSY6 homo sapien
8	67	17.9	912	5 Q8T034	Q8T034 drosophila
9	66.5	17.7	521	13 Q90XPI	Q90XPI salmo salar
10	66.5	17.7	522	13 Q8QGP2	Q8QGP2 salmo salar
11	66.5	17.7	522	13 Q9PRH3	Q9PRH3 oncorhynch
12	66	17.6	808	10 Q82073	Q82073 triticum ae
13	65.5	17.5	258	16 Q8DSX6	Q8DSX6 streptococc
14	65	17.3	137	4 Q96EW8	Q96EW8 homo sapien
15	65	17.3	459	17 Q9UZH9	Q9UZH9 pyrococcus
16	64.5	17.2	254	5 Q95W96	Q95W96 helioidari

17	64.5	17.2	291	2 Q9F1T8	Q9F1T8 acidovorax
18	64.5	17.2	871	16 Q97K23	Q97K23 clostridium
19	64	17.1	519	13 Q9PTY6	Q9PTY6 anguilla ja
20	64	17.1	519	13 Q9PTY7	Q9PTY7 anguilla ja
21	64	17.1	521	13 Q8QGI8	Q8QGI8 anguilla an
22	64	17.1	819	16 Q8DEP2	Q8DEP2 vibrio vuln
23	63.5	16.9	129	16 Q8CYK6	Q8CYK6 streptococc
24	63	16.8	304	16 Q8XVQ2	Q8XVQ2 raietonia s
25	63	16.8	521	13 Q9Y164	Q9Y164 fundulus he
26	63	16.8	1213	5 Q9XTC7	Q9XTC7 caenorhabdi
27	62.5	16.7	359	16 Q8R863	Q8R863 thermoanaer
28	62.5	16.7	519	13 Q9PT96	Q9PT96 dlicentrarch
29	62.5	16.7	522	16 Q9JZB2	Q9JZB2 neisseria m
30	62.5	16.7	522	16 Q9JUH1	Q9JUH1 neisseria m
31	62	16.5	253	5 Q95W97	Q95W97 helioidari
32	61.5	16.4	506	9 Q64068	Q64068 bacterioph
33	61.5	16.4	506	16 Q31953	Q31953 bacillus su
34	61.5	16.4	647	16 Q8F0E4	Q8F0E4 leptospira
35	61	16.3	254	16 Q9K7J1	Q9K7J1 bacillus ha
36	61	16.3	439	13 Q98SK5	Q98SK5 ammodytes m
37	61	16.3	519	13 Q8UW07	Q8UW07 brachydanio
38	61	16.3	519	13 Q8QGS5	Q8QGS5 brachydanio
39	61	16.3	736	16 Q98068	Q98068 mycoplasma
40	61	16.3	2344	3 Q74539	Q74539 schizosacch
41	60.5	16.1	276	16 Q9X0H7	Q9X0H7 thermotoga
42	60.5	16.1	395	13 Q98TE5	Q98TE5 oreochromis
43	60.5	16.1	854	12 Q995Z2	Q995Z2 enterovirus
44	60.5	16.1	854	12 Q995Z1	Q995Z1 enterovirus
45	60.5	16.1	1232	17 Q58318	Q58318 methanococc

#### ALIGNMENTS

RESULT 1	ID	Q8UES9	PRELIMINARY;	PRT;	390 AA.
AC	Q8UES9	01-JUN-2002 (TREMBLrel. 21, Created)			
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)				
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
DB	Para-aminobenzoate synthase component I.				
GN	PABP OR ATU1676 OR AGR_C_3082.				
OS	Agrobacterium tumefaciens (strain C58 / ATCC 33970).				
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;				
OC	Rhizobiaceae; Rhizobium.				
OX	NCBI_TaxID=176299;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21608550; PubMed=11743193;				
RA	Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,				
RA	Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Woo L.,				
RA	Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,				
RA	Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,				
RA	Kutyavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,				
RA	Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,				
RA	Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,				
RA	Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,				
RA	Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,				
RA	Nester E.W.;				
RT	"The genome of the natural genetic engineer Agrobacterium tumefaciens				
RT	C58.";				
RL	Science 294:2317-2323 (2001).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21608551; PubMed=11743194;				
RA	Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,				
RA	Quarles B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,				
RA	Houmlel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,				
RA	Wollam C., Allinger J., Douglty D., Scott C., Iapacs C., Markelz B.,				
RA	Flanagan C., Crowell C., Girsan J., Lomo C., Sear C., Strub G.,				
RA	Cielo C., Slater S.;				
RT	"Genome sequence of the plant pathogen and biotechnology agent				

RT	Agrobacterium tumefaciens C58."
RL	Science 294:2323-2328(2001).
DR	EMBL; AE009124; AAL42676.1; ALT_INIT.
DR	EMBL; AE008089; AAK87448.1; -.
DR	InterPro; IPR005801; Anth_synch_chor.
DR	Pfam; PF00425; chorismate_bind_1.
DR	PRINTS; PR00095; ANTSNTHASEI.
DR	ProDom; PD000779; Anth_synch_chor; 1.
KW	Complete proteome.
SQ	SEQUENCE 390 AA; 43232 MW; 65EB9BD09E7FF16 CRC64;

  

Query Match	19.2%; Score 72; DB 16; Length 390;
Best local Similarity	35.6%; Pred. No. 2.5;
Matches 26; Conservative 11; Mismatches 24; Indels 12; Gaps 4;	

  

QY	10 ASRPEAFNTPLINIDKLRSAFK-ADEFLNMHA--LFE-----SIKRKLPELNWDAF-- 57
	::::      ::::      :  :      :
DB	34 ADEPEAFTTALQRMEELRRAGKYLGYMSYEAGFLFEPKLAFPAALEPRNVPELNFVFSG 93
	::::      ::::      :  :      :
QY	58 PKLGLRSATPDA 70
	:
DB	94 PQPDEGRFARPD 106

RESULT 2	
ID Q935B8	PRELIMINARY; PRT; 251 AA.
AC Q935B8;	
DT 01-DEC-2001 (TReMBLrel. 19, Created)	
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)	
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)	
DE Hypothetical protein HCM2.0044C.	
GN HCM2.0044C.	
OS Salmonella typhi.	
OG plasmid pHCM2.	
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
OC Enterobacteriaceae; Salmonella.	
OX NCBI_TaxID=601;	
OX [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=CT18;	
RX MEDLINE=21534947; PubMed=11677608;	
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,	
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,	
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,	
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,	
RA Feltham T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,	
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,	
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,	
RA Whitehead S., Barrell B.G.;	
RT "Complete genome sequence of a multiple drug resistant Salmonella	
RT enterica serovar Typhi CT18.";	
RT Nature 413:848-852(2001).	
RL EMBL; AL513384; CAD09911.1; -	
KW Hypothetical protein; Plasmid; Complete proteome.	
SO SEQUENCE 251 AA; 29282 MW; DA64A8B1473B4AA3 CRC64;	
Query Match	18.7%; Score 70; DB 16; Length 251;
Best Local Similarity	28.4%; Pred. No. 2.6;
Matches 21; Conservative 13; Mismatches 16; Indels 24; Gaps 4	
QY 3 ESTIEN--YASRPEAFNTPF-----LNIDKLRSAPKAD-----EFLNHALFE 43	
DB 19 DAFVNGTIYASRPLDFNDPALKVIILDFEADPDVICKKFFADNPEKTEEEFLAWYSSFD 78	
QY 44 SIKRKLPLINWDAF 57	
DB 79 ERAK-----SWIAY 87	
RESULT 3	
Q8C4L6 PRELIMINARY; PRT; 407 AA.	
ID Q8C4L6	

AC Q8C4L6;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)  
DE Inferred: RIKEN cDNA 1110014F24.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Head;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
DR EMBL; AK081753; BAC38319.1; -.  
SQ SEQUENCE 407 AA; 42735 MW; 9D243DA7077983F6 CRC64;

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Query Match          18.5% ; Score 69.5 ; DB 11 ; Length 407 ;
Best Local Similarity 31.1% ; Pred. No. 5.3 ;
Matches 19 ; Conservative 5 ; Mismatches 16 ; Indels 21 ; Gaps 3 ;

QY      14 EAFNTPFLNIDKLRSAPKA-DEFLNWH-----LFSIKRKLPFLN 53
      : | | | | : | | | | | | | | | | | | | | | |
Db       265 DASTLPF-NIDNFWENLKSXTRFLINWDAINKGHAPSPSTRALLYFRKLTWENFKRSTPFFN 323

QY      54 W 54
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Db       324 W 324

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RESULT 4
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ID Q98SG4 PRELIMINARY; PRT; 439 AA.
AC Q98SG4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DB Cytochrome P4501A (Fragment).
GN CYP1A.
OS Scophthalmus maximus (turbot).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoides; Scophthalmidae; Scophthalmus.
OX NCBI_TaxID=52904;
RN [1]
RP SEQUENCE FROM N.A.
RA Craft J.A., Robertson F.E., McPhail M.E., Brown E., Stagg R.M.;
RT "Measurement of cytochrome P4501A induction in dab (Limanda limanda)
RT and other teleosts with species-specific cDNA probes: isolation and
RT characterization of dab cDNA and its use in expression studies with b-
RT naphthoflavone-treated fish.";
RL Comp. Biochem. Physiol. 129:115-127(2001).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AJ310694; CAC34401.1; -.
DR HSSP; P00179; 1DT6.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Heme; Monooxygenase; Oxidoreductase.
FT NON_TER 1
FT NON_TER 439
SQ SEQUENCE 439 AA; 49589 MW; 564ECC5864C696E5 CRC64;

```

Query Match	18.0%;	Score 67.5;	DB 13;	Length 439;
Best Local Similarity	31.7%;	Pred. No. 10;		
Matches	20;	Conservative	11;	Mismatches 23;
				Indels 9;
				Gaps 3;



OC Ephyridae; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkeley;  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
RA Munoz J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,  
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY069595; AAL39740.1; -.  
DR FlyBase; FBgn0034847; CG3502.  
DR InterPro; IPR001930; Ala\_peptase.  
DR InterPro; IPR006025; Zn\_MTPeptase.  
DR Pfam; PF01433; Peptidase\_M1; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
SQ SEQUENCE 912 AA; 105630 MW; 4F07209CD5EBB2A0 CRC64;

Query Match 17.9%; Score 67; DB 5; Length 912;  
Best Local Similarity 31.7%; Pred. No. 27;  
Matches 20; Conservative 7; Mismatches 18; Indels 18; Gaps 2;

OY 24 DKLSAFKADFLNWH-----AL-----FESIKRKLPLNWDAPFKLGLRSA 65  
Db 636 DLLEYLKEQDFLPWQRAIGILNRLGALLNVAENKFKNYMQKLLLLYNRPRLSGIRE 695  
OY 66 ATP 68  
Db 696 AKP 698

RESULT 9  
Q90XP1 PRELIMINARY; PRT; 521 AA.  
AC Q90XP1;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Cytochrome P450 1A.  
OS Salmo salar (Atlantic salmon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.  
OX NCBI\_TaxID=8030;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Arukwe A.;  
RT "Molecular cloning, sequence analysis and expression of the cytochrome  
RT P4501A gene in Atlantic salmon (Salmo salar).";  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
DR EMBL; AF364076; AAK52513.2; -.  
DR InterPro; IPR001128; Cytochrome\_P450.  
DR Pfam; PF00067; P450; 1.  
DR PRINTS; PR00385; P450.  
DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
KW Heme; Monooxygenase; Oxidoreductase.  
SQ SEQUENCE 521 AA; 58574 MW; C1859561E453F5CC CRC64;

Query Match 17.7%; Score 66.5; DB 13; Length 521;  
Best Local Similarity 31.7%; Pred. No. 16;  
Matches 20; Conservative 12; Mismatches 22; Indels 9; Gaps 3;

OY 7 ENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKLGLRSA 66  
Db 106 EDFAGRPDLVSPKFIN-DGKSLAFSTDKAGVWRA-----RRKLAMSALRSFATLEG--S 156  
OY 67 TPD 69  
Db 157 TPE 159

RESULT 10  
Q8QGP2 PRELIMINARY; PRT; 522 AA.  
AC Q8QGP2;  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Cytochrome P450 1A.  
GN CYP1A.  
OS Salmo salar (Atlantic salmon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.  
OX NCBI\_TaxID=8030;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rees C.B., Li W.;  
RT "Cloning and induction of Atlantic salmon CYP1A.";  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
DR EMBL; AF361643; AAM0254.1; -.  
DR InterPro; IPR001128; Cytochrome\_P450.  
DR Pfam; PF00067; P450; 1.  
DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
KW Heme; Monooxygenase; Oxidoreductase.  
SQ SEQUENCE 522 AA; 59192 MW; 560C4E10F704A568 CRC64;

Query Match 17.7%; Score 66.5; DB 13; Length 522;  
Best Local Similarity 31.7%; Pred. No. 16;  
Matches 20; Conservative 12; Mismatches 22; Indels 9; Gaps 3;

OY 7 ENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKLGLRSA 66  
Db 106 EDFAGRPDLVSPKFIN-DGKSLAFSTDKAGVWRA-----RRKLAMSALRSFATLEG--S 156  
OY 67 TPD 69  
Db 157 TPE 159

RESULT 11  
Q9PRH3 PRELIMINARY; PRT; 522 AA.  
AC Q9PRH3;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Cytochrome P450 1A3.  
GN CYP1A3.  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TISSUE=Liver;  
RA Carvan M.J. III, Ponomareva L.V., Solis W.A., Matlib R.S., Puga A.,  
RA Nebert D.W.;  
RT "Trout CYP1A3 Gene: Recognition of Fish DNA Motifs by Mouse Regulatory  
RT Proteins.";  
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
DR EMBL; AF059711; AAD45967.1; -.  
DR EMBL; AF059710; AAD45966.1; -.  
DR HSSP; P00179; 1DT6.  
DR InterPro; IPR001128; Cytochrome\_P450.  
DR Pfam; PF00067; P450; 1.  
DR PRINTS; PR00385; P450.  
DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
KW Heme; Monooxygenase; Oxidoreductase.  
SQ SEQUENCE 522 AA; 59086 MW; AF36786EB19D73DA CRC64;





Query Match 17.3%; Score 65; DB 17; Length 459;  
Best Local Similarity 34.7%; Pred. No. 21;  
Matches 17; Conservative 7; Mismatches 15; Indels 10; Gaps 2;

QY 1 EEESTIENYASR-PEAFNTPEFLNIDKLRSAFKADEFLNWHALFESIKRK 48  
| | : : : : | | | | : |  
Db 59 ESETVLEDFSERLAEEYFNDPFLKENPLR-----NWGAFFAYLAGK 98

Search completed: November 28, 2003, 13:40:31  
Job time : 60 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 08:03:47 ; Search time 19 Seconds

(without alignments)  
501.089 Million cell updates/sec

Title: US-10-059-395-142

Perfect score: 99  
Sequence: 1 MKIPVLPAVLLSLVLSA.....LNWDAPPKLGLRSATPDQ 99

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 76:\*

1: pir1:\*\n2: pir2:\*\n3: pir3:\*\n4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	8	8.1	150	1	NRBO	pancreatic ribonuc
2	8	8.1	167	2	S20066	pancreatic-type ri
3	8	8.1	184	2	AF0298	probable yfeABCD 1
4	8	8.1	219	2	AG0333	heme exporter prot
5	8	8.1	222	2	B82125	heme exporter prot
6	8	8.1	428	2	D97010	5-enolpyruvylshik
7	8	8.1	480	2	F81220	NADH dehydrogenase
8	8	8.1	125	2	D72658	hypothetical prote
9	7	7.1	132	2	H75548	hypothetical prote
10	7	7.1	133	2	E71311	hypothetical prote
11	7	7.1	202	2	A83448	hypothetical prote
12	7	7.1	213	2	F95198	hypothetical prote
13	7	7.1	218	1	S23664	heliB protein - Rho
14	7	7.1	221	1	F64166	heme export protei
15	7	7.1	244	2	A69502	conserved hypothet
16	7	7.1	247	1	OBHOMS	cytochrome-c oxida
17	7	7.1	247	2	S42736	cytochrome-c oxida
18	7	7.1	247	2	S42737	cytochrome-c oxida
19	7	7.1	247	2	S42739	cytochrome-c oxida
20	7	7.1	247	2	AC2699	conserved hypothet
21	7	7.1	260	2	C97481	1828 [imported] -
22	7	7.1	311	1	BYEBT	sulfate-binding pr
23	7	7.1	329	2	AG0942	periplasmic sulpha
24	7	7.1	350	2	S35631	genome polyprotein
25	7	7.1	350	2	A70473	flagellar biosynth
26	7	7.1	361	2	I50505	gene wnt8 protein
27	7	7.1	372	1	WMVZCN	major envelope ant
28	7	7.1	372	2	C72155	E13L protein - var
29	7	7.1	372	2	H36840	C17L protein - var

30	7	7.1	372	2	T28475	hypothetical prote
31	7	7.1	372	2	G90322	hypothetical prote
32	7	7.1	386	1	S41691	ubiquinol-cytochro
33	7	7.1	410	2	S70647	neurosepin precur
34	7	7.1	437	2	D69519	tRNA nucleotidyltr
35	7	7.1	447	2	B82490	probable Na+/H+ an
36	7	7.1	451	2	A38099	glycylpeptide N-te
37	7	7.1	457	2	I73636	neuronal olfactome
38	7	7.1	470	2	B87506	hypothetical prote
39	7	7.1	484	2	H69298	hypothetical prote
40	7	7.1	494	2	AC0133	probable permease
41	7	7.1	519	2	T45764	hypothetical prote
42	7	7.1	542	2	D90944	hypothetical prote
43	7	7.1	542	2	H85792	hypothetical prote
44	7	7.1	542	2	G64942	hypothetical prote
45	7	7.1	546	2	AB0088	probable flagellar

## ALIGNMENTS

## RESULT 1

## NRBO

pancreatic ribonuclease (EC 3.1.27.5) precursor [validated] - bovine

N/Alternate names: ribonuclease 1; ribonuclease A

C/Species: Bos primigenius taurus (cattle)

C/Date: 24-Apr-1984 #sequence revision 05-Aug-1994 #text change 15-Sep-2000

C/Accession: S00897; I45998; A32471; A00804; A92018; A61293; S53757; S05528

R/Carsana, A.; Confalone, E.; Palmieri, M.; Libonati, M.; Furia, A.

Nucleic Acids Res. 16, 5491-5502, 1988

A/Title: Structure of the bovine pancreatic ribonuclease gene: the unique intervening se

A/Reference number: S00897; MUID:88262557; PMID:2838818

A/Accession: S00897

A/Molecule type: DNA

A/Residues: 1-150 <CAR>

A/Cross-references: EMBL:X07283; NID:g671; PIDN:CAA30263.1; PID:g672

R/Vasantha, N.; Filpula, D.

Gene 76, 53-60, 1989

A/Title: Expression of bovine pancreatic ribonuclease A coded by a synthetic gene in Bac

A/Reference number: I45998; MUID:89306659; PMID:2501158

A/Accession: I45998

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 'M', 27-150 <VAS>

A/Cross-references: EMBL:X15802; NID:g93; PIDN:CAA33801.1; PID:g94

A/Note: recombinant gene expressed in E. coli

R/Robertson, A.D.; Purisima, E.O.; Eastman, M.A.; Scheraga, H.A.

Biochemistry 28, 5930-5938, 1989

A/Title: Proton NMR assignments and regular backbone structure of bovine pancreatic ribo

A/Reference number: A32471; MUID:89375325; PMID:2775743

A/Accession: A32471

A/Molecule type: protein

A/Residues: 27-150 <ROB>

R/Smyth, D.G.; Stein, W.H.; Moore, S.

J. Biol. Chem. 238, 227-234, 1963

A/Title: The sequence of amino acid residues in bovine pancreatic ribonuclease: revisior

A/Reference number: A92016

A/Accession: A00804

A/Molecule type: protein

A/Residues: 27-150 <SMY>

A/Note: disulfide bonds were determined

R/Plummer Jr., T.H.; Hirs, C.H.W.

J. Biol. Chem. 239, 2530-2538, 1964

A/Title: On the structure of bovine pancreatic ribonuclease B. Isolation of a glycopepti

A/Reference number: A92018

A/Accession: A92018

A/Molecule type: protein

A/Residues: 27-150 <PLU>

R/Kumagai, H.; Yoshihara, K.; Umemoto, M.; Igataashi, K.; Hirose, S.; Ohgi, K.; Irie, M.

J. Biochem. 93, 865-874, 1983

A/Title: Studies on salivary gland ribonucleases. III. Purification and properties of th

A/Reference number: A61293; MUID:83265672; PMID:6874668

A/Accession: A61293

A:Molecule type: protein  
 A:Residues: 27-40,'XX','43','X','45-46 <KUM>  
 R:Yang, H.J.; Tsou, C.L.  
 Biochem. J. 305, 379-384, 1995  
 A:Title: Inactivation during denaturation of ribonuclease A by guanidinium chloride is a  
 A:Reference number: S53757; MUID:95134214; PMID:7832749  
 A:Accession: S53757  
 A:Molecule type: protein  
 A:Residues: 27-53;60-63;69-73 <YAN>  
 R:Birdsall, D.L.; McPherson, A.  
 submitted to the Brookhaven Protein Data Bank, August 1992  
 A:Reference number: A51385; PDB:1RTB  
 A:Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 27-150  
 R:Birdsall, D.L.; McPherson, A.  
 J. Biol. Chem. 267, 22230-22236, 1992  
 A:Title: Crystal structure disposition of thymidylc acid tetramer in complex with ribon  
 A:Reference number: A44321; MUID:93054504; PMID:1429575  
 A:Contents: annotation; X-ray crystallography, 2.5 angstroms  
 R:Williams, R.L.; Greene, S.M.; McPherson, A.  
 submitted to the Brookhaven Protein Data Bank, September 1987  
 A:Reference number: A50330; PDB:1RBB  
 A:Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 27-150  
 R:Wlodawer, A.  
 submitted to the Brookhaven Protein Data Bank, April 1985  
 A:Reference number: A50927; PDB:5RSA  
 A:Contents: annotation; X-ray and neutron crystallography, 2.0 angstroms, residues 27-15  
 R:Wlodawer, A.; Bolt, R.; Sjoln, L.  
 J. Biol. Chem. 257, 1325-1332, 1982  
 A:Title: The refined crystal structure of ribonuclease A at 2.0 angstrom resolution.  
 A:Reference number: A92350; MUID:82120062; PMID:6276380  
 A:Contents: annotation; X-ray crystallography, 2.0 angstroms  
 R:Howlin, B.; Moss, D.S.; Harris, G.W.; Palmer, R.A.  
 submitted to the Brookhaven Protein Data Bank, October 1991  
 A:Reference number: A50626; PDB:3RNN  
 A:Contents: annotation; X-ray crystallography, 1.45 angstroms, residues 27-150  
 R:Carlisle, C.H.; Palmer, R.A.; Mazumdar, S.K.; Gorinsky, B.A.; Yeates, D.G.R.  
 J. Mol. Biol. 85, 1-18, 1974  
 A:Title: The structure of ribonuclease at 2.5 angstrom resolution.  
 A:Reference number: A92949; MUID:74253324; PMID:4835726  
 A:Contents: annotation; X-ray crystallography, 2.5 angstroms  
 R:Wyckoff, H.W.; Tsernoglou, D.; Hanson, A.W.; Knox, J.R.; Lee, B.; Richards, F.M.  
 J. Biol. Chem. 245, 305-328, 1970  
 A:Title: The three-dimensional structure of ribonuclease-S. Interpretation of an electro  
 A:Reference number: A92059; MUID:70092235; PMID:5460889  
 A:Contents: annotation; X-ray crystallography, 2.0 angstroms  
 R:Santero, J.; Gonzalez, C.; Bruix, M.; Neira, J.L.; Nieto, J.L.; Herranz, J.; Rico, M.  
 submitted to the Brookhaven Protein Data Bank, November 1992  
 A:Reference number: A52045; PDB:2AAS  
 A:Contents: annotation; conformation by (1)H-NMR, residues 27-150  
 R:Rico, M.; Bruix, M.; Santero, J.; Gonzalez, C.; Neira, J.L.; Nieto, J.L.; Herranz, J.  
 Eur. J. Biochem. 183, 623-638, 1989  
 A:Title: Sequential (1)H-NMR assignment and solution structure of bovine pancreatic ribo  
 A:Reference number: S05528; MUID:89377830; PMID:2776756  
 A:Contents: annotation; confirmation by (1)H-NMR  
 R:Shall, S.; Barnard, B.A.  
 J. Mol. Biol. 41, 237-251, 1969  
 A:Title: Heavy atom-labelled derivatives of bovine pancreatic ribonuclease. I. Specific  
 A:Reference number: A92946; MUID:69260123; PMID:5801478  
 A:Contents: annotation; active site  
 R:Heinriksen, R.L.; Stein, W.H.; Crestfield, A.M.; Moore, S.  
 J. Biol. Chem. 240, 2921-2934, 1965  
 A:Title: The reactivities of the histidine residues at the active site of ribonuclease b  
 A:Reference number: A92020  
 A:Contents: annotation; active site  
 C:Function:  
 A:Description: ribonuclease endonucleolytically hydrolyzes RNA to produce 3'-phosphomono  
 A:Pathway: ribonucleic acid digestion  
 A>Note: this enzyme can also destabilize or unwind the DNA helix by complexing with sing  
 rginine residues of the enzyme and the phosphate groups of the nucleotides  
 C:Superfamily: pancreatic ribonuclease  
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
 F:1-26/Domain: signal sequence #status predicted <SIG>  
 F:27-150/Product: pancreatic ribonuclease #status experimental <MAT>

F:38,67,145/Active site: His, Lys, His #status experimental  
 F:52-110,66-121,84-136,91-98/Disulfide bonds: #status experimental  
 F:60/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 8.1%; Score 8; DB 1; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 2.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLLSLVLT 17  
 |||||  
 Db 7 VLLSLVLT 14

## RESULT 2

S20066

pancreatic-type ribonuclease (EC 3.1.27.5) BRB precursor, brain - bovine

C:Species: Bos primigenius taurus (cattle)

C&gt;Date: 22-Nov-1993 #sequence\_revision 12-May-1995 #text\_change 22-Jun-1999

C:Accession: S20066; JX0056

R:Sasso, M.P.; Carsana, A.; Confalone, E.; Costi, C.; Sorrentino, S.; Viola, M.; Palmieri  
 Nucleic Acids Res. 19, 6469-6474, 1991

A:Title: Molecular cloning of the gene encoding the bovine brain ribonuclease and its e

A:Reference number: S20066; MUID:92093604; PMID:1754384

A:Accession: S20066

A:Molecule type: DNA

A:Residues: 1-167 &lt;SAS&gt;

A:Cross-references: EMBL:X59767; NID:9150; PIDN:CAA42439.1; PID:9151

R:Watanabe, H.; Katoh, H.; Ishii, M.; Komoda, Y.; Sando, A.; Takizawa, Y.; Ohgi, K.; It

J. Biochem. 104, 939-945, 1988

A:Title: Primary structure of a ribonuclease from bovine brain.

A:Reference number: JX0056; MUID:89214015; PMID:3243767

A:Accession: JX0056

A:Molecule type: protein

A:Residues: 27-154,'S',156-166 &lt;WAT&gt;

A:Experimental source: brain

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase

F:38,67,145/Active site: His, Lys, His #status predicted

F:52-110,66-121,84-136,91-98/Disulfide bonds: #status predicted

F:88/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:155/Binding site: carbohydrate (Thr) (covalent) #status experimental

F:159/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 8.1%; Score 8; DB 2; Length 167;

Best Local Similarity 100.0%; Pred. No. 2.5;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLLSLVLT 17  
 |||||  
 Db 7 VLLSLVLT 14

## RESULT 3

AF0298

probable yfeABCD locus regulator yfeB [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis

C&gt;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Nov-2001

C:Accession: AF0298

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.E  
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;

11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AF0298

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-184 &lt;KUR&gt;

A:Cross-references: GB:AL590842; PIDN:CAC91250.1; PID:915980439; GSPDB:GN00175

C:Genetics:

A:Gene: yfeB

C:Superfamily: Escherichia coli probable membrane protein b1726

Query Match 8.1%; Score 8; DB 2; Length 184;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 FNTPLINI 51  
|||||  
Db 63 FNTPLINI 70

RESULT 4  
AG0333  
heme exporter protein B [imported] - Yersinia pestis (strain CO92)  
C/Species: Yersinia pestis  
C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Nov-2001  
C/Accession: AG0333  
R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001  
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A/Reference number: AB0001; MUID:21470413; PMID:11586360  
A/Accession: AG0333  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-219 <KUR>  
A/Cross-references: GB:AE00842; PIDN:CAC92974.1; PID:g15980713; GSPDB:GN00175  
C/Genetics:  
A/Gene: ccmB  
C/Superfamily: cytochrome c biogenesis protein Cym

Query Match 8.1%; Score 8; DB 2; Length 219;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLISLVL 17  
|||||  
Db 158 VLISLVL 165

RESULT 5  
B82125  
heme exporter protein B VC2056 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
C/Species: Vibrio cholerae  
C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
C/Accession: B82125  
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, R. 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000  
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A/Reference number: A82035; MUID:20406833; PMID:10952301  
A/Accession: B82125  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-222 <HEI>  
A/Cross-references: GB:AE004279; GB:AE003852; NID:g9656590; PIDN:AAF95202.1; GSPDB:GN001  
A/Experimental source: serogroup O1, strain N16961, biotype El Tor  
C/Genetics:  
A/Gene: VC2056  
A/Map position: 1  
C/Superfamily: cytochrome c biogenesis protein Cym

Query Match 8.1%; Score 8; DB 2; Length 222;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLISLVL 17  
|||||  
Db 161 VLISLVL 168

RESULT 6  
D97010

5-enolpyruvylshikimate-3-phosphate synthase [imported] - Clostridium acetobutylicum  
C/Species: Clostridium acetobutylicum  
C/Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 30-Sep-2001  
C/Accession: D97010  
R/Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, .; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001  
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc  
A/Reference number: A96900; MUID:21359325; PMID:21359325  
A/Accession: D97010  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-428 <KUR>  
A/Cross-references: GB:AE001437; PIDN:AAK78871.1; PID:g15023793; GSPDB:GN00168  
A/Experimental source: Clostridium acetobutylicum ATCC824  
C/Genetics:  
A/Gene: CAC0895  
C/Superfamily: 3-phosphoshikimate 1-carboxyvinyltransferase; 3-phosphoshikimate 1-carbox

Query Match 8.1%; Score 8; DB 2; Length 428;  
Best Local Similarity 100.0%; Pred. No. 5.6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 EEESTIEN 36  
|||||  
Db 35 EEESTIEN 42

RESULT 7  
F81220  
NADH dehydrogenase I, N chain NMB0259 [imported] - Neisseria meningitidis (strain MC58 s  
C/Species: Neisseria meningitidis  
C/Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C/Accession: F81220  
R/Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Maignan, V.; Pizza, M. Science 287, 1809-1815, 2000  
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A/Reference number: A81000; MUID:20175755; PMID:10710307  
A/Accession: F81220  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-480 <TET>  
A/Cross-references: GB:AE002382; GB:AE002098; NID:g7225470; PIDN:AAF40713.1; PID:g722548 A/Experimental source: serogroup B, strain MC58  
C/Genetics:  
A/Gene: NMB0259  
C/Superfamily: NADH dehydrogenase (ubiquinone) chain 2

Query Match 8.1%; Score 8; DB 2; Length 480;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLISLVL 17  
|||||  
Db 16 VLISLVL 23

RESULT 8  
D72658  
hypothetical protein APE0692 - Aeropyrum pernix (strain K1)  
C/Species: Aeropyrum pernix  
C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jun-2000  
C/Accession: D72658  
R/Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999  
A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A/Reference number: A72450; MUID:99310339; PMID:10382966  
A/Accession: D72658  
A/Status: preliminary



A/Molecule type: DNA  
A/Residues: 1-125 <KAM>  
A/Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79668.1; PID:d1043454; PID:g510  
A/Experimental source: strain K1  
C/Genetics:  
A/Gene: APE0692  
C/Superfamily: Aeropyrum pernix hypothetical protein APE0692

Query Match 7.1%; Score 7; DB 2; Length 125;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PVLPAVV 10  
|||||  
Db 70 PVLPAVV 76

RESULT 9  
H75548  
hypothetical protein - Deinococcus radiodurans (strain R1)

C/Species: Deinococcus radiodurans  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
C/Accession: H75548  
R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999

A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A/Reference number: A75250; MUID:20036896; PMID:10567266

A/Accession: H75548

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-132 <WHI>

A/Cross-references: GB:AE001882; GB:AE000513; NID:g6457865; PIDN:AAF09794.1; PID:g645787  
A/Experimental source: strain R1  
C/Genetics:  
A/Gene: DR0206  
A/Map position: 1

Query Match 7.1%; Score 7; DB 2; Length 132;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLISLV 16  
|||||  
Db 107 VLISLV 113

RESULT 10  
E71311

hypothetical protein TP0536 - syphilis spirochete  
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 05-Nov-1999

C/Accession: E71311

R/Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin  
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo  
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998

A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A/Reference number: A71250; MUID:98332770; PMID:9665876

A/Accession: E71311

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-133 <COL>

A/Cross-references: GB:AE001229; GB:AE000520; NID:g3322827; PIDN:AAC65529.1; PID:g332283  
A/Experimental source: strain Nichols  
C/Genetics:  
A/Gene: TP0536

Query Match 7.1%; Score 7; DB 2; Length 133;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LLSLV 17  
|||||  
Db 112 LLSLV 118

RESULT 11  
A83448

hypothetical protein PA1579 [imported] - Pseudomonas aeruginosa (strain PA01)

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C/Accession: A83448

R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim  
.i. Lo, S.; Olson, M.V.  
Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path  
A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: A83448

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-202 <STO>

A/Cross-references: GB:AE004586; GB:AE004091; NID:g9947536; PIDN:AAG04968.1; GSPDB:GN00  
A/Experimental source: strain PA01  
C/Genetics:  
A/Gene: PA1579

Query Match 7.1%; Score 7; DB 2; Length 202;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 LKGLRSA 94  
|||||  
Db 192 LKGLRSA 198

RESULT 12  
F95198

hypothetical protein SP1705 [imported] - Streptococcus pneumoniae (strain TIGR4)

C/Species: Streptococcus pneumoniae

C/Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001

C/Accession: F95198

R/Tetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple,  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001

A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison  
A/Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A/Reference number: A95000; MUID:21357209; PMID:11463916

A/Accession: F95198

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-213 <KUR>

A/Cross-references: GB:AE005672; PIDN:AAK75783.1; PID:g14973199; GSPDB:GN00164; TIGR:SP  
A/Experimental source: strain TIGR4  
C/Genetics:  
A/Gene: SP1705

Query Match 7.1%; Score 7; DB 2; Length 213;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLISLV 16  
|||||  
Db 193 VLISLV 199

RESULT 13

S23664

helB protein - Rhodobacter capsulatus

C/Species: Rhodobacter capsulatus

C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C/Accession: S23664

R/Beckman, D.L.; Trawick, D.R.; Kranz, R.G.

Genes Dev. 6, 268-283, 1992

A;Title: Bacterial cytochromes c biogenesis.

A;Reference number: S23662; MUID:92146961; PMID:1310666

A;Accession: S23664

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-218 <BEC>

A;Cross-references: EMBL:X63462; NID:g46022; PIDN:CAA45062.1; PID:g46025

C;Superfamily: cytochrome c biogenesis protein CycW

C;Keywords: transmembrane protein

Query Match

Best Local Similarity 7.1%; Score 7; DB 1; Length 218;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LLSLV 17

DB 158 LLSLV 164

#### RESULT 14

F64166

heme export protein B - Haemophilus influenzae (strain Rd KW20)

C;Species: Haemophilus influenzae

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C;Accession: F64166

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.

; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: F64166

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-221 <TIGR>

A;Cross-references: GB:U32789; GB:I42023; NID:g1574642; PIDN:AAC22747.1; PID:g1574645; T

C;Superfamily: cytochrome c biogenesis protein CycW

C;Keywords: transmembrane protein

Query Match

Best Local Similarity 7.1%; Score 7; DB 1; Length 221;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLSLV 16

DB 159 VLSLV 165

#### RESULT 15

A69502

conserved hypothetical protein AF2018 - Archaeoglobus fulgidus

C;Species: Archaeoglobus fulgidus

C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999

C;Accession: A69502

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlisch, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae

A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: A69502

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-244 <KLE>

A;Cross-references: GB:AE000963; GB:AE000782; NID:g2689286; PIDN:AAB89232.1; PID:g264851

Query Match

Best Local Similarity 7.1%; Score 7; DB 2; Length 244;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AVVLSL 14

DB 226 AVVLSL 232

Search completed: November 28, 2003, 08:05:30  
Job time : 24 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2003, 07:57:12 ; Search time 11 Seconds  
(without alignments)  
423.240 Million cell updates/sec

Title: US-10-059-395-142  
Perfect score: 99  
Sequence: 1 MKIPVLPAVVLSTLVLSA.....LNWDAFPKLGKRSATPDQA 99

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues  
Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	8.1	150	1 RNP_BOVIN	P00656 bos taurus
2	8	8.1	167	1 RNP_BOVIN	P39873 bos taurus
3	8	8.1	184	1 YFEE_YERPE	Q56956 yersinia pe
4	8	8.1	428	1 AROA_CLOAB	Q97km2 clostridium
5	7	7.1	133	1 EPTI_HUMAN	O95925 homo sapien
6	7	7.1	133	1 EPTI_HUMAN	Q9bdl1 macaca mula
7	7	7.1	133	1 SECG_TREPA	O83547 treponema p
8	7	7.1	202	1 YF79_PSEAE	Q913d8 pseudomonas
9	7	7.1	205	1 EPIB_YEAST	P32471 saccharomyc
10	7	7.1	218	1 CCMB_RHOCA	P29960 rhodobacter
11	7	7.1	221	1 CCMB_HAEIN	P45033 haemophilus
12	7	7.1	239	1 GIDB_CLOPE	Q8xh32 clostridium
13	7	7.1	247	1 COX2_WILMR	P47918 williopsis
14	7	7.1	247	1 COX2_WILSA	P06029 williopsis
15	7	7.1	283	1 ICAL_CERAE	P49342 cercopithec
16	7	7.1	320	1 MCA2_HUMAN	Q13155 homo sapien
17	7	7.1	325	1 CYK2_ORYSA	O9xeas oryza sativ
18	7	7.1	329	1 SUBI_SALTY	P02906 salmonella
19	7	7.1	350	1 FLHB_AQUAE	O67813 aquifex aeo
20	7	7.1	359	1 WNT8_BRARE	P51028 brachydanio
21	7	7.1	372	1 VENV_VACCC	P20638 vaccinia vi
22	7	7.1	372	1 VENV_VARV	P33815 vaccinia vi
23	7	7.1	373	1 MGE1_HUMAN	Q9ubf1 homo sapien
24	7	7.1	410	1 NEUS_CHICK	O90935 gallus gall
25	7	7.1	437	1 CCA_ARCFU	O28126 archaeglob
26	7	7.1	451	1 NMT_CANAL	P30418 candida alb
27	7	7.1	532	1 YOAD_ECOLI	P76261 escherichia
28	7	7.1	554	1 PIGS_SCHPO	Q10351 schizosacch
29	7	7.1	636	1 CTR4_HUMAN	O43246 homo sapien
30	7	7.1	708	1 ICAL_HUMAN	P20810 homo sapien
31	7	7.1	713	1 ICAL_PIG	P12675 sus scrofa
32	7	7.1	814	1 AD15_HUMAN	Q13444 homo sapien
33	7	7.1	1061	1 OAR_MYXXA	P38370 myxococcus

34	7	7.1	1803	1 YUL3_YEAST	P47024 saccharomyc
35	7	7.1	8797	1 SNE1_HUMAN	O8nf91 homo sapien
36	6	6.1	75	1 REGB_PSEAE	O03381 pseudomonas
37	6	6.1	77	1 LLP_BPT5	Q38162 bacterioph
38	6	6.1	85	1 FCEG_BOVIN	Q9bdr7 bos taurus
39	6	6.1	86	1 FCEG_CAVPO	Q07249 cavia porce
40	6	6.1	86	1 FCEG_HUMAN	P30273 homo sapien
41	6	6.1	86	1 FCEG_PIG	O9xs26 sus scrofa
42	6	6.1	88	1 FXY3_MOUSE	Q61835 mus musculu
43	6	6.1	88	1 FXY3_RAT	P59645 rattus norv
44	6	6.1	92	1 VB05_VACC8	P24284 vaccinia vi
45	6	6.1	97	1 NTLM_LOCM1	Q36423 locusta mlg

ALIGNMENTS

RESULT 1  
RNP\_BOVIN  
ID RNP\_BOVIN STANDARD; PRT; 150 AA.  
AC P00656;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ribonuclease pancreatic precursor (EC 3.1.27.5) (RNase 1) (RNase A).  
GN RNASE1 OR RNS1.  
OS Bos taurus (Bovine), and  
OS Bison bison (American bison).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913, 9901;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Bovine;  
RX MEDLINE=88262557; PubMed=2838818;  
RA Carsana A., Confalone E., Palmieri M., Libonati M., Furia A.;  
RT "Structure of the bovine pancreatic ribonuclease gene: the unique  
RT intervening sequence in the 5' untranslated region contains a  
RT promoter-like element.";  
RL Nucleic Acids Res. 16:5491-5502(1988).  
RN [2]  
RP SEQUENCE OF 23-150 FROM N.A.  
RC SPECIES=Bovine;  
RX MEDLINE=96093920; PubMed=7479688;  
RA Delcardayre S.B., Ribc M., Yokel E.M., Quirk D.J., Rutter W.J.,  
RA Raines R.T.;  
RT "Engineering ribonuclease A: production, purification and  
RT characterization of wild-type enzyme and mutants at Gln11.";  
RL Protein Eng. 8:261-273(1995).  
RN [3]  
RP SEQUENCE OF 27-150, AND DISULFIDE BONDS.  
RC SPECIES=Bovine;  
RX Smyth D.G., Stein W.H., Moore S.;  
RT "The sequence of amino acid residues in bovine pancreatic  
RT ribonuclease: revisions and confirmations.";  
RL J. Biol. Chem. 238:227-234(1963).  
RN [4]  
RP SEQUENCE OF 27-150.  
RC SPECIES=Bovine;  
RX Plummer T.H. Jr., Hirs C.H.W.;  
RT "On the structure of bovine pancreatic ribonuclease B. Isolation of  
RT a glycopeptide.";  
RL J. Biol. Chem. 239:2530-2538(1964).  
RN [5]  
RP ACTIVE SITE.  
RC SPECIES=Bovine;  
RX Heinrichson R.L., Stein W.H., Crestfield A.M., Moore S.;  
RT "The reactivities of the histidine residues at the active site of  
RT ribonuclease toward halo acids of different structures.";  
RL J. Biol. Chem. 240:2921-2934(1965).  
RN [6]  
RP ACTIVE SITE.

RC SPECIES=Bovine;  
RX MEDLINE=69260123; PubMed=5801478;  
RN Shall S., Barnard E.A.;  
RA "Heavy atom-labelled derivatives of bovine pancreatic ribonuclease.  
RT I. Specific reactions of ribonuclease with N-acetylhomocysteine  
thiolactone and silver ion.";  
RT J. Mol. Biol. 41:237-251(1969).  
RL [7]  
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RP SPECIES=Bovine;  
RC MEDLINE=70092235; PubMed=5460889;  
RX Wyckoff H.W., Tsernoglou D., Hanson A.W., Knox J.R., Lee B.,  
RA Richards F.W.;  
RT "The three-dimensional structure of ribonuclease-S. Interpretation of  
an electron density map at a nominal resolution of 2 A.";  
RL J. Biol. Chem. 245:305-328(1970).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
RC SPECIES=Bovine;  
RX MEDLINE=74253324; PubMed=4835726;  
RA Carlisle C.H., Palmer R.A., Mazumdar S.K., Gorlinsky B.A.;  
RA Yeates D.G.R.;  
RT "The structure of ribonuclease at 2.5-A resolution.";  
RL J. Mol. Biol. 85:1-18(1974).  
RN [9]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RC SPECIES=Bovine;  
RX MEDLINE=82120062; PubMed=6276380;  
RA Wlodawer A., Bott R., Sjoelin L.;  
RT "The refined crystal structure of ribonuclease A at 2.0-A  
resolution.";  
RL J. Biol. Chem. 257:1325-1332(1982).  
RN [10]  
RP X-RAY CRYSTALLOGRAPHY (1.26 ANGSTROMS).  
RC SPECIES=Bovine;  
RX MEDLINE=88294009; PubMed=3401445;  
RA Wlodawer A., Svensson L.A., Sjoelin L., Gilliland G.L.;  
RT "Structure of phosphate-free ribonuclease A refined at 1.26 A.";  
RL Biochemistry 27:2705-2717(1988).  
RN [11]  
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).  
RX MEDLINE=97299793; PubMed=9154942;  
RA Leonidas D.D., Shapiro R., Irons L.I., Russo N., Acharya K.R.;  
RT "Crystal structures of ribonuclease A complexes with 5'-  
diphosphadenosine 3'-phosphate and 5'-diphosphadenosine  
2'-phosphate at 1.7-A resolution.";  
RL Biochemistry 36:5578-5588(1997).  
RN [12]  
RP STRUCTURE BY NMR.  
RC SPECIES=Bovine;  
RX MEDLINE=89375325; PubMed=2775743;  
RA Robertson A.D., Purisima E.O., Eastman M.A., Scheraga H.A.;  
RT "Proton NMR assignments and regular backbone structure of bovine  
pancreatic ribonuclease A in aqueous solution.";  
RL Biochemistry 28:5930-5938(1989).  
RN [13]  
RP STRUCTURE BY NMR.  
RC SPECIES=Bovine;  
RX MEDLINE=89377830; PubMed=2776756;  
RA Rico M., Bruix M., Santoro J., Gonzalez C., Neira J.L., Nieto J.L.,  
RA Herranz J.;  
RT "Sequential 1H-NMR assignment and solution structure of bovine  
pancreatic ribonuclease A.";  
RL Eur. J. Biochem. 183:623-638(1989).  
RN [14]  
RP STRUCTURE BY NMR.  
RC SPECIES=Bovine;  
RX MEDLINE=93044359; PubMed=1841699;  
RA Rico M., Santoro J., Gonzalez C., Bruix M., Neira J.L., Nieto J.L.,  
RA Herranz J.;  
RT "3D structure of bovine pancreatic ribonuclease A in aqueous  
solution: an approach to tertiary structure determination from a  
small basis of 1H NMR NOE correlations.";

RL J. Biomol. NMR 1:283-298(1991).  
RN [15]  
RP DNA-BINDING.  
RC SPECIES=Bovine;  
RX MEDLINE=86179900; PubMed=3961503;  
RA McPherson A., Brayer G., Cascio D., Williams R.;  
RT "The mechanism of binding of a polynucleotide chain to pancreatic  
ribonuclease.";  
RL Science 232:765-768(1986).  
RN [16]  
RP SEQUENCE OF 27-150.  
RC SPECIES=B.bison;  
RX MEDLINE=76259396; PubMed=955781;  
RA Muskiet F.A.J., Welling G.W., Belintema J.J.;  
RT "Studies on the primary structure of bison pancreatic ribonuclease.";  
RL Int. J. Pept. Protein Res. 8:345-348(1976).  
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
with 2',3'-cyclic phosphate intermediates.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Pancreas.  
CC -1- MISCELLANEOUS: RIBONUCLEASE CAN DESTABILIZE OR UNWIND THE DNA  
HEXIL BY COMPLEXING WITH SINGLE-STRANDED DNA; THIS COMPLEX ARISES  
BY AN EXTENDED MULTISITE CATION-ANION INTERACTION BETWEEN THE  
LYSINE AND ARGININE RESIDUES OF THE ENZYME AND THE PHOSPHATE  
GROUPS OF THE NUCLEOTIDES.  
CC -1- MISCELLANEOUS: THE BISON SEQUENCE APPEARS TO BE IDENTICAL WITH  
THAT OF BOVINE.  
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
CC -1- DATABASE: NAME=Worthington enzyme manual;  
WWW="http://www.worthington-biochem.com/manual/R/RNASE.html".  
CC -----  
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CC -----  
DR EMBL; X07283; CAA30263.1; -.  
DR EMBL; S80747; AAB35594.1; -.  
DR PIR; S00897; NRBO.  
DR PDB; 1RBB; 15-JUL-92.  
DR PDB; 3RN3; 15-OCT-91.  
DR PDB; 2RNS; 31-JAN-94.  
DR PDB; 1RSM; 15-OCT-89.  
DR PDB; 1SRN; 15-JUL-92.  
DR PDB; 5RSA; 15-APR-93.  
DR PDB; 6RSA; 15-OCT-89.  
DR PDB; 7RSA; 15-JAN-93.  
DR PDB; 8RSA; 15-APR-91.  
DR PDB; 9RSA; 15-APR-91.  
DR PDB; 1RAT; 15-JUL-93.  
DR PDB; 2RAT; 15-JUL-93.  
DR PDB; 3RAT; 15-JUL-93.  
DR PDB; 4RAT; 15-JUL-93.  
DR PDB; 5RAT; 15-JUL-93.  
DR PDB; 6RAT; 15-JUL-93.  
DR PDB; 7RAT; 15-JUL-93.  
DR PDB; 8RAT; 15-JUL-93.  
DR PDB; 9RAT; 15-JUL-93.  
DR PDB; 1RBC; 31-OCT-93.  
DR PDB; 1RBD; 31-OCT-93.  
DR PDB; 1RBE; 31-OCT-93.  
DR PDB; 1RBF; 31-OCT-93.  
DR PDB; 1RBG; 31-OCT-93.  
DR PDB; 1RBH; 31-OCT-93.  
DR PDB; 1RBI; 31-OCT-93.  
DR PDB; 1RBJ; 07-DEC-95.  
DR PDB; 1RBN; 20-DEC-94.  
DR PDB; 1RBW; 15-OCT-95.  
DR PDB; 1RBX; 15-OCT-95.

Query Match 8.1%; Score 8; DB 1; Length 150;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLSLVL 17  
|||||  
Db 7 VLSLVL 14

## RESULT 2

RNBR\_BOVIN STANDARD; PRT; 167 AA.  
ID RNBR\_BOVIN  
AC P39873;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ribonuclease, brain precursor (EC 3.1.27.-) (BRB).  
GN BRN.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]

SEQUENCE FROM N.A.  
RA SASSO M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,  
RA Viola M., Palmieri M., Russo E., Furia A.,  
RT "Molecular cloning of the gene encoding the bovine brain ribonuclease  
RT and its expression in different regions of the brain.";  
RL Nucleic Acids Res. 19:6469-6474(1991).  
RN [2]

SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.  
RC TISSUE=Brain;  
RX MEDLINE=89214015; PubMed=3243767;  
RA Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,  
RA Ohgi K., Irie M.,  
RT "Primary structure of a ribonuclease from bovine brain.";  
RL J. Biochem. 104:939-945(1988).  
RN [3]

SEQUENCE OF 27-167 FROM N.A.  
RX MEDLINE=96139017; PubMed=8587129;  
RA Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,  
RA Vento M.T., Furia A.,  
RT "Molecular evolution of genes encoding ribonucleases in ruminant  
RT species.";  
RL J. Mol. Evol. 41:850-858(1995).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.

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CC -----

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DR EMBL; X59767; CAA42439.1; -.  
DR EMBL; S81744; AAB36138.1; -.  
DR PIR; S20066; S20066.  
DR HSSP; P00656; 2RNS.  
DR GlycoSuiteDB; P39873; -.  
DR InterPro; IPR001427; RNaseA.  
DR Pfam; PF00074; rnaaseA; 1.  
DR PRINTS; PR00794; RIBONUCLEASE.  
DR PRODOM; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNase\_Pc; 1.  
DR PROSITE; PS00127; RNase\_PANCREATIC; 1.  
KM Hydroxylase; Nuclease; Endonuclease; Glycoprotein; Signal.  
FT SIGNAL 1 26  
FT CHAIN 27 167 RIBONUCLEASE, BRAIN.

FT ACT\_SITE 38 38 BY SIMILARITY.  
FT ACT\_SITE 67 67 BY SIMILARITY.  
FT ACT\_SITE 145 145 BY SIMILARITY.  
FT DISULFID 52 110 BY SIMILARITY.  
FT DISULFID 66 121 BY SIMILARITY.  
FT DISULFID 84 136 BY SIMILARITY.  
FT DISULFID 91 98 BY SIMILARITY.  
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .).  
FT CARBOHYD 155 155 /FTID-CAR\_000005.  
FT CARBOHYD 159 159 O-LINKED.  
FT CONFLICT 155 155 T -> S (IN REF. 2).  
SQ SEQUENCE 167 AA; 18450 MW; 681CAAC3CC2FC459 CRC64;

Query Match 8.1%; Score 8; DB 1; Length 167;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLSLVL 17  
|||||  
Db 7 VLSLVL 14

## RESULT 3

YFEE\_YERPE STANDARD; PRT; 184 AA.  
ID YFEE\_YERPE  
AC Q56956;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Putative yfABCD regulator yfee.  
GN YFEE OR YP02445 OR Y1891.  
OS Yersinia pestis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Yersinia.  
OX NCBI\_TaxID=632;  
RN [1]

SEQUENCE FROM N.A.  
RA STRAIN=KIM6;  
RA Bearden S.W.;  
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]

SEQUENCE FROM N.A.  
RC STRAIN=CO-92 / Biovar Orientalis;  
RX MEDLINE=21470413; PubMed=11586360;  
RA Parthill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,  
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,  
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,  
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
RA Felwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,  
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,  
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.,  
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";  
RL Nature 413:523-527(2001).  
RN [3]

SEQUENCE FROM N.A.  
RC STRAIN=KIM5 / Biovar Mediaevalis;  
RX MEDLINE=22137863; PubMed=12142430;  
RA Deng W., Burland V., Plunkett G., III, Boutin A., Mayhew G.F., Liss P.,  
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,  
RA Fetherston J.D., Landler L.E., Brubaker R.R., Plano G.V.,  
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,  
RA Perry R.D.,  
RT "Genome sequence of Yersinia pestis KIM.";  
RL J. Bacteriol. 184:4601-4611(2002).  
CC -1- FUNCTION: PUTATIVE REGULATOR OF YFEEABCD, AN ABC TRANSPORTER LOCUS  
CC INVOLVED IN INORGANIC IRON TRANSPORT.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -1- SIMILARITY: STRONG, TO E.COLI YNIB.

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CC -----
DR EMBL; U50903; AAC46151.1; -.
DR EMBL; AJ414152; CAC91250.1; -.
DR EMBL; AE013792; AAM85458.1; -.
DR PIR; AF0298; AF0298.
KW Transmembrane; Complete proteome.
FT TRANSMEM 15 35 POTENTIAL.
FT TRANSMEM 84 104 POTENTIAL.
FT TRANSMEM 162 182 POTENTIAL.
SQ SEQUENCE 184 AA; 20913 MW; 99860ED024E8A51A CRC64;

Query Match      8.1%; Score 8; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 44 ENTPLNI 51
Db 63 ENTPLNI 70

RESULT 4
AROA_CIOAB STANDARD; PRT; 428 AA.
ID AROA_CIOAB
AC O97KM2;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
  enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).
GN AROA OR CAC0895.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OK NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koenin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
  bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
  phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
  sixth step.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
CC -----
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CC -----
DR EMBL; AE007605; AAK78871.1; -.
DR PIR; D97010; D97010.
DR HAMAP; MF_00210; -; 1.
DR InterPro; IPR006264; AROA.
DR InterPro; IPR001986; EPSP_synthase.
DR Pfam; PF00275; EPSP_synthase; 1.
DR ProDom; PD001867; EPSP_synthase; 1.
DR TIGRfam; TIGR01356; aroA; 1.

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DR PROSITE; PS00104; EPSP_SYNTHASE_1; FALSE_NEG.
DR PROSITE; PS00885; EPSP_SYNTHASE_2; 1.
KW Aromatic amino acid biosynthesis; Transferase; Complete proteome.
SQ SEQUENCE 428 AA; 46960 MW; D3A9BF1F46E9C547 CRC64;

Query Match      8.1%; Score 8; DB 1; Length 428;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 EESTIEN 36
Db 35 EESTIEN 42

RESULT 5
BPPI_HUMAN STANDARD; PRT; 133 AA.
ID BPPI_HUMAN
AC O95925; Q96SD7; Q9HD30;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
  inhibitor-like with Kunitz and WAP domains 1).
GN SPINLM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OK NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Epididymis, and Testis;
RX MEDLINE=21297183; PubMed=11404006;
RA Richardson R.T., Sivasubramanian P., Hall S.H., Hamil K.G., Moore P.A.,
RA Ruben S.M., French F.S., O'Rand M.G.;
RT "Cloning and sequencing of human Eppin: a novel family of protease
  inhibitors expressed in the epididymis and testis.";
RL Gene 270:93-102(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Stavrides G.S., Huckie E.J., Deloukas P.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckie E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Leivaesialho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLeay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams D.R., Beck S.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- ALTERNATIVE PRODUCTS:

```

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CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=1;
CC      Iacid=O95925-1; Sequence=Displayed;
CC      Name=2;
CC      Iacid=O95925-2; Sequence=VSP 006755;
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN EPIDIDYMS AND TESTIS.
CC      -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC      -1- SIMILARITY: Contains 1 WAP-type domain.
CC      -----
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CC      -----
DR      EMBL; AF286370; AAG00548.1; -
DR      EMBL; AF286369; AAG00547.1; -
DR      EMBL; AF286368; AAG00546.1; -
DR      EMBL; AL118493; CAB56343.1; -
DR      EMBL; AL031663; CAB37635.1; -
DR      EMBL; AL031663; CAC36265.1; -
DR      HSSP; P00974; 1BPI.
DR      Genew; HGNC:15932; SPINLW1.
DR      InterPro; IPR002223; Kunitz_BPTI.
DR      InterPro; IPR002221; WAP.
DR      Pfam; PF00014; Kunitz_BPTI; 1.
DR      Pfam; PF00095; WAP; 1.
DR      PRINTS; PR00759; BASICPTASE.
DR      ProDom; PD000222; Kunitz_BPTI; 1.
DR      SMART; SM00131; KU; 1.
DR      SMART; SM00217; WAP; 1.
DR      PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR      PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR      PROSITE; PS00279; BPTI_KUNITZ_2; 1.
DR      KMW Serine protease inhibitor; Signal; Alternative splicing.
FT      SIGNAL 1 21 POTENTIAL.
FT      CHAIN 22 133 EPPIN.
FT      DOMAIN 29 73 WAP.
FT      DOMAIN 77 127 BPTI/KUNITZ INHIBITOR.
FT      DISULFID 33 61 BY SIMILARITY.
FT      DISULFID 40 65 BY SIMILARITY.
FT      DISULFID 48 60 BY SIMILARITY.
FT      DISULFID 54 69 BY SIMILARITY.
FT      DISULFID 77 127 BY SIMILARITY.
FT      DISULFID 86 110 BY SIMILARITY.
FT      DISULFID 102 123 BY SIMILARITY.
FT      VARSPLIC 1 31 MGSSGLSLVLFVLLANVQSGPLTDLFPR -> MLSKAH
FT      GCKTALSLG (in isoform 2).
FT      /FTID=VSP 006755.
SQ      SEQUENCE 133 AA; 15284 MW; F7831B203366D9DC CRC64;

Query Match 7.1%; Score 7; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 LLSLV 17
      |||||
      6 LLSLV 12

Db

RESULT 6
EPI_MACMU STANDARD; PRT; 133 AA.
AC Q9BDL1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
  inhibitor-like with Kunitz and WAP domains 1).
DE SPINLW1.
GN Macaca mulatta (Rhesus macaque).
OS

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OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC      Cercopitheciinae; Macaca.
OC      NCBI_TaxID=9544;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Epididymis, and Testis;
RA      Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA      Richardson R.T.;
RT      "Characterization of monkey and mouse Eppin, a protease inhibitor from
RT      epididymis and testis."
RL      Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC      -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN EPIDIDYMS AND TESTIS.
CC      -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC      -1- SIMILARITY: Contains 1 WAP-type domain.
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF346414; AAK31336.1; -
DR      HSSP; P00974; 1BPI.
DR      InterPro; IPR002223; Kunitz_BPTI.
DR      InterPro; IPR002221; WAP.
DR      Pfam; PF00014; Kunitz_BPTI; 1.
DR      Pfam; PF00095; WAP; 1.
DR      PRINTS; PR00759; BASICPTASE.
DR      ProDom; PD000222; Kunitz_BPTI; 1.
DR      SMART; SM00131; KU; 1.
DR      SMART; SM00217; WAP; 1.
DR      PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR      PROSITE; PS00279; BPTI_KUNITZ_2; 1.
DR      KMW Serine protease inhibitor; Signal.
FT      SIGNAL 1 21 POTENTIAL.
FT      CHAIN 22 133 EPPIN.
FT      DOMAIN 29 73 WAP.
FT      DOMAIN 77 127 BPTI/KUNITZ INHIBITOR.
FT      DISULFID 33 61 BY SIMILARITY.
FT      DISULFID 40 65 BY SIMILARITY.
FT      DISULFID 48 60 BY SIMILARITY.
FT      DISULFID 54 69 BY SIMILARITY.
FT      DISULFID 77 127 BY SIMILARITY.
FT      DISULFID 86 110 BY SIMILARITY.
FT      DISULFID 102 123 BY SIMILARITY.
SQ      SEQUENCE 133 AA; 15279 MW; 433AE946E39A35E9 CRC64;

Query Match 7.1%; Score 7; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 LLSLV 17
      |||||
      6 LLSLV 12

Db

RESULT 7
SECG_TREPA STANDARD; PRT; 133 AA.
AC O83547;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable protein-export membrane protein secg.
GN SECG OR TP0536.
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OC NCBI_TaxID=160;
RN      [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khakhal H., Richardson D., Howell J.K., Chidambaram M., Uterback T.,
RA McDonald L., Artlisch P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky W., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT Spirochete.";
RL Science 281:375-388(1998).
CC -1- FUNCTION: INVOLVED IN PROTEIN EXPORT. PARTICIPATES IN AN EARLY
CC EVENT OF PROTEIN TRANSLATION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SECY FAMILY.
CC -----
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CC -----
DR EMBL; AE001229; AAC65529.1; -.
DR PIR; E71311; E71311.
DR TIGR; TP0536; -.
DR InterPro; IPR004692; SecG.
DR Pfam; PF03840; SecG; 1.
DR PRINTS; PR01651; SECSEXPORT.
DR TIGRFAMs; TIGR00810; secG; 1.
DR Protein transport; Translocation; Transmembrane; Complete proteome.
FT TRANSMEM 3 23 POTENTIAL.
FT TRANSMEM 52 72 POTENTIAL.
SQ SEQUENCE 133 AA; 14279 MW; 43557E45AF1D6DAB CRC64;

Query Match
Best Local Similarity 7.1%; Score 7; DB 1; Length 133;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LLSLVL 17
Db 112 LLSLVL 118

RESULT 8
YF79_PSEAE STANDARD; PRT; 202 AA.
ID YF79_PSEAE
AC Q913D8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein PA1579.
GN PA1579.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).

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RN [2]
RX POTENTIAL FUNCTION.
RX MEDLINE=21173595; PubMed=11276083;
RA Iyer L.M., Koonin E.V., Aravind L.;
RT "Adaptations of the helix-grip fold for ligand binding and catalysis
RT in the START domain superfamily.";
RL Proteins 43:134-144(2001).
CC -1- FUNCTION: May play a role in the interaction of the bacterium with
CC animal cells.
CC -1- SIMILARITY: Contains 1 START domain.
CC -----
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CC -----
DR EMBL; AE004586; AAG04968.1; -.
DR PIR; A83448; A83448.
DR InterPro; IPR002913; START.
DR Pfam; PF01852; START; 1.
DR PROSITE; PS50848; START; 1.
KW Hypothetical protein; Complete proteome.
FT DOMAIN 1 202 START.
SQ SEQUENCE 202 AA; 22110 MW; 9F1C9B71F61ED95E CRC64;

Query Match
Best Local Similarity 7.1%; Score 7; DB 1; Length 202;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 LKGLRSA 94
Db 192 LKGLRSA 198

RESULT 9
EF1B_YEAST STANDARD; PRT; 205 AA.
ID EF1B_YEAST
AC P32471;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Elongation factor 1-beta (EF-1-beta).
DE Elongation factor 1-beta (EF-1-beta).
GN EF1B OR TEF5 OR YAL003W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=93131037; PubMed=8420802;
RA Hiraga K., Suzuki K., Tsuchiya E., Miyakawa T.;
RT "Cloning and characterization of the elongation factor EF-1 beta
RT homologue of Saccharomyces cerevisiae. EF-1 beta is essential for
RT growth.";
RL FEBS Lett. 316:165-169(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=95028152; PubMed=7941740;
RA Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B.,
RA Delaney S., Ouellette B.F.F., Barton A.B., Kaback D.B., Bussey H.;
RT "Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of
RT the 42 kbp SPO7-CEN1-CDC15 region.";
RL Yeast 10:535-541(1994).
RN [3]
RP SEQUENCE OF 167-177.
RC STRAIN=S288C;
RX MEDLINE=95203288; PubMed=7895733;
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;

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RT "Protein identifications for a Saccharomyces cerevisiae protein
RT database."
RL Electrophoresis 15:1466-1486(1994).
RN [4]
RP SEQUENCE OF 13-21 AND 50-55.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE=97089742; PubMed=8935650;
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
RT Saccharomyces cerevisiae."
RL FEMS Microbiol. Lett. 137:1-8(1996).
RN [5]
RP ACETYLATION, AND PHOSPHORYLATION.
RA Garels J.I., Futcher B., Kobayashi R., Iatter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -1- FUNCTION: EF-1-BETA AND EF-1-DELTA STIMULATE THE EXCHANGE OF
CC GDP BOUND TO EF-1-ALPHA TO GTP.
CC -1- SUBUNIT: EF-1 IS COMPOSED OF FOUR SUBUNITS: ALPHA, BETA,
CC DELTA, AND GAMMA.
CC -1- PTM: PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO THE EF-1-BETA/EF-1-DELTA FAMILY.
CC -----
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CC -----
DR EMBL; D14080; BAA03165.1; -.
DR EMBL; L22015; AAC04954.1; -.
DR PIR; S43445; S43445.
DR PDB; 1F60; 22-NOV-00.
DR PDB; 1G7C; 30-MAY-01.
DR PDB; 1IJF; 06-JUN-01.
DR PDB; 1IJF; 06-JUN-01.
DR SWISS-2DPAGE; P32471; YEAST.
DR SGD; S0000003; EFB1.
DR InterPro; IPR001326; EFL BD.
DR InterPro; IPR004046; GST_Cterm.
DR Pfam; PF00736; EFLBD; 1.
DR PROSITE; PS00824; EFLBD_1; 1.
DR PROSITE; PS00825; EFLBD_2; 1.
KW Elongation factor; Protein biosynthesis; Acetylation; Phosphorylation;
KW 3D-structure.
FT INIT MET 0 0
FT MOD_RES 1 1 ACETYLATION.
FT CONFLICT 48 48 F -> S (IN REF. 2).
FT CONFLICT 56 56 F -> S (IN REF. 2).
FT CONFLICT 97 97 W -> L (IN REF. 2).
FT CONFLICT 167 167 L -> E (IN REF. 3).
SQ SEQUENCE 205 AA; 22689 MW; E47782908998DED6 CRC64;

Query Match 7.1%; Score 7; DB 1; Length 205;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 AFKADEF 63
DB 55 AFKADEF 61

RESULT 10
CCMB_RHOCA STANDARD; PRT; 218 AA.
AC P29360;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heme exporter protein B (Cytochrome c-type biogenesis protein hclB).
RA HELB.

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OS Rhodobacter capsulatus (Rhodopseudomonas capsulata).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SB1003 / St Louis;
RX MEDLINE=92146961; PubMed=1310666;
RA Beckman D.L., Trawick D.R., Kranz R.G.;
RT "Bacterial cytochromes c biogenesis."
RL Genes Dev. 6:268-283(1992).
CC -1- FUNCTION: REQUIRED FOR THE EXPORT OF HEME TO THE PERIPLASM FOR THE
CC BIOGENESIS OF C-TYPE CYTOCHROMES.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Probable).
CC -1- SIMILARITY: BELONGS TO THE CCMB/CYCW/HELH FAMILY.
CC -----
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CC -----
DR EMBL; X63462; CAA45062.1; -.
DR PIR; S23664; S23664.
DR InterPro; IPR003544; Cyt_c_biolg_CcMB.
DR Pfam; PF03379; CcMB; 1.
DR PRINTS; PR01414; CCMBBIOGNIS.
DR TIGRFAMs; TIGR01190; ccmb; 1.
KW Cytochrome c-type biogenesis; Transport; Transmembrane;
KW Inner membrane.
FT TRANSMEM 18 38 POTENTIAL.
FT TRANSMEM 43 63 POTENTIAL.
FT TRANSMEM 99 119 POTENTIAL.
FT TRANSMEM 131 151 POTENTIAL.
FT TRANSMEM 155 175 POTENTIAL.
FT TRANSMEM 185 205 POTENTIAL.
SQ SEQUENCE 218 AA; 22611 MW; CA2382FBD4B447F4 CRC64;

Query Match 7.1%; Score 7; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LLSLVL 17
DB 158 LLSLVL 164

RESULT 11
CCMB_HAEIN STANDARD; PRT; 221 AA.
AC P45033;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heme exporter protein B (Cytochrome c-type biogenesis protein ccmb).
GN CCMB OR H11090.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-T., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spitzgs T., Hedblom B., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudex D.M., Brandon R.C.,

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RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,  
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
 RA Venter J.C.;  
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae  
 RT Rd.";  
 RL Science 269:496-512(1995).  
 CC -1- FUNCTION: REQUIRED FOR THE EXPORT OF HEME TO THE PERIPLASM FOR THE  
 CC BIOGENESIS OF C-TYPE CYTOCHROMES (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
 CC (Probable).  
 CC -1- SIMILARITY: BELONGS TO THE CCMB/CYCW/HELB FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; U32789; AAC22747.1; -.  
 CC PIR; F64166; F64166.  
 DR TIGR; H1090; -.  
 DR InterPro; IPR003544; Cyt\_c\_biolg\_CcMB.  
 DR Pfam; PF03379; CcMB; 1.  
 DR PRINTS; PR01414; CCMBBIOGNIS.  
 DR TIGRFAMs; TIGR01190; ccmb; 1.  
 KW Cytochrome c-type biogenesis; Transport; Transmembrane;  
 KW Inner membrane; Complete proteome.  
 FT TRANSMEM 21 41 POTENTIAL.  
 FT TRANSMEM 46 66 POTENTIAL.  
 FT TRANSMEM 101 121 POTENTIAL.  
 FT TRANSMEM 126 146 POTENTIAL.  
 FT TRANSMEM 157 177 POTENTIAL.  
 FT TRANSMEM 193 213 POTENTIAL.  
 SQ SEQUENCE 221 AA; 23643 MW; 2FF8EAFDC5228EF8 CRC64;  
 Query Match 7.1%; Score 7; DB 1; Length 221;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 VLSLVLV 16  
 Db 159 VLSLVLV 165  
 RESULT 12  
 GIDB\_CLOPE STANDARD; PRT; 239 AA.  
 ID GIDB\_CLOPE  
 AC Q8XH32;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Methyltransferase gidB (EC 2.1.-.-) (Glucose inhibited division  
 DE protein B).  
 OS GIDB OR CPE2653.  
 GN Clostridium perfringens.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1502;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=13 / Type A;  
 RX MEDLINE=21664373; PubMed=11792842;  
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,  
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;  
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic  
 RT flesh-eater";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).  
 CC -1- FUNCTION: Probable S-adenosyl-L-methionine dependent  
 CC methyltransferase specific for a sterol and/or lipid substrate (By  
 CC similarity).  
 CC -1- SIMILARITY: BELONGS TO THE GIDB FAMILY.

CC -----  
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 CC -----  
 CC EMBL; AP003194; BAB82359.1; -.  
 CC HAMAP; MF\_00074; -; 1.  
 DR InterPro; IPR003682; GidB.  
 DR Pfam; PF02527; GidB; 1.  
 DR ProDom; PD004441; GidB; 1.  
 DR TIGRFAMs; TIGR00138; gidB; 1.  
 KW Transferase; Methyltransferase; Complete proteome.  
 SQ SEQUENCE 239 AA; 26886 MW; 5F1024A3E3C1C71E CRC64;  
 Query Match 7.1%; Score 7; DB 1; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 57 AFKADEF 63  
 Db 62 AFKADEF 68  
 RESULT 13  
 COX2\_WILMR STANDARD; PRT; 247 AA.  
 ID COX2\_WILMR  
 AC P47918;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide II precursor (EC 1.9.3.1).  
 GN COX2.  
 OS Williopsis mrakii (Yeast) (Hansenula mrakii).  
 OG Mitochondrion.  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Williopsis.  
 OX NCBI\_TaxID=4963;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CBS 1707;  
 RX MEDLINE=94287716; PubMed=8017108;  
 RA Drissi R., Sor F., Fukuhara H.;  
 RT "Genes of the linear mitochondrial DNA of Williopsis mrakii: coding  
 RT sequences for a maturase-like protein, a ribosomal protein VAR1  
 RT homologue, cytochrome oxidase subunit 2 and methionyl tRNA.";  
 RL Yeast 10:391-398(1994).  
 CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 CC 3 form the functional core of the enzyme complex. Subunit 2  
 CC transfers the electrons from cytochrome c via its dinuclear copper  
 CC A center to the bimetallic center of the catalytic subunit 1.  
 CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -1- COFACTOR: Copper A.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- PTM: THE SIGNAL SEQUENCE OF COX2 IS PROCESSED BY IMP1 (BY  
 CC SIMILARITY).  
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 CC -----  
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 CC -----  
 CC EMBL; X66595; CAA47160.1; -.



DR PIR; S42736; S42736.  
 DR InterPro; IPR001505; Copper CUA.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper CUA; 1.  
 DR PROSITE; PS00078; COX2; 1.  
 KW Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;  
 KM Electron transport; Respiratory chain; Signal.  
 FT SIGNAL 1 11  
 FT CHAIN 12 247  
 FT DOMAIN 12 38  
 FT TRANSMEM 39 59  
 FT DOMAIN 60 78  
 FT TRANSMEM 79 101  
 FT DOMAIN 102 247  
 FT METAL 182 182  
 FT METAL 217 217  
 FT METAL 221 221  
 FT METAL 225 225  
 SQ SEQUENCE 247 AA; 27941 MW; 98EF8346730BECA CRC64;

Query Match 7.1%; Score 7; DB 1; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LPAVVLL 12  
 |||||  
 Db 84 LPAVVLL 90

RESULT 14  
 COX2\_WILSA STANDARD; PRT; 247 AA.  
 ID COX2\_WILSA  
 AC P06029;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide II precursor (EC 1.9.3.1).  
 GN COX2 OR OX11.  
 OS Williopsis saturnus (Yeast) (Hansenula saturnus).  
 OG Mitochondrion.  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Williopsis.  
 OX NCBI\_TaxID=4906;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88223501; PubMed=2836090;  
 RA Lawson J.E.; Deters D.W.;  
 RT "Nucleotide sequence of the mitochondrial cytochrome oxidase subunit  
 II gene in the yeast Hansenula saturnus.";  
 RL Curr. Genet. 9:351-360(1985).  
 CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 3 form the functional core of the enzyme complex. Subunit 2  
 transfers the electrons from cytochrome c via its binuclear copper  
 A center to the bimetallic center of the catalytic subunit 1.  
 CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
 c + 2 H(2)O.  
 CC -1- COFACTOR: Copper A.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 inner membrane.  
 CC -1- PTM: THE SIGNAL SEQUENCE OF COX2 IS PROCESSED BY IMP1 (BY  
 SIMILARITY).  
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 -----  
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 -----  
 DR EMBL; X02439; CA26284.1; -.  
 DR PIR; S07165; OEHQMS.  
 DR InterPro; IPR001505; Copper CUA.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper CUA; 1.  
 DR PROSITE; PS00078; COX2; 1.  
 KW Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;  
 KM Electron transport; Respiratory chain; Signal.  
 FT SIGNAL 1 11  
 FT CHAIN 12 247  
 FT DOMAIN 12 38  
 FT TRANSMEM 39 59  
 FT DOMAIN 60 78  
 FT TRANSMEM 79 101  
 FT DOMAIN 102 247  
 FT METAL 182 182  
 FT METAL 217 217  
 FT METAL 221 221  
 FT METAL 225 225  
 SQ SEQUENCE 247 AA; 27927 MW; 8AFABE9A1EA249CA CRC64;

Query Match 7.1%; Score 7; DB 1; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LPAVVLL 12  
 |||||  
 Db 84 LPAVVLL 90

RESULT 15  
 ICAL\_CERAE STANDARD; PRT; 283 AA.  
 ID ICAL\_CERAE  
 AC P49342;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Calpain inhibitor (Calpastatin) (Fragment).  
 GN CAST.  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92235069; PubMed=1569094;  
 RA Lee W.J.; Ma H.; Takano E.; Yang H.Q.; Hatanaka M.; Maki M.;  
 RT "Molecular diversity in amino-terminal domains of human calpastatin  
 by exon skipping.";  
 RL J. Biol. Chem. 267:8437-8442(1992).  
 CC -1- FUNCTION: Specific inhibition of calpain (calcium-dependent  
 cysteine protease). Plays a key role in postmortem tenderization  
 of meat and have been proposed to be involved in muscle protein  
 degradation in living tissue.  
 CC -1- DOMAIN: HAS FOUR INHIBITORY DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE CALPASTATIN FAMILY.  
 -----  
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 -----  
 DR EMBL; M86248; AAA52753.1; -.  
 DR InterPro; IPR001259; Calpain\_inh1b.

DR Pfam; PF00748; Calpain\_inhib; 2.  
KW Repeat; Thiol protease inhibitor; Alternative splicing.  
FT REPEAT 170 222 INHIBITORY DOMAIN 1.  
FT NON TER 283 283  
SQ SEQUENCE 283 AA; 30170 MW; 02743390B5D6F0F8 CRC64;

Query Match 7.1%; Score 7; DB 1; Length 283;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 TLGGPBE 30  
Db 163 TLGGPBE 169

Search completed: November 28, 2003, 08:04:04  
Job time : 15 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: November 28, 2003, 07:57:48 ; Search time 30 Seconds  
(without alignments)  
851.574 Million cell updates/sec

Title: US-10-059-395-142

Perfect score: 99  
Sequence: 1 MKIPVLPAVVLSTLVLSA.....LNMWDAFPKLGKLSATPDQA 99

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	8.1	219	2 Q9Z650	Q9Z650 pantoea cit
2	8	8.1	219	16 Q8ZD57	Q8ZD57 yersinia pe
3	8	8.1	222	16 Q9KQ84	Q9KQ84 vibrio chol
4	8	8.1	228	16 Q8D0V2	Q8D0V2 yersinia pe
5	8	8.1	372	8 Q8HN36	Q8HN36 paragonimus
6	8	8.1	390	16 Q8ETM3	Q8ETM3 oceanobacil
7	8	8.1	404	12 Q9ICB8	Q9ICB8 human adeno
8	8	8.1	409	12 Q9ICB6	Q9ICB6 human adeno
9	8	8.1	414	12 Q8JZH6	Q8JZH6 human adeno
10	8	8.1	422	12 Q9ICB7	Q9ICB7 human adeno
11	8	8.1	480	16 Q9K1A8	Q9K1A8 neisseria m
12	8	8.1	956	10 Q9LKI5	Q9LKI5 arabidopsis
13	8	8.1	1197	5 Q9VLB3	Q9VLB3 drosophila
14	7	7.1	48	16 Q9I204	Q9I204 streptomyce
15	7	7.1	77	6 Q8HZ44	Q8HZ44 papio hamad
16	7	7.1	77	8 Q9TA10	Q9TA10 caefeceria r

17	7	7.1	102	10 Q9FIS3	Q9FIS3 arabidopsis
18	7	7.1	103	2 P7I310	P7I310 escherichia
19	7	7.1	110	8 Q9T9Z6	Q9T9Z6 telestes mu
20	7	7.1	125	11 Q9IXK8	Q9IXK8 mus musculu
21	7	7.1	125	17 Q9YE78	Q9YE78 aeropyrum p
22	7	7.1	132	16 Q9RXV0	Q9RXV0 deinococcus
23	7	7.1	133	6 Q8HZ45	Q8HZ45 papio papio
24	7	7.1	162	2 Q8GI22	Q8GI22 pseudomonas
25	7	7.1	163	2 Q9AQM7	Q9AQM7 pseudomonas
26	7	7.1	170	2 Q9AQM6	Q9AQM6 pseudomonas
27	7	7.1	170	2 Q8GI21	Q8GI21 pseudomonas
28	7	7.1	173	16 Q8D808	Q8D808 vibrio vuln
29	7	7.1	189	8 Q94S57	Q94S57 arxiozyma t
30	7	7.1	190	8 Q94NV5	Q94NV5 arxiozyma t
31	7	7.1	190	10 Q8GSB4	Q8GSB4 oryza sativ
32	7	7.1	192	8 Q94S58	Q94S58 arxiozyma t
33	7	7.1	195	5 Q97369	Q97369 calpodes et
34	7	7.1	196	8 Q94S60	Q94S60 arxiozyma t
35	7	7.1	200	8 Q94S59	Q94S59 arxiozyma t
36	7	7.1	213	16 Q97PD3	Q97PD3 streptococc
37	7	7.1	218	2 Q33571	Q33571 rhodobacter
38	7	7.1	221	16 Q9CPN1	Q9CPN1 pasteurella
39	7	7.1	222	8 Q9MG12	Q9MG12 kongobatha
40	7	7.1	227	8 Q8LXM4	Q8LXM4 myadestes g
41	7	7.1	227	8 Q9G9A0	Q9G9A0 myadestes g
42	7	7.1	227	8 Q8LVX2	Q8LVX2 myadestes g
43	7	7.1	229	8 Q9B8S3	Q9B8S3 rhagoletis
44	7	7.1	229	8 Q8HN00	Q8HN00 monchelea m
45	7	7.1	233	5 Q8MNE4	Q8MNE4 dictyosteli

#### ALIGNMENTS

RESULT 1	
Q9Z650	PRELIMINARY; PRT; 219 AA.
ID Q9Z650	
AC Q9Z650;	
DT 01-MAY-1999 (TREMBLrel. 10, Created)	
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)	
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
DE CcMB.	
GN CcMB.	
OS Pantoea citrea.	
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
OC Enterobacteriaceae; Pantoea.	
OX NCBI_TaxID=53336;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=1056R;	
RX MEDLINE=20200361; PubMed=10735866;	
RA Pujol C.J., Kado C.I.;	
RT "Genetic and Biochemical characterization of the pathway in Pantoea	
RT citrea leading to pink disease of pineapple.";	
RL J. Bacteriol. 182:2230-2237(2000).	
DR EMBL; AF103874; AADI9538.1; -.	
DR InterPro; IPR003544; CytC_blog_CcMB.	
DR Pfam; PF03379; CcMB; 1.	
DR PRINTS; PR01414; CCMBBIQNSIS.	
DR TIGRFAMs; TIGR01190; CcMB; 1.	
SQ SEQUENCE 219 AA; 23088 MW; A7A86D08EA0EE028 CRC64;	
Query Match	8.1%; Score 8; DB 2; Length 219;
Best Local Similarity	100.0%; Pred. No. 7.7;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 VLSTLV 17	
Db 158 VLSTLV 165	
RESULT 2	
Q8ZD57	

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ID Q8ZD57 PRELIMINARY; PRT; 219 AA.
AC Q8ZD57;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Heme exporter protein B.
GN CCMB OR YPO2735.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Felwell T., Hamlin N., Holroyd S., Jagsels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
DR EMBL; AJ414153; CAC92974.1; -.
DR InterPro; IPR003544; CytC_bilog_CcMB.
DR Pfam; PF03379; CcMB; 1.
DR PRINTS; PR01414; CCMBBIOGNIS.
DR TIGRFAMs; TIGR01190; ccmb; 1.
KW Complete proteome.
SQ SEQUENCE 219 AA; 23127 MW; 2BBE66D122D1093A CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 16; Length 219;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLLSLVL 17
Db 158 VLLSLVL 165

RESULT 3
ID Q9KQE4 PRELIMINARY; PRT; 222 AA.
AC Q9KQE4;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Heme exporter protein B.
GN VC2056.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eissen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AB004279; AAF95202.1; -.
DR TIGR; VC2056; -.
DR InterPro; IPR003544; CytC_bilog_CcMB.
DR Pfam; PF03379; CcMB; 1.
DR PRINTS; PR01414; CCMBBIOGNIS.

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DR TIGRFAMs; TIGR01190; ccmb; 1.
KW Complete proteome.
SQ SEQUENCE 222 AA; 23697 MW; 9F6CD1ECA214EC60 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 16; Length 222;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLLSLVL 17
Db 161 VLLSLVL 168

RESULT 4
ID Q8D0V2 PRELIMINARY; PRT; 228 AA.
AC Q8D0V2;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Heme exporter protein B.
GN CCMB OR Y1568.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
DR EMBL; AE013760; AAM85137.1; -.
SQ SEQUENCE 228 AA; 24114 MW; 3E6AFC5025D7AE55 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 16; Length 228;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLLSLVL 17
Db 167 VLLSLVL 174

RESULT 5
ID Q8HN36 PRELIMINARY; PRT; 372 AA.
AC Q8HN36;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Cytochrome b.
GN CYTB.
OS Paragonimus westermani.
OC Mitochondrion.
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Plagiorchiida; Troglotremata; Paragonimidae; Paragonimus.
OX NCBI_TaxID=34504;
RN [1]
RP SEQUENCE FROM N.A.
RA Iwagami M., Sato Y., Iwashita A., Abe T., Hong S.-J., Agatsuma T.;
RT "Paragonimus westermani (2n) mitochondrial genome.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF540958; AAN15171.1; -.
KW Mitochondrion.
SQ SEQUENCE 372 AA; 41636 MW; 7B529C6B241B0BFD CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 8; Length 372;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLLSLV 17  
DB 223 VLLSLV 230

## RESULT 6

Q8ETM3 PRELIMINARY; PRT; 390 AA.  
AC Q8ETM3;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
GN OB0237.  
OS Oceanobacillus iheyensis.  
OC Bacteria; Firmicutes; Bacillales; Oceanobacillus.  
OX NCBI\_TaxID=182710;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;  
RX MEDLINE=2220767; PubMed=12235376;  
RA Takami H., Takaki Y., Uchiyama I.;  
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya  
RT Ridge and its unexpected adaptive capabilities to extreme  
RT environments.";  
RL Nucleic Acids Res. 30:3927-3935(2002).  
DR EMBL; AF004593; BAC12193.1;  
KM Hypothetical protein; Complete proteome.  
SQ SEQUENCE 390 AA; 43262 MW; B2CE189BE0A63D2B CRC64;

Query Match 8.1%; Score 8; DB 16; Length 390;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 PFLNIDKL 54  
DB 200 PFLNIDKL 207

## RESULT 7

Q91CB8 PRELIMINARY; PRT; 404 AA.  
AC Q91CB8;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Early E3 48K glycoprotein.  
OS Human adenovirus type 8.  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
OX NCBI\_TaxID=31545;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Blusch J.H., Deryckere F., Windheim M., Adrian T., Burgert H.G.;  
RT "E3-49K: a novel early region 3 protein expressed by adenoviruses of  
RT subgroup D.";  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF233391; AAL01120.1;  
DR InterPro; IPR003471; Adeno\_E3\_CR1.  
DR InterPro; IPR003470; Adeno\_E3\_CR2.  
DR Pfam; PF02440; Adeno\_E3\_CR1; 3.  
DR Pfam; PF02439; Adeno\_E3\_CR2; 1.  
SQ SEQUENCE 404 AA; 45541 MW; 5B5B62A9A37B99EF CRC64;

Query Match 8.1%; Score 8; DB 12; Length 404;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VVLSLVLV 16  
DB 7 VVLSLVLV 14

## RESULT 8

Q91CB6 PRELIMINARY; PRT; 409 AA.  
AC Q91CB6;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Early E3 46K glycoprotein.  
OS Human adenovirus type 9.  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
OX NCBI\_TaxID=10527;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Blusch J.H., Deryckere F., Windheim M., Adrian T., Burgert H.G.;  
RT "E3-49K: a novel early region 3 protein expressed by adenoviruses of  
RT subgroup D.";  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF233394; AAL01123.1;  
DR InterPro; IPR003471; Adeno\_E3\_CR1.  
DR InterPro; IPR003470; Adeno\_E3\_CR2.  
DR InterPro; IPR006895; zf-Sec23\_Sec24.  
DR Pfam; PF02440; Adeno\_E3\_CR1; 3.  
DR Pfam; PF02439; Adeno\_E3\_CR2; 1.  
DR Pfam; PF04810; zf-Sec23\_Sec24; 1.  
SQ SEQUENCE 409 AA; 45846 MW; 562F6807B279A95E CRC64;

Query Match 8.1%; Score 8; DB 12; Length 409;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VVLSLVLV 16  
DB 7 VVLSLVLV 14

## RESULT 9

Q8JZH6 PRELIMINARY; PRT; 414 AA.  
AC Q8JZH6;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE E3/49K.  
OS Human adenovirus type 19p.  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
OX NCBI\_TaxID=134640;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=587;  
RA Blusch J.H., Deryckere F., Windheim M., Ruzsics Z., Arnborg N.,  
RA Adrian T., Burgert H.-G.;  
RT "E3/49K: A Novel Early Region 3 Protein Specifically Expressed By  
RT Adenoviruses of Subgroup D.";  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF271153; AAM43819.1;  
DR InterPro; IPR003471; Adeno\_E3\_CR1.  
DR InterPro; IPR003470; Adeno\_E3\_CR2.  
DR Pfam; PF02440; Adeno\_E3\_CR1; 3.  
DR Pfam; PF02439; Adeno\_E3\_CR2; 1.  
SQ SEQUENCE 414 AA; 46289 MW; D5F388514FC95A92 CRC64;

Query Match 8.1%; Score 8; DB 12; Length 414;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VVLSLVLV 16  
DB 7 VVLSLVLV 14

## RESULT 10



Q91CB7 PRELIMINARY; PRT; 422 AA.  
 AC Q91CB7;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Early E3 50K glycoprotein.  
 OS Human adenovirus type 15.  
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
 NCBI\_TaxID=28276;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Blusch J.H., Deryckere F., Windheim M., Adrian T., Burgert H.G.;  
 RT "E3-49K: a novel early region 3 protein expressed by adenoviruses of  
 RT subgroup D.";  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF233392; AAL01121.1; -  
 DR InterPro; IPR003471; Adeno\_E3\_CR1.  
 DR InterPro; IPR003470; Adeno\_E3\_CR2.  
 DR Pfam; PF02440; Adeno\_E3\_CR1; 3.  
 DR Pfam; PF02439; Adeno\_E3\_CR2; 1.  
 SQ SEQUENCE 422 AA; 47877 MW; 6551F6FC54BC8399 CRC64;

Query Match 8.1%; Score 8; DB 12; Length 422;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VLLSLV 16  
 Db 7 VLLSLV 14

## RESULT 11

Q9K1A8 PRELIMINARY; PRT; 480 AA.  
 AC Q9K1A8;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE NADH dehydrogenase I, N subunit.  
 GN NMB0259.  
 OS Neisseria meningitidis (serogroup B).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 NCBI\_TaxID=491;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MC58 / Serogroup B;  
 RX MEDLINE=20175755; PubMed=10710307;  
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,  
 RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,  
 RA Nelson W.C., Gwin M.L., DeBoy R., Peterson J.D., Hickey E.K.,  
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,  
 RA Mason T., Clecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,  
 RA Cotton M.D., Uitterback T.R., Khoult H., Qin H., Vamathevan J.,  
 RA Gill J., Scarlato V., Maignan V., Piza M., Grandi G., Sun L.,  
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;  
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain  
 RT MC58.";  
 RL Science 287:1809-1815(2000).  
 CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: TO NADH-UBIQUINONE/PLASTOQUINONE (COMPLEX I), VARIOUS  
 CC CHAINS.  
 CC -1- SIMILARITY: TO ONE OF THE POLYPEPTIDE CHAINS OF THE NADH-UBIQUINOL  
 CC OXIDOREDUCTASE OF CHLOROPLASTS OR MITOCHONDRIA.  
 DR EMBL; AE002382; AAF40713.1; -  
 DR TIGR; NMB0259; -  
 DR InterPro; IPR003916; NADH\_oxred5.  
 DR InterPro; IPR001750; Oxidored\_q1.  
 DR Pfam; PF00361; oxidored q1; 1.  
 DR PRINTS; PR01434; NADHDHGNASE5.  
 KW NAD; Oxidoreductase; Transmembrane; Complete proteome.

SQ SEQUENCE 480 AA; 52125 MW; D05A272BAB24EB15 CRC64;

Query Match 8.1%; Score 8; DB 16; Length 480;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLLSLV 17  
 Db 16 VLLSLV 23

## RESULT 12

Q9LK15 PRELIMINARY; PRT; 956 AA.  
 AC Q9LK15;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE 5' repair endonuclease.  
 GN UVH1.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Landsberg erecta;  
 RX MEDLINE=20484028; PubMed=11027708;  
 RA Fidanter A.L., Mitchell D.L., Britt A.B.;  
 RT "The Arabidopsis UVH1 Gene Is a Homolog of the Yeast Repair  
 RT Endonuclease RAD1.";  
 RL Plant Physiol. 124:579-586(2000).  
 DR EMBL; AF277377; AAF81910.1; -  
 DR InterPro; IPR006166; ERCC4.  
 DR Pfam; PF02732; BRCC4; 1.  
 KW Endonuclease.

Query Match 8.1%; Score 8; DB 10; Length 956;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LSLVLHS 19  
 Db 830 LSLVLHS 837

## RESULT 13

Q9VLB3 PRELIMINARY; PRT; 1197 AA.  
 AC Q9VLB3;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE CG3811 protein.  
 GN CG3811.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadien E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry B., Moris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleab J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,  
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,  
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
 RA Pacleab J., Paragas V., Park S., Patel S., Pfeiffer B.,  
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
 RA Stapleton M., Strong R., Svirskaas R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,  
 RT "Sequencing of Drosophila melanogaster genome.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,  
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,  
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,  
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,  
 RT "Annotation of Drosophila melanogaster genome.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.,  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA FlyBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB003625; AAF52781.2; -;  
 DR FlyBase; FBgn0032123; CG3811.  
 DR InterPro; IPR007114; MPS.  
 DR InterPro; IPR004156; OATP\_Nterm.  
 DR Pfam; PF03132; OATP\_N; 1.  
 DR PROSITE; PS50850; MFS; 1.

SEQ SEQUENCE 1197 AA; 130193 MW; 369C217AAB4B754C CRC64;  
 Query Match 8.1%; Score 8; DB 5; Length 1197;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 VVLSLV 16  
 DB 173 VVLSLV 180  
 RESULT 14  
 Q9L204 PRELIMINARY; PRT; 48 AA.  
 ID Q9L204;  
 AC Q9L204;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Hypothetical protein SCO2629.  
 GN SCO2629 OR SC8E4.04.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2) / M145;  
 RX MEDLINE=21996410; PubMed=12000953;  
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,  
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete Streptomyces  
 coelicolor A3(2).";  
 RL Nature 417:141-147(2002).  
 DR EMBL; AL939113; CAB71804.1; -;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 48 AA; 5012 MW; 4CC4B4D1F265858E CRC64;  
 Query Match 7.1%; Score 7; DB 16; Length 48;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 VVLSLV 16  
 DB 17 VVLSLV 23  
 RESULT 15  
 Q8HZ44 PRELIMINARY; PRT; 77 AA.  
 ID Q8HZ44;  
 AC Q8HZ44;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Epididymal protease inhibitor 2.  
 GN EPPIN.  
 OS Papio hamadryas (Hamadryas baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Papio.  
 OX NCBI\_TaxID=9557;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RA Sivashanmugam P., O'Rand M.G., Richardson R.T.,  
 RT "Characterization of Baboon Eppin.";  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY141975; AAN08509.1; -.  
KM Protease.  
SQ SEQUENCE 77 AA; 8787 MW; B86E5868C57CEBD0 CRC64;

Query Match 7.1%; Score 7; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 LLSLVL 17  
|||  
Db 6 LLSLVL 12

Search completed: November 28, 2003, 08:04:43  
Job time : 37 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 09:26:39 ; Search time 1716 Seconds  
(without alignments)  
1402.181 Million cell updates/sec

Title: US-10-059-395-142  
Perfect score: 99  
Sequence: 1 MKIPVLPVAVLISLVLSA.....LNMDAFPKLKGSRATPDQ 99

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Word size: 1

Total number of hits satisfying chosen parameters: 45562604

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=x1h  
-Q=/cgn2\_1/USPTO\_spool/US10059395/runat\_25112003\_140755\_7412/app\_query.fasta\_1.263  
-DB=EST -QFMT=fastap -SUFFIX=01.rst -MINMATCH=0.1 -LOOFC=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR\_SCORE=quality -THR\_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10059395 @CGN 1\_1 2810 @runat\_25112003\_140755\_7412 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est4:\*  
13: gb\_est5:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vr1:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	99	100.0	334	9	AA297512	AA297512 EST113061
2	99	100.0	432	13	BX112106	BX112106 BX112106
3	98	99.0	424	14	W69083	W69083 zd44b06.s1
4	88	88.9	394	14	W60320	W60320 zd29g01.s1
5	86	86.9	348	9	AW238758	AW238758 xp03e08.x
6	80	80.8	381	14	W69108	W69108 zd44c04.s1
7	78	78.8	339	9	AA778414	AA778414 zt39e05.s
8	76	76.8	373	9	AA722694	AA722694 zg82b06.s
9	72	72.7	412	14	W60268	W60268 zd29g01.r1
10	72	72.7	432	14	W69233	W69233 zd44c04.r1
11	71	71.7	318	9	AA586846	AA586846 nm67e11.s
12	71	71.7	359	10	BE466728	BE466728 h224g06.x
13	71	71.7	362	9	AI140605	AI140605 ge05f03.x
14	66	66.7	326	9	AA297513	AA297513 EST113062
15	59	59.6	431	14	W69227	W69227 zd44b06.r1
16	58	58.6	377	9	AA582988	AA582988 nm72h02.s
17	58	58.6	413	9	AA393296	AA393296 zt74f05.r
18	57	57.6	345	9	AI217565	AI217565 qd43d02.x
19	56	56.6	241	9	AA595989	AA595989 nm64g08.s
20	53	53.5	359	10	BG150312	BG150312 7f98g03.x
21	51	51.5	334	9	AI217587	AI217587 qd43f04.x
22	43	43.4	345	9	AA583942	AA583942 nm64f07.s
23	43	43.4	376	14	W95920	W95920 ze08d01.r1
24	39	39.4	221	9	AA584333	AA584333 nm73a09.s
25	37	37.4	358	9	AW003825	AW003825 wg83f12.x
26	35	35.4	330	14	W95883	W95883 ze08d01.s1
27	33	33.3	218	9	AA398638	AA398638 zt74f05.s
28	29	29.3	249	13	BX476814	BX476814 DKFZp686H
29	27	27.3	339	14	W52030	W52030 zd13b01.s1
30	27	27.3	378	9	AI184682	AI184682 qd68b02.x
31	27	27.3	368	9	AW260965	AW260965 EQUK0243
32	24	24.2	436	9	AV597545	AV597545 AV597545
33	24	24.2	163	9	AA776980	AA776980 zt23d05.s
34	18	18.2	377	9	AW260982	AW260982 EQUK0196
35	15	15.2	421	9	AV618771	AV618771 AV618771
36	14	14.1	581	9	AV597546	AV597546 AV597546
37	13	13.1	323	10	BE715771	BE715771 MR2-HT075
38	12	12.1	601	10	BE033529	BE033529 ME04C12 M
39	10	10.1	612	28	AO587040	AO587040 RPCI-11-4
40	10	10.1	766	13	BU327477	BU327477 603495367
41	10	10.1	523	9	AA066639	AA066639 ml74g12.x
42	9	9.1	528	13	BU829711	BU829711 K046P81P
43	9	9.1	532	28	BZ169340	BZ169340 CH230-247
44	9	9.1	538	10	BE879658	BE879658 601491847
45	9	9.1				

ALIGNMENTS

RESULT 1  
AA297512 334 bp mRNA linear EST 18-APR-1997  
LOCUS AA297512 Fetal skin Homo sapiens cDNA 5' end, mRNA sequence.  
DEFINITION AA297512  
ACCESSION AA297512  
VERSION AA297512.1 GI:1949866  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 334)  
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult

, C.J., Lee, N.H., Kirkness, E.F., Weinstein, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wal, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodok, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligriano, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Sauder, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferris, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

**TITLE**  
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

**JOURNAL**  
Nature 377 (6547 Suppl), 3-174 (1995)

**MEDLINE**  
96026280

**PUBMED**  
7566098

**COMMENT**  
Other ESTs: THC151622  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tcdb/hgi/hgi.html>)  
Seq primer: M13 Reverse.

# FEATURES

**Source**  
1.334  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="ATCC (Inhost):141532"  
/db\_xref="taxon:9606"  
/tissue\_type="epithelium"  
/cell\_type="epithelial cell"  
/dev\_stage="fetus"  
/clone\_lib="Fetal skin"  
/note="Organ: skin; Vector: pBluescript SK-; Site\_1: EcoRI  
; Site\_2: XhoI"

**BASE COUNT** 77 a 100 c 78 g 78 t 1 others

**ORIGIN**

**Alignment Scores:**  
Pred. No.: 1.11e-86 Length: 334  
Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-059-395-142 (1-99) x AA297512 (1-334)

**QY** 1 MetlySILEProValLeuProAlaValValLeuLeuSerLeuLeuValLeuHisSerAla 20  
|||||  
**Db** 14 ATGAAGATCCCGGTCCTTCCTGCGGTGTGCTCCTCTCTGCTGCTCCACTCTGCC 73  
|||||  
**QY** 21 GInGIyAlaThrLeuGIyGIyProGIuGIuGIuSerThrIleGIuAsnTyraLaserArg 40  
|||||  
**Db** 74 CAGGAGCCACCCCTGGGTGCTGAGGAAGAACACCAATTGAGAAATGCGTCA 133  
|||||  
**QY** 41 ProGIuAlaPheAsnThrProPheLeuAsnIleAspLyLeuArgSerAlaPheLySAla 60  
|||||  
**Db** 134 CCGAGGCTTTAAACACCCCGTCTCGAATCGAACAAATGCGATCTGCGTTAAGCT 193  
|||||  
**QY** 61 AspGIuPheLeuAsnTyroPheIleAlaLeuPheGIuSerIleLySArgLyLeuProPheLeu 80  
|||||  
**Db** 194 GATGAGTTCCTGAAGTGGACGCGCTCTTGTAGTCTATCAAAAGAAACTTCTTCCTC 253  
|||||

**QY** 81 AsnTrpAspAlaPheProLyLeuLyGIyLeuArgSerAlaThrProAspAlaGln 99  
|||||  
**Db** 254 AACTGGATGCTTCTTCTTAAGCTGAAGAGACTNAGAGCGCACTCTGATGCCAG 310  
|||||

**RESULT 2**  
BX112106  
**LOCUS** BX112106 432 bp mRNA linear EST 07-FEB-2003  
**DEFINITION** BX112106 Soares fetal heart NbH19W Homo sapiens cDNA clone  
IMAGE998D01781 ; IMAGE:342096, mRNA sequence.

**ACCESSION** BX112106  
**VERSION** BX112106.1 GI:27878783  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens

**REFERENCE** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 432)  
Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,  
Radelof, U., Schneider, D. and Korn, B.

**TITLE** Human Unigeneset - RZPD3  
**JOURNAL** Unpublished  
**COMMENT** Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD, IMAGE998D01781.  
RZPDLIB: I.M.A.G.E. cDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No.972)  
<http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi?response?libNo=972> Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de  
This clone is available royalty-free from RZPD;  
contact RZPD ([clone@rzpd.de](mailto:clone@rzpd.de)) for further information. Seq primer:  
M13r, Primer sequence: TTTCAACAGCAAGAAAGCTATGAC.

# FEATURES

**Source**  
1.432  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE998D01781 ; IMAGE:342096"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal heart NbH19W"  
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by  
M.FaciMa Bonaldo. This library was constructed from the  
same fetus as the fetal lung library, Soares fetal lung  
NbH19W."

**BASE COUNT** 113 a 129 c 92 g 98 t

# ORIGIN

**Alignment Scores:**  
Pred. No.: 1.46e-86 Length: 432  
Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-10-059-395-142 (1-99) x BX112106 (1-432)







4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

This clone is available royalty-free through LML; contact the  
IMAGE Consortium (info@image.lml.gov) for further information.  
Insert length: 442 Std Error: 0.00

Seq primer: mob.REGA+ET  
High quality sequence stop: 347.

## FEATURES

## Source

1..381  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:1268869"  
/db\_xref="taxon:9606"  
/clone="IMAGE:343494"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares\_fetal\_heart\_NbHL19W"  
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by  
M.Fatima Bonaldo. This library was constructed from the  
same fetus as the fetal lung library, Soares fetal lung  
NbHL19W."

BASE COUNT 91 a 86 c 114 g 89 t 1 others  
ORIGIN

## Alignment Scores:

Pred. No.: 4.41e-68 Length: 381  
Score: 80.00 Matches: 80  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 80.81% Indels: 0  
DB: 14 Gaps: 0

US-10-059-395-142 (1-99) x W69108 (1-381)

QY 20 AlAGlNGlYAlaThrLeuGlyGlyProGlUGlUGlUSeRThrIleGlUAsnTYrAlaSer 39  
|||  
Db 344 GCCCAGGAGGCCACCCCTGGGTGCTCTGAGGAAGAAGCACATTGAGAAATTAATGCGTCA 285  
|||  
QY 40 ArgPRoGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLys 59  
|||  
Db 284 CGACCCGAGGCCTTTAAACCCCGTCTGAAACATGCAAAATGCGATCTGCGTTAAG 225  
|||  
QY 60 AlaAspGluPheLeuAsnThrPheAlaLeuPheGluSerIleLysArgLysLeuProPhe 79  
|||  
Db 224 GCTGATGAGTCTCTGAACCTGGCAGCCCTCTTGAATCTATCAAAAGAACTTCTTTC 165  
|||  
QY 80 LeuAsnTPAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
|||  
Db 164 CTCAACTGGGATGCTTCTTAAGCTGAAGAGACTGAGAGCGCAACTCTGATGCCAG 105  
|||

## RESULT 7

AA778414/c

LOCUS AA778414 339 bp mRNA linear EST 05-FEB-1998

DEFINITION zf39e05.b1 Soares\_fetal\_heart\_NbHL19W Homo sapiens cDNA clone  
IMAGE:379328 3', mRNA sequence.

ACCESSION AA778414

VERSION AA778414.1 GI:2837745

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE 1 (bases 1 to 339)

## AUTHORS

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Maria, M., Martin,  
J., Moore, B., Scheinberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.

## TITLE

WashU-NCI human EST Project

## JOURNAL

Unpublished

## COMMENT

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LML; contact the  
IMAGE Consortium (info@image.lml.gov) for further information.  
Seq primer: -40m13 fwd. ET from Amersham.

## FEATURES

## Source

1..339  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:1287584"  
/db\_xref="taxon:9606"  
/clone="IMAGE:379328"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares\_fetal\_heart\_NbHL19W"  
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by  
M.Fatima Bonaldo. This library was constructed from the  
same fetus as the fetal lung library, Soares fetal lung  
NbHL19W."

BASE COUNT 79 a 77 c 96 g 87 t  
ORIGIN

## Alignment Scores:

Pred. No.: 3.49e-66 Length: 339  
Score: 78.00 Matches: 78  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 78.79% Indels: 0  
DB: 9 Gaps: 0

US-10-059-395-142 (1-99) x AA778414 (1-339)

QY 22 GlYAlaThrLeuGlyGlyProGlUGlUGlUSeRThrIleGlUAsnTYrAlaSerArgPro 41  
|||  
Db 337 GGAGCCACCCCTGGGTGCTCTGAGGAAGAAGCACATTGAGAAATTAATGCGTCAAGACC 278  
|||  
QY 42 GlUAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAlaAsp 61  
|||  
Db 277 GAGGCTTTAAACCCCGTCTCTGAAACATGCAAAATGCGATCTGCGTTAAGCTGAT 218  
|||  
QY 62 GluPheLeuAsnThrPheAlaLeuPheGluSerIleLysArgLysLeuProPheLeuAsn 81  
|||  
Db 217 GAGTTCCTGAACCTGGCAGCCCTCTTGAATCTATCAAAAGAACTTCTTCTCAAC 158  
|||  
QY 82 TPAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
|||  
Db 157 TGGGATGCTTCTTAAGCTGAAGAGACTGAGAGCGCAACTCTGATGCCAG 104  
|||

## RESULT 8

AA722694/c

LOCUS AA722694 373 bp mRNA linear EST 02-JAN-1998

DEFINITION zg82b06.b1 Soares\_fetal\_heart\_NbHL19W Homo sapiens cDNA clone  
IMAGE:399827 3', mRNA sequence.





Oy	48	PheLeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHis	67
Db	154	TTCCTGAACATCGACAATTGGCATCTGCCTTAAGGTGATGAGTTCCTGAACGTGCAC	213
Oy	68	AlaLeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLys	87
Db	214	GCCCTCTTGAGTTATCAAAAGAAACTTCCTTCTCACACTGGATGCCCTTCTAAG	273
Oy	88	LeuLysGlyLeuArgSerAlaThrProAspAlaGln	99
Db	274	CTGAAGGACTGAGGAGCGCAACTCCTGATGCCAC	309
RESULT 10			
W69233		LOCUS	432 bp mRNA linear EST 16-OCT-1996
DEFINITION			z44c04.r1 Soares fetal heart NBHHL19W Homo sapiens cDNA clone
IMAGE:343494			5', mRNA sequence.
W69233			
VERSION			W69233.1 GI:1378493
KEYWORDS			EST.
SOURCE			Homo sapiens (human)
ORGANISM			Homo sapiens
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS			Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,B., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
TITLE			The WashU-Merck EST Project
JOURNAL			Unpublished
COMMENT			Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAG Consortium (info@image.lnl.gov) for further information. Insert Length: 442 Std Error: 0.00 Seq primer: mob.REGA+ET High quality sequence stop: 341.
FEATURES			Location/Qualifiers
source			1..432
			/organism="Homo sapiens"
			/mol_type="mRNA"
			/db_xref="GDB:1268869"
			/db_xref="taxon:9606"
			/clone="IMAGE:343494"
			/sex="unknown"
			/dev_stage="19 weeks"
			/lab_host="DH10B (ampicillin resistant)"
			/clone_lib="Soares_fetal_heart_NBHHL19W"
			/note="Organ: heart; Vector: pTZ19 (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' GTTACCACATCTGAAGTGGAGCGCGCCGATCTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTZ19 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHHL19W."
BASE COUNT			106 a 127 c 94 g 102 t 3 others
ORIGIN			
Alignment Scores:			
Pred. No.:			3.23e-60
Score:			72.00
Percent Similarity:			98.99%
Best Local Similarity:			98.99%
			Mismatches: 1

Query Match:	72.73%	Indels:	1
DB:	14	Gaps:	0
US-10-059-395-142 (1-99) x W69233 (1-432)			
QY	1 MetLysIleProValLeuProAlaValLeuLeuSerLeuLeuValLeuHisSerAla 20		
Db	13 ATGAAGATCCCGTCTTCTCCTGCGGTGGTCTCTCTCCCTCGTGGTCTCCACTCTGCC 72		
QY	21 GInGlyAlaThrLeuGlyGlyProGInGluGluSerThrIleGluAsnTyraLSerArg 40		
Db	73 CAGGAGCCACCTGGGTGT-CCTGAGGAAGAAAGACCATTTGAGATTATGCTACGA 131		
QY	41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60		
Db	132 CCCGAGGCTTTAACACCCCGTCTCTGAACATCGACAATTGCGATCTGCTTTAAGGCT 191		
QY	61 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80		
Db	192 GATGAGTTCCTGAACGTGGACGCGCCCTCTTGAGTCTATCAAAAGAACTCTCTCCTC 251		
QY	81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99		
Db	252 AACTGGATGCTTTCTTCTTAAGCTGAAGAAAGACTGAGGAGCGCAACTCTGATGCCCA 308		
RESULT 11			
AA586846/c	318 bp	mRNA	linear
LOCUS	nm67ell.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088972 3',		
DEFINITION	mRNA sequence.		
ACCESSION	AA586846		
VERSION	AA586846.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 318)		
JOURNAL	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .		
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Tumor Gene Index		
	Unpublished		
	Contact: Robert Strausberg, Ph.D.		
	Email: <a href="mailto:cgaps-r@mail.nih.gov">cgaps-r@mail.nih.gov</a>		
	Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.		
	Emmert-Buck, M.D., Ph.D.		
	CDNA Library Preparation: Stratagene, Inc.		
	CDNA Library Arrayed by: Greg Lennon, Ph.D.		
	DNA Sequencing by: Washington University Genome Sequencing Center		
	Clone distribution: NCI-CGAP clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LINL at:		
	<a href="http://www-bio.ln1.gov/bbrp/image/image.html">www-bio.ln1.gov/bbrp/image/image.html</a>		
	Insert Length: 465 Std Error: 0.00		
	Seq primer: -40ml3 fwd. ET from Amersham.		
FEATURES			
Source	Location/Qualifiers		
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	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:1088972"		
	/tissue_type="larynx"		
	/lab_host="SOLR (kanamycin resistant)"		
	/clone_lhb="NCI CGAP_Lar1"		
	/note="Organ: larynx; Vector: Bluescript SK-; Site_1:		
	EcORI; Site_2: XhoI; Cloned unidirectionally. Primer:		
	Oligo dT. larynx. 5' adaptor sequence: 5' GAATTCGACACGAG		
	3' 3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'		
	Average insert size: 0.9 kb."		
BASE COUNT	76 a 67 c 90 g 85 t		
ORIGIN			
Alignment Scores:	2.21e-59	Length:	318
Pred. No.:			



Score: 71.00 Matches: 71  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 71.72% Indels: 0  
 DB: 9 Gaps: 0

US-10-059-395-142 (1-99) x AA586846 (1-318)

QY 29 GUGUGUGUSeThriIleGluAsnTYrAlaSerArgProGluAlaPheAsnThrProPhe 48  
 DB 316 GAGGAGAAAGCACCATTGAGAAATTATGCGTCACGACCCGAGGCTTTAAACACCCCGTTC 257  
 QY 49 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 68  
 DB 256 CTGAACATCGACAATTGCGATCGCTTTAAGGCTGATGAGTTCTGAACTGGCACGCC 197  
 QY 69 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 88  
 DB 196 CTCTTTGAGTCTATCAAAAGAAACTTCTTCTCAACTGGGATGCCCTTCTTAAGCTG 137  
 QY 89 LysGlyLeuArgSerAlaThrProAspAlaGln 99  
 DB 136 AAAGACTGAGAGCGCAACTCTGATGCCAG 104

RESULT 12  
 BE466728/c 359 bp mRNA linear EST 27-JUL-2000  
 LOCUS hz24G06.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:3208954 3',  
 DEFINITION mRNA sequence.

ACCESSION BE466728  
 VERSION BE466728.1 GI:9512503  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 359)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL Tumor Gene Index

COMMENT Unpublished

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL, send email to:

Info@image.lnl.gov  
 Seq primer: -40UP from Gibco.

FEATURES  
 Source location/Qualifiers

1..359

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3208954"

/tissue\_type="pooled germ cell tumors"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP\_GC6"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA

from the normalized library NCI\_CGAP\_GC4 was prepared, and

as circles were made in vitro. Following HAP purification,

this DNA was used as tracer in a subtractive hybridization

reaction. The driver was PCR-amplified cDNAs from a pool

of 5,000 clones made from the same library (clonids

1257096-1258631, 1469064-1470983, and 1475592-1476743).

Subtraction by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 77 a 80 c 96 g 106 t

Alignment Scores:  
 Pred. No.: 2.51e-59 Length: 359  
 Score: 71.00 Matches: 71  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 71.72% Indels: 0  
 DB: 10 Gaps: 0

US-10-059-395-142 (1-99) x BE466728 (1-359)

QY 29 GUGUGUGUSeThriIleGluAsnTYrAlaSerArgProGluAlaPheAsnThrProPhe 48  
 DB 332 GAGGAGAAAGCACCATTGAGAAATTATGCGTCACGACCCGAGGCTTTAAACACCCCGTTC 273  
 QY 49 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 68  
 DB 272 CTGAACATCGACAATTGCGATCTGCGTTTAAAGGCTGATGAGTTCTGAACTGGCACGCC 213  
 QY 69 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 88  
 DB 212 CTCTTTGAGTCTATCAAAAGAAACTTCTTCTCAACTGGGATGCCCTTCTTAAGCTG 153  
 QY 89 LysGlyLeuArgSerAlaThrProAspAlaGln 99  
 DB 152 AAAGACTGAGAGCGCAACTCTGATGCCAG 120

RESULT 13  
 A1140605 362 bp mRNA linear EST 29-OCT-1998  
 LOCUS ge05f03.x1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1738109  
 DEFINITION 3', mRNA sequence.

ACCESSION A1140605  
 VERSION A1140605.1 GI:3648062  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 362)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL Tumor Gene Index

COMMENT Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo

Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

www-bio.lnl.gov/bbrp/image/image.html

Insert Length: 425 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham.

FEATURES

Source location/Qualifiers

1..362

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1738109"

/sex="male"

/lab\_host="DH10B"

/clone\_lib="Soares testis NHT"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was prepared from mRNA obtained from Clontech Laboratories

, Inc., and primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGAGGCGCCGCAATTTTCTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT7T3 vector. Library

went through one round of normalization to Cot5, and was

BASE COUNT 77 a 81 c 99 g 105 t  
 ORIGIN

## Alignment Scores:

Pred. No.: 2.53e-59 Length: 362  
 Score: 71.00 Matches: 71  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 71.72% Indels: 0  
 DB: 9 Gaps: 0

US-10-059-395-142 (1-99) x AII140605 (1-362)

OY 29 GluGlulSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 48  
 |||||  
 DB 331 GAGGAAGAAAGCACCATTGAGATATATGCGTCACGACCGAGCCCTTAACACCCGCTC 272

OY 49 LeuAsnIleAspIleuArgSerAlaPheLysAlaAspGluPheLeuAsnThrHisAla 68  
 |||||  
 DB 271 CTGAACATCGACAATGCGATCTGCGTTAAGGCTGATGAGTTCTTGAACCTGGCAGCC 212

OY 69 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 88  
 |||||  
 DB 211 CTCTTGAGTCTATCAAAAGAACTTCTTCTCACTGGATGCTTCTTAAGCTG 152

OY 89 LysGlyLeuArgSerAlaThrProAspAlaGln 99  
 |||||  
 DB 151 AAAGACTGAGAGCGCACTCTGATGCCAG 119

RESULT 14  
 AA297513

LOCUS AA297513 326 bp mRNA linear EST 18-APR-1997  
 DEFINITION EST113062 Fetal skin Homo sapiens cDNA 5' end, mRNA sequence.  
 AA297513  
 AA297513.1 GI:1949867

KEYWORDS  
 EST.

SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens

REFERENCE  
 AUTHORS  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 326)  
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult  
 ,C.J., Lee,N.H., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D., White  
 ,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,  
 Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald  
 ,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,  
 Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,  
 Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,  
 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,  
 Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,  
 Small,K.V., Spriggs,T.A., Utterback,T.R., Weldman,J.F., Li,Y.,  
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,  
 Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.,  
 Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,  
 Kunsch,C., Hungjun,J., Li,H., Melsner,P.S., Olsen,H., Raymond,L.,  
 Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon  
 ,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and  
 Venter,J.C.

TITLE  
 Initial assessment of human gene diversity and expression patterns

JOURNAL  
 MEDLINE  
 PUBMED  
 Nature 377 (6547 Suppl), 3-174 (1995)  
 96026280  
 7566098

COMMENT

Other\_ESTs: THC151622  
 Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlav@tigr.org  
 For clone availability, additional sequence and expression

Information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse.  
 Location/Qualifiers  
 1..326

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="ATCC (inhost):141549"  
 /db\_xref="taxon:9606"  
 /issue\_type="epithelium"  
 /cell\_type="epithelial cell"  
 /dev\_stage="fetus"  
 /clone\_lib="Fetal skin"  
 /note="Organ: skin; Vector: pBluescript SK-; Site\_1: EcoRI  
 ; Site\_2: XhoI"

BASE COUNT 76 a 95 c 76 g 77 t 2 others  
 ORIGIN

## Alignment Scores:

Pred. No.: 1.71e-54 Length: 326  
 Score: 66.00 Matches: 66  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 66.67% Indels: 0  
 DB: 9 Gaps: 0

US-10-059-395-142 (1-99) x AA297513 (1-326)

OY 2 LysIleProValLeuProAlaValValLeuSerLeuLeuValLeuHisSerAlaGln 21  
 |||||  
 DB 1 AAGATCCCGGTCTTCTCCGCGTGTGCTCTCTCCCTCGTGTCTCACTGCCCCAG 60

OY 22 GlyAlaThrLeuGlyGlyProGluGluSerThrIleGluAsnTyrAlaSerArgPro 41  
 |||||  
 DB 61 GGAGCCACCCTGGGTGTCTCTGAGGAAGAACACCATGAGATATATGCGTCACGACCC 120

OY 42 GluAlaPheAsnThrProPheLeuAsnIleAspIleuArgSerAlaPheLysAlaAsp 61  
 |||||  
 DB 121 GAGGCTTTAACCACCCCGTTCTGTAACATGACAAATTGCGATCGTTTAAAGCTGAT 180

OY 62 GluPheLeuAsnTrpHis 67  
 |||||  
 DB 181 GAGTTCTGAACTGGCAC 198

RESULT 15

LOCUS W69227 431 bp mRNA linear EST 16-OCT-1996  
 DEFINITION z44b06.r1 Soares fetal heart NBH119W Homo sapiens cDNA clone  
 IMAGE:343475 5', mRNA sequence.  
 W69227  
 W69227.1 GI:1378487

KEYWORDS  
 EST.

SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens

REFERENCE  
 AUTHORS  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 431)  
 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman  
 ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,  
 Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston  
 ,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE  
 The WashU-Merck EST Project

JOURNAL  
 MEDLINE  
 PUBMED  
 Unpublished

COMMENT  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information.  
 Insert Length: 466 Std Error: 0.00  
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FEATURES High quality sequence stop: 410.  
Location/Qualifiers  
1..431  
source

/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:343475"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal heart NbHL19W"  
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTACCAATCTGAAGTGGAGCGGCCGACATCTTTTCTTTT 3']',  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by  
M.Patima Bonaldo. This library was constructed from the  
same fetus as the fetal lung library, Soares fetal lung  
NbHL19W."

BASE COUNT 106 a 127 c 94 g 102 t 2 others  
ORIGIN

Alignment Scores:

Pred. No.: 1.56e-47 Length: 431  
Score: 59.00 Matches: 59  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 59.60% Indels: 0  
DB: 14 Gaps: 0

US-10-059-395-142 (1-99) x W69227 (1-431)

QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
Db 134 CCGAGGCCCTTTAACACCCCGTTCTTGAACATCGACAAATTGCGATCTGCGTTAAGGCT 193  
QY 61 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
Db 194 GATGAGTTCCTGAACCTGGCAGCCCTCTTGAAGTCTATCAAAAGAACTCTTCCTC 253  
QY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
Db 254 AACTGGGATGCCTTCTCTAAGCTGAAGAACTGAGGAGCGCACTCCTGATGCCAG 310

Search completed: November 28, 2003, 10:52:28  
Job time : 1720 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2003, 07:55:01 ; Search time 22 Seconds

(without alignments)  
190.399 Million cell updates/sec

Title: US-10-059-395-142

Perfect score: 510  
Sequence: 1 MKIPVLPVAVLISLVLSA.....LNWDAFPKLGKRSATPDQA 99

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	510	100.0	99	4	US-09-996-243-201 Sequence 201, App
2	66.5	13.0	692	4	US-09-198-452A-966 Sequence 966, App
3	65.5	12.8	77	4	US-09-107-532A-5662 Sequence 5662, App
4	64.5	12.6	1350	2	US-08-319-866-9 Sequence 9, Appli
5	62	12.2	311	4	US-09-252-991A-18334 Sequence 18334, A
6	62	12.2	400	4	US-09-150-347-1 Sequence 1, Appli
7	62	12.2	400	4	US-09-665-313-1 Sequence 1, Appli
8	62	12.2	432	4	US-09-403-089A-1 Sequence 1, Appli
9	61.5	12.1	276	4	US-09-328-352-7013 Sequence 7013, Ap
10	61	12.0	192	4	US-09-134-001C-5386 Sequence 5386, Ap
11	61	12.0	256	4	US-09-252-991A-29587 Sequence 29587, A
12	60.5	11.9	292	4	US-09-051-755-10 Sequence 10, Appl
13	60.5	11.9	934	4	US-09-252-991A-19515 Sequence 19515, A
14	59.5	11.7	233	4	US-09-328-352-6059 Sequence 6059, Ap
15	59.5	11.7	15281	2	US-08-471-119A-2 Sequence 2, Appli
16	59	11.6	324	4	US-08-311-731A-262 Sequence 262, App
17	59	11.6	2509	4	US-09-252-991A-16642 Sequence 16642, A
18	58.5	11.5	370	4	US-09-107-532A-5920 Sequence 5920, Ap
19	58	11.4	174	4	US-09-252-991A-16812 Sequence 16812, A
20	58	11.4	713	3	US-08-872-855-5 Sequence 5, Appli
21	57.5	11.3	93	4	US-09-134-001C-3205 Sequence 3205, Ap
22	57	11.2	252	2	US-07-885-089B-7 Sequence 7, Appli
23	57	11.2	281	4	US-09-107-532A-4985 Sequence 4985, Ap
24	57	11.2	505	4	US-09-627-216A-12 Sequence 12, Appl
25	57	11.2	505	4	US-09-126-420A-22 Sequence 22, Appl
26	57	11.2	505	4	US-09-765-873A-12 Sequence 12, Appl
27	57	11.2	1070	2	US-08-633-770A-2 Sequence 2, Appli

28	57	11.2	3724	2	US-08-804-227C-10 Sequence 10, Appl
29	57	11.2	3724	2	US-08-804-198-4 Sequence 4, Appli
30	56.5	11.1	374	4	US-09-252-991A-18651 Sequence 18651, A
31	56.5	11.1	400	4	US-09-150-347-2 Sequence 2, Appli
32	56.5	11.1	400	4	US-09-665-313-2 Sequence 2, Appli
33	56.5	11.1	429	2	US-09-074-512-1 Sequence 1, Appli
34	56.5	11.1	518	3	US-08-999-723-2 Sequence 2, Appli
35	56.5	11.1	518	3	US-09-434-427-2 Sequence 2, Appli
36	56.5	11.1	518	4	US-09-548-372D-2 Sequence 2, Appli
37	56.5	11.1	518	4	US-09-548-367D-2 Sequence 2, Appli
38	56.5	11.1	518	4	US-09-551-853D-2 Sequence 2, Appli
39	56.5	11.1	543	4	US-09-252-991A-30375 Sequence 30375, A
40	56.5	11.1	1066	2	US-08-633-770A-1 Sequence 1, Appli
41	56	11.0	135	4	US-09-288-143-69 Sequence 69, Appl
42	56	11.0	373	4	US-09-328-352-7009 Sequence 7009, Ap
43	55.5	10.9	186	1	US-08-117-083-22 Sequence 22, Appl
44	55	10.8	431	4	US-09-134-001C-3051 Sequence 3051, Ap
45	55	10.8	513	4	US-09-595-857B-30 Sequence 30, Appl

## ALIGNMENTS

RESULT 1  
US-09-996-243-201  
Sequence 201, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottfredsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996,243  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28





; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 510; DB 4; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4.8e-59;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKIPVPAVLLSLVLSAAGATLGPEESTIENYASRPEAFNTPLNIDKLSAFKA 60  
1 MKIPVPAVLLSLVLSAAGATLGPEESTIENYASRPEAFNTPLNIDKLSAFKA 60

OY 61 DEFNWMALFESIKRKLPLNWDAPFKLGLRSATPDAQ 99  
61 DEFNWMALFESIKRKLPLNWDAPFKLGLRSATPDAQ 99

RESULT 2  
US-09-198-452A-966

; Sequence 966, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 966

; LENGTH: 692

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-966

Query Match 13.0%; Score 66.5; DB 4; Length 692;  
Best Local Similarity 29.2%; Pred. No. 5.6;  
Matches 19; Conservative 11; Mismatches 28; Indels 7; Gaps 1;

OY 11 LLSLVLSAAGATLGPEESTIENYASRPEAFNTPLNIDKLSAFKADFLNWMALF 70  
11 LLSLVLSAAGATLGPEESTIENYASRPEAFNTPLNIDKLSAFKADFLNWMALF 70

OY 71 ESIRK 75  
71 ESIRK 75

Db 253 SSIRK 257  
253 SSIRK 257

RESULT 3

US-09-107-532A-5662

; Sequence 5662, Application US/09107532A

; Patent No. 6583275

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 7310

; CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arinello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 5662:

SEQUENCE CHARACTERISTICS:

LENGTH: 77 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1..77

SEQUENCE DESCRIPTION: SEQ ID NO: 5662:

Query Match 12.8%; Score 65.5; DB 4; Length 77;  
Best Local Similarity 26.4%; Pred. No. 0.37;  
Matches 24; Conservative 13; Mismatches 33; Indels 21; Gaps 4;

OY 4 PVLPAVLLSLVLSAAGATLGPEESTIENYASRPEAFNTPLNIDKLSAFKAD 61  
4 PVLPAVLLSLVLSAAGATLGPEESTIENYASRPEAFNTPLNIDKLSAFKAD 61

Db 6 PILP-----SHGTTIPDPAIQQLVEMY--PRVLTPHVGSTDEALSNMIST 50  
6 PILP-----SHGTTIPDPAIQQLVEMY--PRVLTPHVGSTDEALSNMIST 50

OY 62 EFLNWMALFESIKRKLPLNWDAPFKLGLR 92  
62 EFLNWMALFESIKRKLPLNWDAPFKLGLR 92

Db 51 SFENFREIEITGKTK---NEVSLPKARQLR 77  
51 SFENFREIEITGKTK---NEVSLPKARQLR 77

RESULT 4

US-08-319-866-9

; Sequence 9, Application US/08319866

; Patent No. 5929223

; GENERAL INFORMATION:

; APPLICANT: Tully, Timothy P.

; APPLICANT: Yin, Jerry C.

; APPLICANT: Regulski, Michael

; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/319,866

FILING DATE: 7-OCT-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL94-03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1350 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-319-866-9

Query Match 12.6%; Score 64.5; DB 2; Length 1350;  
Best Local Similarity 35.2%; Pred. No. 26;  
Matches 19; Conservative 9; Mismatches 19; Indels 7; Gaps 1;

QY 8 AVVLLSLVLSAGATLGPEESTIENTYASRPEAFNTPLNIDKLSAFKAD 61  
DB 543 AVVEMNIAVLHSYQSRNV-----TIVDHTASESFMKHFENESKLRNGCPAD 589

RESULT 5  
US-09-252-991A-18334  
Sequence 18334, Application US/09252991A  
Patent No. 6551795

GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 18334  
LENGTH: 311  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18334

Query Match 12.2%; Score 62; DB 4; Length 311;  
Best Local Similarity 28.4%; Pred. No. 7.2;  
Matches 25; Conservative 20; Mismatches 23; Indels 20; Gaps 5;

QY 18 HSAQATLGPEESTIENTYASRPEAFNTPLNIDKLSAFKAD-----FLNWA 68  
DB 218 NASVGASFFGGEEPLDLSR---FS--VNLKLCQAPONDEIARALRSVAIKWHY 271  
QY 69 LFESIK---RKLPL-NWDAPPKL 91  
DB 272 IERSLRNYNQNSVPFLVNKNADRIIDGL 299

RESULT 6  
US-09-150-347-1  
Sequence 1, Application US/09150347  
Patent No. 6372269  
GENERAL INFORMATION:  
APPLICANT: Rangel-Aldao, Rafael  
APPLICANT: Bravo, Adriana  
APPLICANT: Sanchez, Beatriz  
APPLICANT: Galindo-Castro, Ivan  
TITLE OF INVENTION: Malt Beverage Having Stabilized Flavor and Methods of Production  
FILE REFERENCE: 1390.0070004  
CURRENT APPLICATION NUMBER: US/09/150,347

CURRENT FILING DATE: 1998-09-09  
EARLIER APPLICATION NUMBER: 60/058,398  
EARLIER FILING DATE: 1997-09-09  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 400  
TYPE: PRT  
ORGANISM: Saccharomyces carlsbergensis  
US-09-150-347-1

Query Match 12.2%; Score 62; DB 4; Length 400;  
Best Local Similarity 23.4%; Pred. No. 10;  
Matches 18; Conservative 10; Mismatches 31; Indels 18; Gaps 3;

QY 28 PEEESTIENTYASRPE-----AFNTPL-NIDKLSAFKADFLNWAFLFESIKRK 76  
DB 49 PNRDWAVEYTYQRAQRPPTMITTEGAFISPOAGGYDNAPGVWSEEQWVEWTKIFNAIHEK 108  
QY 77 LPF-----LNWDAPF 86  
DB 109 KSFWVQVLWVLGWAAPF 125

RESULT 7  
US-09-665-313-1  
Sequence 1, Application US/09665313  
Patent No. 6468567

GENERAL INFORMATION:  
APPLICANT: Rangel-Aldao, Rafael  
APPLICANT: Bravo, Adriana  
APPLICANT: Sanchez, Beatriz  
APPLICANT: Galindo-Castro, Ivan  
TITLE OF INVENTION: Malt Beverage Having Stabilized Flavor and Methods of Production  
FILE OF INVENTION: Thereof  
FILE REFERENCE: 1390.0070004  
CURRENT APPLICATION NUMBER: US/09/665,313  
CURRENT FILING DATE: 2000-09-19  
PRIOR APPLICATION NUMBER: 09/150,347  
PRIOR FILING DATE: 1998-09-09  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 400  
TYPE: PRT  
ORGANISM: Saccharomyces carlsbergensis  
US-09-665-313-1

Query Match 12.2%; Score 62; DB 4; Length 400;  
Best Local Similarity 23.4%; Pred. No. 10;  
Matches 18; Conservative 10; Mismatches 31; Indels 18; Gaps 3;

QY 28 PEEESTIENTYASRPE-----AFNTPL-NIDKLSAFKADFLNWAFLFESIKRK 76  
DB 49 PNRDWAVEYTYQRAQRPPTMITTEGAFISPOAGGYDNAPGVWSEEQWVEWTKIFNAIHEK 108  
QY 77 LPF-----LNWDAPF 86  
DB 109 KSFWVQVLWVLGWAAPF 125

RESULT 8  
US-09-403-089A-1  
Sequence 1, Application US/09403089A  
Patent No. 6429286  
GENERAL INFORMATION:  
APPLICANT: SUGIMURA, Kazuhisa  
TITLE OF INVENTION: Immunoregulatory Molecules and Process for Preparing the Same  
FILE REFERENCE: 0020-4637P  
CURRENT APPLICATION NUMBER: US/09/403,089A  
CURRENT FILING DATE: 1999-10-15  
PRIOR APPLICATION NUMBER: PCT/JP97/02540  
PRIOR FILING DATE: 1997-07-23





OY 60 ADE-----FLNWHALFESIKRKLPLFNWDAFPKLGJRSAT 95  
Db 5889 ENDNFESLVRVRSTATAFANQDVPFESIVSSL-----LPGSRDAS 5930

Search completed: November 28, 2003, 07:57:05  
Job time : 25 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 09:32:09 ; Search time 55 Seconds

(without alignments)  
794.490 Million cell updates/sec

Title: US-10-059-395-142

Perfect score: 99  
Sequence: 1 MKIPVLPVAVLSTLVLSA.....LNWDAFPKXGLRSATPDAQ 99

Scoring table:

OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1135290

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO.spool/US10059395/runat\_25112003\_140756\_7426/app\_query.fasta\_1.263  
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=ol1.rn1 -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10059395 @CGN 1 1 56 @runat\_25112003\_140756\_7426 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA: \*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	100.0	415	4	US-09-996-243-200 Sequence 200, Appli
2	9	9.1	666	4	US-09-252-991A-5754 Sequence 5754, Ap
3	9	9.1	837	4	US-09-252-991A-5702 Sequence 5702, Ap
4	9	9.1	1035	4	US-09-252-991A-5715 Sequence 5715, Ap
5	9	9.1	1245	4	US-09-252-991A-5725 Sequence 5725, Ap
6	9	9.1	36159	4	US-09-749-588-3 Sequence 3, Appli
7	8	8.1	45	2	US-08-860-882A-8 Sequence 8, Appli
8	8	8.1	240	4	US-09-107-532A-3419 Sequence 3419, Ap
9	8	8.1	278	4	US-09-313-294A-1198 Sequence 1198, Ap
10	8	8.1	330	4	US-09-107-532A-931 Sequence 931, Appl
11	8	8.1	441	4	US-09-107-532A-2246 Sequence 2246, Ap
12	8	8.1	1002	4	US-09-107-532A-2821 Sequence 2821, Ap

C	13	8	8.1	1059	4	US-09-576-160B-8	Sequence 8, Appli
	14	8	8.1	5919	4	US-09-221-017B-584	Sequence 584, Appl
	15	7	7.1	61	1	US-08-391-339-31	Sequence 31, Appl
	16	7	7.1	61	1	US-08-484-274A-31	Sequence 31, Appl
	17	7	7.1	243	2	US-08-747-121-6	Sequence 6, Appli
	18	7	7.1	283	4	US-09-313-294A-1241	Sequence 1241, Ap
C	19	7	7.1	340	4	US-09-404-879A-203	Sequence 203, Appl
C	20	7	7.1	340	4	US-09-338-933-203	Sequence 203, Appl
C	21	7	7.1	340	4	US-09-215-681-203	Sequence 203, Appl
	22	7	7.1	341	4	US-09-404-879A-204	Sequence 204, Appl
	23	7	7.1	341	4	US-09-338-933-204	Sequence 204, Appl
	24	7	7.1	341	4	US-09-215-681-204	Sequence 204, Appl
C	25	7	7.1	375	4	US-09-107-532A-1682	Sequence 1682, Ap
	26	7	7.1	400	4	US-09-404-879A-250	Sequence 250, Appl
	27	7	7.1	400	4	US-09-338-933-250	Sequence 250, Appl
	28	7	7.1	400	4	US-09-215-681-250	Sequence 250, Appl
	29	7	7.1	426	4	US-09-205-258-95	Sequence 95, Appl
	30	7	7.1	527	4	US-09-404-879A-172	Sequence 172, Appl
	31	7	7.1	527	4	US-09-338-933-172	Sequence 172, Appl
	32	7	7.1	527	4	US-09-215-681-172	Sequence 172, Appl
	33	7	7.1	572	4	US-09-404-879A-174	Sequence 174, Appl
	34	7	7.1	572	4	US-09-338-933-174	Sequence 174, Appl
	35	7	7.1	572	4	US-09-215-681-174	Sequence 174, Appl
C	36	7	7.1	653	4	US-09-404-879A-370	Sequence 370, Appl
	37	7	7.1	691	4	US-09-404-879A-240	Sequence 240, Appl
	38	7	7.1	691	4	US-09-338-933-240	Sequence 240, Appl
	39	7	7.1	691	4	US-09-215-681-240	Sequence 240, Appl
C	40	7	7.1	697	4	US-09-404-879A-243	Sequence 243, Appl
C	41	7	7.1	697	4	US-09-338-933-243	Sequence 243, Appl
C	42	7	7.1	723	4	US-09-215-681-243	Sequence 243, Appl
C	43	7	7.1	723	4	US-09-447-356-4	Sequence 4, Appli
C	44	7	7.1	747	4	US-09-404-879A-209	Sequence 209, Appl
C	45	7	7.1	747	4	US-09-338-933-209	Sequence 209, Appl

#### ALIGNMENTS

RESULT 1  
US-09-996-243-200  
Sequence 200, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996,243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16



PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
Pred. No.: 2.32e-92 Length: 415  
Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-059-395-142 (1-99) x US-09-996-243-200 (1-415)

OY 1 MetLySleProValLeuProAlaValLeuSerLeuValLeuHisSerAla 20  
DB 13 ATGAAGATCCCGGTCCTCTCGCGGTGCTCTCTCCCTCGGTGCTCCACTTGC 72  
OY 21 GInGlyAlaThrLeuGlyGlyProGluGluSerThrIleGluAsnTyrAlaSerArg 40  
DB 73 CAGGAGCCACCTGGTGTCTGAGGAAGAAGACCATTTGATGCGTACGGA 132  
OY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
DB 133 CCGAGGCTTTAACAACCCGTTCTGAAACATGACAATTCGATCGGTTAAGGCT 192  
OY 61 AspGluPheLeuAsnThrPheAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
DB 193 GATGAGTTCCTGAAGTGGACGCGCTTTTGAGTCTATCAAAAGAACTTCCTTCC 252  
OY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
DB 253 AACTGGAGTCTTCTTAAGCTGAAGAGACTGAGAGCGCACTCTGATGCCAG 309

## RESULT 2

US-09-252-991A-5754/C  
Sequence 5754, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 5754  
LENGTH: 666  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5754

Alignment Scores:  
Pred. No.: 1.97 Length: 666  
Score: 9.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 9.09% Indels: 0  
DB: 4 Gaps: 0

US-10-059-395-142 (1-99) x US-09-252-991A-5754 (1-666)

OY 90 GlyLeuArgSerAlaThrProAspAla 98  
DB 62 GGGCTGGGAGCGCCACGCGGACGCT 36

## RESULT 3

US-09-252-991A-5702  
Sequence 5702, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 5702  
LENGTH: 837  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5702

Alignment Scores:  
Pred. No.: 2.47 Length: 837  
Score: 9.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 9.09% Indels: 0  
DB: 4 Gaps: 0

US-10-059-395-142 (1-99) x US-09-252-991A-5702 (1-837)

OY 90 GlyLeuArgSerAlaThrProAspAla 98  
DB 218 GGGCTGGGAGCGCCACGCGGACGCT 244

## RESULT 4

US-09-252-991A-5715  
Sequence 5715, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 5715  
LENGTH: 1035  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5715

Alignment Scores:

Pred. No.: 3.05 Length: 1035  
Score: 9.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 9.09% Indels: 0  
DB: 4 Gaps: 0

US-10-059-395-142 (1-99) x US-09-252-991A-5715 (1-1035)

OY 90 G1yleuArgSera1aThProaSPa1a 98  
Db 628 GGGCTGCGAGCGCCACGCCGCGACGCT 654

## RESULT 5

US-09-252-991A-5725/c  
; Sequence 5725, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 5725  
; LENGTH: 1245  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5725

## Alignment Scores:

Pred. No.: 3.66 Length: 1245  
Score: 9.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 9.09% Indels: 0  
DB: 4 Gaps: 0

US-10-059-395-142 (1-99) x US-09-252-991A-5725 (1-1245)

OY 90 G1yleuArgSera1aThProaSPa1a 98  
Db 631 GGGCTGCGAGCGCCACGCCGCGACGCT 605

## RESULT 6

US-09-749-588-3  
; Sequence 3, Application US/09749588  
; Patent No. 6423521  
; GENERAL INFORMATION:  
; APPLICANT: CHANDRAMOULISWARAN, Ishwar et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CI001068  
; CURRENT APPLICATION NUMBER: US/09/749,588  
; CURRENT FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 36159  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(36159)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-749-588-3

Alignment Scores:  
Pred. No.: 104 Length: 36159  
Score: 9.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 9.09% Indels: 0  
DB: 4 Gaps: 0

US-10-059-395-142 (1-99) x US-09-749-588-3 (1-36159)

OY 5 ValleuProa1aVal1euleuSer 13  
Db 9029 GTTTACCGCAGTGTCTCTTAAGC 9055

## RESULT 7

US-08-860-882A-8  
; Sequence 8, Application US/08860882A  
; Patent No. 5985281  
; GENERAL INFORMATION:  
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN  
; APPLICANT: EGGELTE, HENDRIKUS JOHANNES  
; APPLICANT: TARRAGONA-FIOL, ANTONIO  
; APPLICANT: RABIN, BRIAN ROBERT  
; APPLICANT: BOYLE, FRANCIS THOMAS  
; APPLICANT: HENNAM, JOHN FREDERICK  
; APPLICANT: BLAKELY, DAVID CHARLES  
; APPLICANT: MARSHAM, PETER ROBERT  
; APPLICANT: HEATON, DAVID WILLIAM  
; APPLICANT: DAVIES, DAVID HUW  
; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/860,882A  
; FILING DATE: JUNE 23, 1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DONALD J. BIRD  
; REGISTRATION NUMBER: 25,323  
; REFERENCE/DOCKET NUMBER: 9901/238653  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3027  
; TELEFAX: (202) 822-0944  
; TELEX: 6174627 CUSH  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 45 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-860-882A-8

## Alignment Scores:

Pred. No.: 1.41 Length: 45  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 8.08% Indels: 0  
DB: 2 Gaps: 0

US-10-059-395-142 (1-99) x US-08-860-882A-8 (1-45)

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Qy      10 ValleuSerleuValleu 17
      |||||
Db      21 GTCCTGTTGCTGTTGCTG 44

RESULT 8
US-09-107-532A-3419/c
; Sequence 3419, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3419:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...240
; SEQUENCE DESCRIPTION: SEQ ID NO: 3419:
US-09-107-532A-3419

Alignment Scores:
Pred. No.: 7.45 Length: 240
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.08% Indels: 0
DB: 4 Gaps: 0

US-10-059-395-142 (1-99) x US-09-107-532A-3419 (1-240)

Qy      10 ValleuSerleuValleu 17
      |||||
Db      229 GTGCTACTTTCATCTCGTACTC 206

RESULT 9
US-09-313-294A-1198/c

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: Sequence 1198, Application US/09313294A
: Patent No. 6476212
: GENERAL INFORMATION:
: APPLICANT: Lalgucl, Raghnunath V.
: APPLICANT: Ito, Laura Y.
: APPLICANT: Sherman, Bradley K.
: TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
: FILE REFERENCE: PL-0017 US
: CURRENT APPLICATION NUMBER: US/09/313,294A
: CURRENT FILING DATE: 1999-05-14
: NUMBER OF SEQ ID NOS: 7600
: SOFTWARE: PERL Program
: SEQ ID NO 1198
: LENGTH: 278
: TYPE: DNA
: ORGANISM: Zea mays
: FEATURE:
: NAME/KEY: misc feature
: OTHER INFORMATION: Incyte ID No. 6476212 700550532H1
: NAME/KEY: unsure
: LOCATION: 277
: OTHER INFORMATION: a, t, c, g, or other
: US-09-313-294A-1198

Alignment Scores:
Pred. No.:      8.62      Length:      278
Score:          8.00      Matches:      8
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      8.08%      Indels: 0
DB:               4      Gaps: 0

US-10-059-395-142 (1-99) X US-09-313-294A-1198 (1-278)
QY      11 LeuLeuSerLeuLeuValLeuHis 18
Db      126 CTCCTTCCCTCCTCGTCCTGCAC 103

RESULT 10
US-09-107-532A-931
: Sequence 931, Application US/09107532A
: Patent No. 6583275
: GENERAL INFORMATION:
: APPLICANT: Lynn A Doucette-Stamm and David Bush
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
: NUMBER OF SEQUENCES: 7310
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: GENOME THERAPEUTICS CORPORATION
: STREET: 100 Beaver Street
: CITY: Waltham
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02354
: COMPUTER READABLE FORM:
: MEDIUM TYPE: CD/ROM ISO9660
: COMPUTER: PC
: OPERATING SYSTEM: <Unknown>
: SOFTWARE: ASCII
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/107,532A
: FILING DATE: 30-Jun-1998
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/085,598
: FILING DATE: 14 May 1998
: APPLICATION NUMBER: 60/051571
: FILING DATE: July 2, 1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Ariniello, Pamela Deneke
: REGISTRATION NUMBER: 40,489
: REFERENCE/DOCKET NUMBER: GTC-012
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (781) 893-5007

```



TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 931:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 330 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...330  
; SEQUENCE DESCRIPTION: SEQ ID NO: 931:  
US-09-107-532A-931  
  
Alignment Scores:  
Pred. No.: 10.2 Length: 330  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 8.08% Indels: 0  
DB: 4 Gaps: 0  
  
US-10-059-395-142 (1-99) x US-09-107-532A-931 (1-330)  
  
Qy 10 ValleuLeuSerLeuValleu 17  
Db 33 GTGCTGCTTTCGCTGCTGCTT 56  
  
RESULT 11  
US-09-107-532A-2246  
; Sequence 2246, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 2246:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 441 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double

TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...441  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2246:  
US-09-107-532A-2246  
  
Alignment Scores:  
Pred. No.: 13.6 Length: 441  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 8.08% Indels: 0  
DB: 4 Gaps: 0  
  
US-10-059-395-142 (1-99) x US-09-107-532A-2246 (1-441)  
  
Qy 10 ValleuLeuSerLeuValleu 17  
Db 124 GTGCTGCTTTCGCTGCTGCTT 147  
  
RESULT 12  
US-09-107-532A-2821/c  
; Sequence 2821, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 2821:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1002 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium

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;   FEATURE:
;   NAME/KEY:  misc feature
;   LOCATION:  (B) LOCATION 1...1002
;   SEQUENCE DESCRIPTION: SEQ ID NO: 2821:
US-09-107-532A-2821

Alignment Scores:
Pred. No.:      30.8      Length:      1002
Score:          8.00      Matches:       8
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:     8.08%      Indels:    0
DB:              4         Gaps:      0

US-10-059-395-142 (1-99) x US-09-107-532A-2821 (1-1002)

QY      10 ValleuSerleuValleu 17
      |||||
Db      722 GTGCTGCTTCGCTGCTGCTGCTGCT 699

RESULT 13
US-09-576-160B-8/c
; Sequence 8, Application US/09576160B
; Patent No. 6469150
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert
; APPLICANT: Zhao, Jinguo
; APPLICANT: Swanson, Robert
; APPLICANT: Webb, Maria
; APPLICANT: Strohl, Barbara
; TITLE OF INVENTION: Cloning and Characterization of Genes Encoding
; TITLE OF INVENTION: Bradykinin B1 Receptor Homologues From Five Mammalian
; FILE REFERENCE: 1073.058
; CURRENT APPLICATION NUMBER: US/09/576,160B
; CURRENT FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Macaca mulatta
US-09-576-160B-8

Alignment Scores:
Pred. No.:      32.6      Length:      1059
Score:          8.00      Matches:       8
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:     8.08%      Indels:    0
DB:              4         Gaps:      0

US-10-059-395-142 (1-99) x US-09-576-160B-8 (1-1059)

QY      8 AlavaValleuSerleu 15
      |||||
Db      746 GCTGTGCTTCCTATCTGCTG 723

RESULT 14
US-09-221-017B-584
; Sequence 584, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
;
```

```

;
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: Windows
;   SOFTWARE: FastSeq for Windows Version 2.0b
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/221,017B
;   FILING DATE: 23-DEC-1998
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PP1182
;   FILING DATE: 31-DEC-1997
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PP1546
;   FILING DATE: 30-JAN-1998
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PP2911
;   FILING DATE: 09-APR-1998
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/AU98/01023
;   FILING DATE: 10-DEC-1998
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Monroy, Gladys H
;   REGISTRATION NUMBER: 32,430
;   REFERENCE/DOCKET NUMBER: 27340-20021.00
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650-813-5600
;   TELEFAX: 650-494-0792
;   TELEX: 706141
;   INFORMATION FOR SEQ ID NO: 584:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 5919 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: circular
;   MOLECULE TYPE: DNA (genomic)
;   HYPOTHETICAL: NO
;   ANTI-SENSE: UNKNOWN
;   ORIGINAL SOURCE:
;   ORGANISM: PORYPHYROMONAS GINGIVALIS
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: 1...5919
US-09-221-017B-584

Alignment Scores:
Pred. No.:      180      Length:      5919
Score:          8.00      Matches:       8
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:     8.08%      Indels:    0
DB:              4         Gaps:      0

US-10-059-395-142 (1-99) x US-09-221-017B-584 (1-5919)

QY      6 LeuProAlaValleuSer 13
      |||||
Db      3611 TTGCCGCGACGTCGTCGTCG 3634

RESULT 15
US-08-391-339-31
; Sequence 31, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESS: Monsanto Co. B44F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
;
```

STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/391,339  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/156,968  
FILING DATE:  
APPLICATION NUMBER: US/07/717,370  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoerner, Dennis R., Jr.  
REGISTRATION NUMBER: 30,914  
REFERENCE/DOCKET NUMBER: 38-21 (10533)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)537-6099  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (synthetic)  
US-08-391-339-31

## Alignment Scores:

Pred. No.:	19.9	Length:	61
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	7.07%	Indels:	0
DB:	1	Gaps:	0

US-10-059-395-142 (1-99) x US-08-391-339-31 (1-61)

QY 10 ValLeuLeuSerLeuLeuVal 16  
|||  
Db 24 GFACTGTTGAGTTGCTGCTC 44

Search completed: November 28, 2003, 10:53:33  
Job time : 61 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2003, 08:04:08 ; Search time 24 Seconds

(without alignments)  
760.829 Million cell updates/sec

Title: US-10-059-395-142

Perfect score: 99

Sequence: 1 MKIPVLPVAVLTLVLSLHSA.....LWDAFPKLGKLSATPPDAQ 99

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 673684 segs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
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- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
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- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	99	100.0	99	9	US-09-989-723-201
3	99	100.0	99	9	US-09-989-723-201
4	99	100.0	99	9	US-09-989-727-201
5	99	100.0	99	10	US-09-989-731-201
6	99	100.0	99	10	US-09-989-732-201
7	99	100.0	99	10	US-09-990-442-201
8	99	100.0	99	10	US-09-991-163-201
9	99	100.0	99	10	US-09-993-604-201
10	99	100.0	99	10	US-09-990-456-201
11	99	100.0	99	10	US-09-990-456-201
12	99	100.0	99	10	US-09-989-721-201
13	99	100.0	99	10	US-09-992-598-201
14	99	100.0	99	10	US-09-984-245-142
15	99	100.0	99	10	US-09-989-293A-201

16	99	100.0	99	10	US-09-989-735-201	Sequence 201, App
17	99	100.0	99	10	US-09-990-444-201	Sequence 201, App
18	99	100.0	99	10	US-09-991-181-201	Sequence 201, App
19	99	100.0	99	10	US-09-989-730-201	Sequence 201, App
20	99	100.0	99	10	US-09-990-436-201	Sequence 201, App
21	99	100.0	99	10	US-09-989-734-201	Sequence 201, App
22	99	100.0	99	11	US-09-997-666-201	Sequence 201, App
23	99	100.0	99	11	US-09-997-653-201	Sequence 201, App
24	99	100.0	99	11	US-09-993-667-201	Sequence 201, App
25	99	100.0	99	11	US-09-997-428-201	Sequence 201, App
26	99	100.0	99	11	US-09-997-562-201	Sequence 201, App
27	99	100.0	99	11	US-09-990-438-201	Sequence 201, App
28	99	100.0	99	11	US-09-990-562-201	Sequence 201, App
29	99	100.0	99	11	US-09-990-711-201	Sequence 201, App
30	99	100.0	99	11	US-09-989-726-201	Sequence 201, App
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33	99	100.0	99	11	US-09-997-573-201	Sequence 201, App
34	99	100.0	99	11	US-09-997-514-201	Sequence 201, App
35	99	100.0	99	11	US-09-997-573-201	Sequence 201, App
36	99	100.0	99	11	US-09-966-262-142	Sequence 142, App
37	99	100.0	99	11	US-09-997-559-201	Sequence 201, App
38	99	100.0	99	11	US-09-997-601-201	Sequence 201, App
39	99	100.0	99	11	US-09-990-443-201	Sequence 201, App
40	99	100.0	99	11	US-09-991-854-201	Sequence 201, App
41	99	100.0	99	11	US-09-997-628-201	Sequence 201, App
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#### ALIGNMENTS

RESULT 1

US-09-989-722-201

Sequence 201, Application US/09989722

Patent No. US20020072067A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730PIC63

CURRENT APPLICATION NUMBER: US/09/989,722

PRIOR FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17





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; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
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Query Match      100.0%; Score 99; DB 9; Length 99;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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## RESULT 2

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; Sequence 201, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
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;; PRIOR APPLICATION NUMBER: 60/091478

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;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 99; DB 9; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.2e-88;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKIPVLPVAVLLSLVLSAQAATLGPEEESTIENYASRPEAFNTPLNIDKLSAFKA 60  
QY 61 DEFLNMHALFESIKRKLPLFNWDAFPKLGKLSATPDQA 99  
Db 61 DEFLNMHALFESIKRKLPLFNWDAFPKLGKLSATPDQA 99

RESULT 3  
US-09-989-279-201  
; Sequence 201, Application US/09989279  
; Patent No. US20020072496A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC56  
; CURRENT APPLICATION NUMBER: US/09/989,279  
;; PRIOR FILING DATE: 2001-11-19  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/065186  
;; PRIOR FILING DATE: 1997-11-12  
;; PRIOR APPLICATION NUMBER: 60/065311  
;; PRIOR FILING DATE: 1997-11-13  
;; PRIOR APPLICATION NUMBER: 60/066770  
;; PRIOR FILING DATE: 1997-11-24

**ପାଠ ୫**

[illegible]

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; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-09
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Query Match      100.0%; Score 99; DB 9; Length 99;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MKIPVLPAVLLSLVLSHSAQATLGGPEESTIENYASRBEAFNTPLNIDKLSAFKA 60
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QY      61 DEFLNMHALFESIKRKLPLFNMDAFPKLKGKLSATPDAQ 99
Db      61 DEFLNMHALFESIKRKLPLFNMDAFPKLKGKLSATPDAQ 99
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## RESULT 4

US-09-989-727-201

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; Sequence 201, Application US/09989727
; Patent No. US20020072497A1
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## GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C65
; CURRENT APPLICATION NUMBER: US/09/989,727
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
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;; PRIOR FILING DATE: 1998-07-07  
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;; PRIOR FILING DATE: 1998-07-07  
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;; PRIOR FILING DATE: 1998-07-09  
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Best Local Similarity 100.0%; Pred. No. 3.2e-88;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKIPVLPVAVLTLVLVLSAQAATLGGPEESTIENYASRPEAFNTPLNIDKLSAFKA 60  
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; Patent No. US20020103125A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C70  
; CURRENT APPLICATION NUMBER: US/09/989,731  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/065186  
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;; PRIOR APPLICATION NUMBER: 60/066770  
;; PRIOR FILING DATE: 1997-11-24  
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;; PRIOR FILING DATE: 1998-02-25  
;; PRIOR APPLICATION NUMBER: 60/078910  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/083322  
;; PRIOR FILING DATE: 1998-04-28



1 PRIOR APPLICATION NUMBER: 60/084600  
2 PRIOR FILING DATE: 1998-05-07  
3 PRIOR APPLICATION NUMBER: 60/087106  
4 PRIOR FILING DATE: 1998-05-28  
5 PRIOR APPLICATION NUMBER: 60/087607  
6 PRIOR FILING DATE: 1998-06-02  
7 PRIOR APPLICATION NUMBER: 60/087609  
8 PRIOR FILING DATE: 1998-06-02  
9 PRIOR APPLICATION NUMBER: 60/087759  
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11 PRIOR APPLICATION NUMBER: 60/087827  
12 PRIOR FILING DATE: 1998-06-03  
13 PRIOR APPLICATION NUMBER: 60/088021  
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73 PRIOR APPLICATION NUMBER: 60/089600

74 PRIOR FILING DATE: 1998-06-17  
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87 PRIOR APPLICATION NUMBER: 60/089952  
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90 PRIOR FILING DATE: 1998-06-22  
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94 PRIOR FILING DATE: 1998-06-22  
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137 PRIOR APPLICATION NUMBER: 60/091478  
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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 99; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.2e-88;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVLPAVVLISLVLSAOGATLGGEESTIENYASRPEAFNTPLNIDKLSAFKA 60  
1 MKIPVLPAVVLISLVLSAOGATLGGEESTIENYASRPEAFNTPLNIDKLSAFKA 60  
Db

QY 61 DEFLNWFALFESIKRKLPLFNWDAPPKLKGLSATPDAQ 99  
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Db

## RESULT 6

US-09-989-732-201  
Sequence 201, Application US/09989732  
Patent No. US20020123463A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Geritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C57

CURRENT APPLICATION NUMBER: US/09/989,732

PRIOR FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

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PRIOR APPLICATION NUMBER: 60/083322

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; PRIOR APPLICATION NUMBER: 60/091982

; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 99; DB 10; length 99;  
Best Local Similarity 100.0%; Pred. No. 3.2e-88;  
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US-09-991-073-201

; Sequence 201, Application US/09991073  
; Patent No. US20020127576A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

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; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730P1C15

; CURRENT APPLICATION NUMBER: US/09/991, 073

; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

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; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
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; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
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; APPLICANT: Kljavin, Ivar J.  
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; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C8  
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Query Match 100.0%; Score 99; DB 10; Length 99;  
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D 61 DEFLNHALFESIKRKLPLNWDAPPKLKGSRATPDAQ 99  
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; Patent No. US20020132253A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C17  
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; GENERAL INFORMATION:  
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; APPLICANT: Baker, Kevin P.  
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PRIOR FILING DATE: 1998-07-09

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APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
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APPLICANT: Ferrara, Napoleone  
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APPLICANT: Gerritsen, Mary E.  
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APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C22  
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APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
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RESULT 13

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; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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; APPLICANT: Zhang, Zemin
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US-09-984-245-142  
; Sequence 142, Application US/09984245  
; Patent No. US20020165374A1

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;; GENERAL INFORMATION:
;; APPLICANT: Young et al.
;; TITLE OF INVENTION: 87 Human Secreted Proteins
;; FILE REFERENCE: P2004P1
;; CURRENT APPLICATION NUMBER: US/09/984,245
;; PRIOR FILING DATE: 2001-10-29
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;; ORGANISM: Homo sapiens
;; US-09-984-245-142

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; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Saton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C66
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;; PRIOR FILING DATE: 1998-07-09

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Db 61 DEFINWHALESIKRKLPIFNWDAPFKLGLSATPDAQ 99

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Job time : 25 Bees

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 08:57:54 ; Search time 2857 Seconds

(without alignments)  
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Title: US-10-059-395-142

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

SUMMARIES

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14	72	72.7	432	6 AX080815	AX080815 Sequence
15	72	72.7	432	6 AX080818	AX080818 Sequence
16	56	56.6	278	6 AX041085	AX041085 Sequence
17	29	29.3	44679	9 CH19F21246	AD001502 Homo sapi
18	10	10.1	140640	9 AC113165	AC113165 Homo sapi
19	10	10.1	159120	2 AC021395	AC021395 Homo sapi
20	10	10.1	168108	9 AC104119	AC104119 Homo sapi
21	10	10.1	222490	9 AL353801	AL353801 Human DNA
22	9	9.1	8714	4 BTU19467	UI9467 Bos taurus
23	9	9.1	28853	3 CBRG18D16	AC084517 Caenorhab
24	9	9.1	36159	6 AR220021	AR220021 Sequence
25	9	9.1	36159	6 AX555110	AX555110 Sequence
26	9	9.1	38518	2 AC094453_7	Continuation (8 of
27	9	9.1	48253	9 AL731797	AL731797 Human DNA
28	9	9.1	48700	9 AP000558	AP000558 Homo sapi
29	9	9.1	82938	6 AX661200	AX661200 Sequence
30	9	9.1	87943	9 AC095064	AC095064 Homo sapi
31	9	9.1	94634	9 AC096592	AC096592 Homo sapi
32	9	9.1	122012	9 AC008388	AC008388 Homo sapi
33	9	9.1	127437	9 AC105312	AC105312 Homo sapi
34	9	9.1	130946	10 AC129310	AC129310 Mus muscu
35	9	9.1	133104	9 AL451070	AL451070 Human DNA
36	9	9.1	137327	8 AC135206	AC135206 Oryza sat
37	9	9.1	149123	2 BX255947	BX255947 Danio rer
38	9	9.1	158696	2 AC025955	AC025955 Homo sapi
39	9	9.1	160525	2 AC027074	AC027074 Homo sapi
40	9	9.1	166447	9 AC018751	AC018751 Homo sapi
41	9	9.1	167441	2 AC092528	AC092528 Papio anu
42	9	9.1	169237	9 AC009516	AC009516 Homo sapi
43	9	9.1	169418	2 AC116507	AC116507 Mus muscu
44	9	9.1	173432	2 AC141166	AC141166 Rattus no
45	9	9.1	176042	2 AL645822	AL645822 Danio rer

RESULT 1

ALIGNMENTS

AX055438  
LOCUS AX055438 414 bp DNA linear PAT 13-JAN-2001  
DEFINITION Sequence 68 from Patent WO0073452.  
ACCESSION AX055438  
VERSION AX055438.1 GI:12228711  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Ashkenazi, A.J., Baker, K.P., Chan, B., Goddard, A., Godowski, P.J., Gurney, A.L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D.L., Tumas, D., Watanabe, C.K. and Wood, W.I.  
TITLE Compositions and methods for the treatment of immune related diseases  
JOURNAL Patent: WO 0073452-A 68 07-DEC-2000;  
FEATURES  
source location/Qualifiers  
1.414  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 98 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 9.6e-96 Length: 414  
Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-059-395-142 (1-99) x AX055438 (1-414)

QY 1 MetLysIleProValLeuProAlaValIleuSerLeuValIleuHisSerAla 20  
DB 13 ATGAAGATCCCGGTCCTTCCCTGCGGTGCTCTCCCTCCCTGCTCCACTGCGC 72  
QY 21 GInGlyAlaThrLeuGlyGlyProGluGluSerThrIleGluAsnTyrAlaSerArg 40  
DB 73 CAGGAGCCACCCTGGGTGCTCTGAGAGAAAGACCATGGAATTATGCGTCACGA 132  
QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
DB 133 CCCGAGGCTTTAAACACCCCGTCTCTGAACATCGACAAATTGCGATCTGAAGGCT 192  
QY 61 AspGluPheLeuAsnThrPheIleAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
DB 193 GATGATTCCTGAACCTGGCAGCGCCCTTTTGAAGTATCAAAAGAACTTCTTCTC 252  
QY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
DB 253 AACTGGGATGCTTCTTCTTAAGCTGAAGAGACTGAGAGCGCACTCTGATGCCAG 309

RESULT 2  
AR252517 415 bp DNA linear PAT 20-DEC-2002  
LOCUS AR252517  
DEFINITION Sequence 200 from patent US 6478825.  
ACCESSION AR252517  
VERSION AR252517.1 GI:27300425  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 415)  
AUTHORS Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.  
TITLE Implant, method of making same and use of the implant for the treatment of bone defects  
JOURNAL Patent: US 6478825-A 200 12-NOV-2002;  
FEATURES  
source location/Qualifiers  
1.415

BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN /organism="unknown"

Alignment Scores:  
Pred. No.: 9.62e-96 Length: 415  
Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-059-395-142 (1-99) x AR252517 (1-415)

QY 1 MetLysIleProValLeuProAlaValIleuSerLeuValIleuHisSerAla 20  
DB 13 ATGAAGATCCCGGTCCTTCCCTGCGGTGCTCTCCCTCCCTGCTCCACTGCGC 72  
QY 21 GInGlyAlaThrLeuGlyGlyProGluGluSerThrIleGluAsnTyrAlaSerArg 40  
DB 73 CAGGAGCCACCCTGGGTGCTCTGAGAGAAAGACCATGGAATTATGCGTCACGA 132  
QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
DB 133 CCCGAGGCTTTAAACACCCCGTCTCTGAACATCGACAAATTGCGATCTGAAGGCT 192  
QY 61 AspGluPheLeuAsnThrPheIleAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
DB 193 GATGATTCCTGAACCTGGCAGCGCCCTTTTGAAGTATCAAAAGAACTTCTTCTC 252  
QY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
DB 253 AACTGGGATGCTTCTTCTTAAGCTGAAGAGACTGAGAGCGCACTCTGATGCCAG 309

RESULT 3  
AX077031 415 bp DNA linear PAT 22-FEB-2001  
LOCUS AX077031  
DEFINITION Sequence 19 from Patent WO0105972.  
ACCESSION AX077031  
VERSION AX077031.1 GI:13121661  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Ashkenazi, A.J., Baker, K.P., Fong, S., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Mark, M.R., Marsters, S.A., Pitti, R.M., Tumas, D., Watanabe, C.K. and Wood, W.I.  
TITLE Compositions and methods for the treatment of immune related diseases  
JOURNAL Patent: WO 0105972-A 19 25-JAN-2001;  
FEATURES  
source location/Qualifiers  
1.415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 9.62e-96 Length: 415  
Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-059-395-142 (1-99) x AX077031 (1-415)

QY 1 MetLysIleProValLeuProAlaValIleuSerLeuValIleuHisSerAla 20  
DB 13 ATGAAGATCCCGGTCCTTCCCTGCGGTGCTCTCCCTCCCTGCTCCACTGCGC 72  
QY 21 GInGlyAlaThrLeuGlyGlyProGluGluSerThrIleGluAsnTyrAlaSerArg 40  
DB 73 CAGGAGCCACCCTGGGTGCTCTGAGAGAAAGACCATGGAATTATGCGTCACGA 132  
QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
DB 133 CCCGAGGCTTTAAACACCCCGTCTCTGAACATCGACAAATTGCGATCTGAAGGCT 192  
QY 61 AspGluPheLeuAsnThrPheIleAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
DB 193 GATGATTCCTGAACCTGGCAGCGCCCTTTTGAAGTATCAAAAGAACTTCTTCTC 252  
QY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
DB 253 AACTGGGATGCTTCTTCTTAAGCTGAAGAGACTGAGAGCGCACTCTGATGCCAG 309

Db 13 ATGAAGATCCGGTCTTCTGCGGTGCTCTCCCTCCGTGCTCCACTCTGCC 72

QY 21 GlnGlyAlaThrLeuGlyGlyProGluGluSerThrIleGluAsnTyrAlaSerArg 40  
|||||  
Db 73 CAGGAGCCACCTGGGTGCTCTGAGGAAGAACCATTTAGATATGCGTCACGA 132

QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
|||||  
Db 133 CCCGAGGCTTTAAACACCCCGTTCTCTGACATGACAAATTGCGATGCGTTAAGGCT 192

QY 61 AspGluPheLeuAsnTyrPheIleAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
|||||  
Db 193 GATGAGTTCCTGAAGTGGACGCGCCCTTTGAGTCTATCAAAAGAACTTCTTCCCTC 252

QY 81 AsnTyrAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
|||||  
Db 253 AACTGGATGCTTCTCTAAGCTGAAGAGACTGAGAGCGCACTCCTGATGCCAG 309

RESULT 4  
AX358892 415 bp DNA linear PAT 13-FEB-2002  
LOCUS  
DEFINITION Sequence 145 from Patent WO0193983.  
ACCESSION AX358892  
VERSION AX358892.1 GI:18675347  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1 Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,  
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,  
Watanabe,C.K. and Wood,W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0193983-A 145 13-DEC-2001;  
Genentech Inc. (US)  
FEATURES  
Source Location/Qualifiers  
1.415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t

ORIGIN

Alignment Scores:  
Pred. No.: 9.62e-96 Length: 415  
Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-10-059-395-142 (1-99) x AX358892 (1-415)

QY 1 MetLysIleProValLeuProAlaValLeuLeuSerLeuLeuValLeuHisSerAla 20  
|||||  
Db 13 ATGAAGATCCCGTCTTCTGCGGTGCTCTCCCTCCGTGCTCCACTCTGCC 72

QY 21 GlnGlyAlaThrLeuGlyGlyProGluGluSerThrIleGluAsnTyrAlaSerArg 40  
|||||  
Db 73 CAGGAGCCACCTGGGTGCTCTGAGGAAGAACCATTTAGATATGCGTCACGA 132

QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
|||||  
Db 133 CCCGAGGCTTTAAACACCCCGTTCTCTGACATGACAAATTGCGATGCGTTAAGGCT 192

QY 61 AspGluPheLeuAsnTyrPheIleAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
|||||  
Db 193 GATGAGTTCCTGAAGTGGACGCGCCCTTTGAGTCTATCAAAAGAACTTCTTCCCTC 252

QY 81 AsnTyrAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
|||||

Db 253 AACTGGATGCTTCTCTAAGCTGAAGAGACTGAGAGCGCACTCCTGATGCCAG 309

RESULT 5  
AX362385 415 bp DNA linear PAT 15-FEB-2002  
LOCUS  
DEFINITION Sequence 145 from Patent WO0208288.  
ACCESSION AX362385  
VERSION AX362385.1 GI:18694650  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1 Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,  
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,  
Watanabe,C.K. and Wood,W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0208288-A 145 31-JAN-2002;  
Genentech, Inc. (US)  
FEATURES  
Source Location/Qualifiers  
1.415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t

ORIGIN

Alignment Scores:  
Pred. No.: 9.62e-96 Length: 415  
Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-10-059-395-142 (1-99) x AX362385 (1-415)

QY 1 MetLysIleProValLeuProAlaValLeuLeuSerLeuLeuValLeuHisSerAla 20  
|||||  
Db 13 ATGAAGATCCCGTCTTCTGCGGTGCTCTCCCTCCGTGCTCCACTCTGCC 72

QY 21 GlnGlyAlaThrLeuGlyGlyProGluGluSerThrIleGluAsnTyrAlaSerArg 40  
|||||  
Db 73 CAGGAGCCACCTGGGTGCTCTGAGGAAGAACCATTTAGATATGCGTCACGA 132

QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
|||||  
Db 133 CCCGAGGCTTTAAACACCCCGTTCTCTGACATGACAAATTGCGATGCGTTAAGGCT 192

QY 61 AspGluPheLeuAsnTyrPheIleAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
|||||  
Db 193 GATGAGTTCCTGAAGTGGACGCGCCCTTTGAGTCTATCAAAAGAACTTCTTCCCTC 252

QY 81 AsnTyrAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
|||||

RESULT 6  
AX403313 415 bp DNA linear PAT 14-JUN-2002  
LOCUS  
DEFINITION Sequence 200 from Patent WO0073454.  
ACCESSION AX403313  
VERSION AX403313.1 GI:21436871  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1 Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,  
Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,

Grimaldi, C.J., Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J.,  
Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,  
Williams, P., Wood, W.I. and Zhang, Z.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same

JOURNAL Patent: WO 0073454-A 200 07-DEC-2000;  
Genentech Inc. (US)

FEATURES Location/Qualifiers  
source 1..415

BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN /organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

## Alignment Scores:

Pred. No.: 9.62e-96 Length: 415  
Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142 (1-99) x AX403313 (1-415)

QY 1 MetLysIleProValIleuProAlaValIleuSerIleuValIleuHisSerAla 20  
Db 13 ATGAAGATCCCGGTCTCTGCGTGTGCTCTCTCCCTCGTGTGCTCCACTGCGC 72  
QY 21 GlnGlyAlaThrIleuGlyGlyProGluGluGluSerThrIleGluAsnTyrAlaSerArg 40  
Db 73 CAGGAGCCACCCTGGGTGTCTGAGGAAGAACACCATGAGATTATGCGTCACGA 132  
QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspIleuArgSerAlaPheIleAla 60  
Db 133 CCCGAGCCCTTAACACCCCGTCTGACATCGACAAATTGCGATCTGCGTTAAGGCT 192  
QY 61 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleIleArgIleuProPheLeu 80  
Db 193 GATGAGTTCCTGAACCTGGACGCCCTCTTTGAGTCTATCAAAAGAACTTCTTCCTC 252  
QY 81 AsnTrpAspAlaPheProIleuLeuGlyLeuArgSerAlaThrProAspAlaGln 99  
Db 253 AACTGGATGCTTCTTAAGCTGAAGAGACTGAGGAGCGCAACTCTGATGCCCGC 309

RESULT 7  
AX454546 415 bp DNA linear PAT 06-JUL-2002  
LOCUS Sequence 131 from Patent WO0208284.

DEFINITION AX454546  
ACCESSION AX454546  
VERSION AX454546.1 GI:21713897  
KEYWORDS

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1  
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
and Ye, W.

TITLE Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis

JOURNAL Patent: WO 0208284-A 131 31-JAN-2002;  
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone

(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,  
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;  
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)  
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;  
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William  
I. (US)

FEATURES Location/Qualifiers  
source 1..415

BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN /organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

## Alignment Scores:

Pred. No.: 9.62e-96 Length: 415  
Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142 (1-99) x AX454546 (1-415)

QY 1 MetLysIleProValIleuProAlaValIleuSerIleuValIleuHisSerAla 20  
Db 13 ATGAAGATCCCGGTCTCTGCGTGTGCTCTCTCCCTCGTGTGCTCCACTGCGC 72  
QY 21 GlnGlyAlaThrIleuGlyGlyProGluGluGluSerThrIleGluAsnTyrAlaSerArg 40  
Db 73 CAGGAGCCACCCTGGGTGTCTGAGGAAGAACACCATGAGATTATGCGTCACGA 132  
QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspIleuArgSerAlaPheIleAla 60  
Db 133 CCCGAGCCCTTAACACCCCGTCTGACATCGACAAATTGCGATCTGCGTTAAGGCT 192  
QY 61 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleIleArgIleuProPheLeu 80  
Db 193 GATGAGTTCCTGAACCTGGACGCCCTCTTTGAGTCTATCAAAAGAACTTCTTCCTC 252  
QY 81 AsnTrpAspAlaPheProIleuLeuGlyLeuArgSerAlaThrProAspAlaGln 99  
Db 253 AACTGGATGCTTCTTAAGCTGAAGAGACTGAGGAGCGCAACTCTGATGCCCGC 309

RESULT 8  
AX491024 415 bp DNA linear PAT 16-AUG-2002  
LOCUS Sequence 131 from Patent WO0200690.

DEFINITION AX491024  
ACCESSION AX491024  
VERSION AX491024.1 GI:22323849  
KEYWORDS

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1  
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
and Ye, W.

TITLE Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis

JOURNAL Patent: WO 0200690-A 131 03-JAN-2002;  
Genentech, Inc. (US)

FEATURES Location/Qualifiers  
source 1..415

BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN /organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

## Alignment Scores:

Pred. No.: 9.62e-96 Length: 415  
Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142 (1-99) x AX491024 (1-415)



QY 1 MetLysIleProValIleuProAlaValIleuLeuSerIleuLeuValIleuHisSerAla 20  
Db 13 ATGAAGATCCCGGTCTTCTGCGGTGCTCTCTCCCTCTGCTGCTCACTCTGCC 72  
QY 21 GInGIYAlaThrIleuGIYGIYProGIUGIUGIuSerThrIleGIuAsnTYrAlaSerArg 40  
Db 73 CAGGAGCCACCCCTGGGTGCTCTGAGGAGAAAGACCATGTGAAATTATGCTTCACGA 132  
QY 41 ProGIuAlaPheAsnThrProPheLeuAsnIleAspIYsLeuArgSerAlaPheYsAla 60  
Db 133 CCCGAGGCTTAAACACCCCGTTCCTGACATCGACAAATTGCGATCTGCTTAAAGCT 192  
QY 61 AspGIuPheLeuAsnTYrPheIleAlaLeuPheGIuSerIleYsArgIYsLeuProPheLeu 80  
Db 193 GATGAGTTCCTGAAGTGGACGCCCTCTTGAAGTCTATCAAAAGAAACTTCTTCCTC 252  
QY 81 AsnTYrAspAlaPheProIYsLeuIYsGIYLeuArgSerAlaThrProAspAlaGln 99  
Db 253 AACTGGATGCTTCTCTAAGCTGAAGGAGACTGAGAGCGCAACTCTGATGCCAG 309  
RESULT 9  
AX574494 415 bp DNA linear PAT 07-JAN-2003  
LOCUS Sequence 21 from Patent WO0224888.  
ACCESSION AX574494  
VERSION AX574494.1 GI:27551800  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE  
1 Baker, K.P., Eaton, D.L., Filvaroff, E., Goddard, A., Grimaldi, J.C.,  
Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K., Wood, W.I.,  
Zhang, Z. and Fong, S.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0224888-A 21 28-MAR-2002;  
GENENTECH, INC. (US)  
FEATURES  
source 1. .415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 9.62e-96 length: 415  
Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-10-059-395-142 (1-99) x AX574494 (1-415)  
QY 1 MetLysIleProValIleuProAlaValIleuLeuSerIleuLeuValIleuHisSerAla 20  
Db 13 ATGAAGATCCCGGTCTTCTGCGGTGCTCTCTCCCTCTGCTGCTCACTCTGCC 72  
QY 21 GInGIYAlaThrIleuGIYGIYProGIUGIUGIuSerThrIleGIuAsnTYrAlaSerArg 40  
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LOCUS BD082389  
DEFINITION 87 human secreted proteins.  
ACCESSION BD082389  
VERSION BD082389.1 GI:22627999  
KEYWORDS JP 2001522239-A/31.  
SOURCE Mastadenovirus  
ORGANISM Mastadenovirus  
Viruses; dsDNA viruses, no RNA stage; Adenoviridae.  
REFERENCE  
1 (bases 1 to 456)  
Young, P., Greene, J.M., Ferrie, A.M., Ruben, S.M., Rosen, C.A.,  
Duan, R.D., Hu, J.S., Florence, K.A., Olsen, H.S., Ebner, R.,  
Brewer, L.A., Moore, P.A., Shi, Y., Lafleur, D.W. and Ni, J.  
TITLE 87 human secreted proteins  
JOURNAL Patent: JP 2001522239-A 31 13-NOV-2001;  
HUMAN GENOME SCIENCES INC SECRETARY OF THE DEPARTMENT OF HEALTH  
HUMAN SERVICES  
PN JP 2001522239-A/31  
PD 13-NOV-2001  
PF 19-MAR-1998 JP 1998542119  
PR 21-MAR-1997 US 60/041281, 21-MAR-1997 US 60/041276 PR  
21-MAR-1997 US 60/042344, 21-MAR-1997 US 60/041277 PR  
30-MAY-1997 US 60/048355, 30-MAY-1997 US 60/048096 PR  
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30-MAY-1997 US 60/048160, 30-MAY-1997 US 60/048069 PR  
30-MAY-1997 US 60/048131, 30-MAY-1997 US 60/048186 PR  
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30-MAY-1997 US 60/048099, 30-MAY-1997 US 60/050937 PR  
30-MAY-1997 US 60/048352, 30-MAY-1997 US 60/048135 PR  
30-MAY-1997 US 60/048350, 30-MAY-1997 US 60/048094 PR  
30-MAY-1997 US 60/048350, 05-AUG-1997 US 60/054804 PR  
19-AUG-1997 US 60/056370, 02-OCT-1997 US 60/060862 PI  
YOUNG, JOHN M GREENE, ANN M FERRIE, STEVEN M RUBEN, CRAIG A PI  
ROSEN, C  
PI ROXANNE D DUAN, JING SHAN HU, KIMBERLY A FLORENCE, HENRIK S  
OLSEN, H  
PI REINHARD EBNER, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W  
PI LAFLEUR, D  
PI JIAN NI  
PC C07K14/00  
CC Strandedness: Double;  
CC Topology: Linear;  
FH Key  
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ACCESSION      AX080817
VERSION      AX080817.1  GI:13169786
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SOURCE      .
ORGANISM      synthetic construct
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              artificial sequences.
REFERENCE      1
AUTHORS      Ashkenazi,A.J., Baker,K.P., Goddard,A., Godowski,P.J., Gurney,A.L.,
              Kljavin,I.J., Lafleur,M., Mark,M.R., Marsters,S.A., Pitti,R.M.,
              Watanabe,C.K. and Wood,W.I.
              Method of preventing the injury or death of retinal cells and
              treating ocular diseases
              Patent: WO 0109327-A 63 08-FEB-2001;
              Genentech, Inc. (US)
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      140 CAGGAGACCCACCTGGGTGCTGAGGAAGAACACCATGAGATTATGCTGACGA 199
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Qy      61 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80
      260 GATGAGTTCCTGAACCTGGACAGCGCCCTCTTGAGTCTATCAAAAGAACTCCTTCCCTC 319
Db      81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99
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ACCESSION      AX080816
VERSION      AX080816      GI:13169785
KEYWORDS
SOURCE      .
ORGANISM      synthetic construct
              synthetic construct
              artificial sequences.
REFERENCE      1
AUTHORS      Ashkenazi,A.J., Baker,K.P., Goddard,A., Godowski,P.J., Gurney,A.L.,
              Kljavin,I.J., Lafleur,M., Mark,M.R., Marsters,S.A., Pitti,R.M.,
              Watanabe,C.K. and Wood,W.I.
              Method of preventing the injury or death of retinal cells and
              treating ocular diseases
              Patent: WO 0109327-A 62 08-FEB-2001;
              Genentech, Inc. (US)
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DB:      6
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      75 CAGGAGACCCACCTGGGTGCTGAGGAAGAACACCATGAGATTATGCTGACGA 134
Qy      41 -ProgluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaThrProAspAla 60
      135 CCCGAGGCGCTTTAACACCCCGCTTCTGAAACATGACAAATTGCGATCTGCTTAAGGC 194
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Qy      80 uAsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99
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LOCUS      Homo sapiens mRNA differentially expressed in malignant melanoma,
ACCESSION      clone NM 15.
VERSION      AJ293408
AJ293408.1  GI:27526545
KEYWORDS      differential expression; malignant; melanoma.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1
AUTHORS      Deichmann,M., Thome,M., Wacker,J. and Naehrer,H.
TITLE      Genes differentially expressed in malignant melanoma
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Qy 61 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
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Db 192 GATGAGTTCTGAACTGGCAGCGCCCTTTGAGTCTATCAAAAGAAACTTCTTCTC 251  
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Search completed: November 28, 2003, 10:23:47  
Job time : 2863 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 08:40:10 ; Search time 231 Seconds

(without alignments)  
1156.902 Million cell updates/sec

Title: US-10-059-395-142

Perfect score: 99

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Searched: 2552756 seqs, 1349719017 residues

Word size: 1

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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2	99	100.0	414	24 ABK28600	Human DNA57694-134
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6	99	100.0	415	22 AAC97491	Human angiogenesis
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9	99	100.0	415	24 ABL88137	Human PRO826 cDNA
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19	99	100.0	428	24 ABZ11803	Human polynucleoti
20	99	100.0	456	20 AAX00632	Human secreted pro
21	89	89.9	518	22 ABA09519	Human secreted pro
22	56	56.6	278	21 AAC68806	Human head/neck tu
23	56	56.6	305	24 ABZ11886	Human polynucleoti
24	44	44.4	386	24 ABZ11804	Human polynucleoti
25	9	9.1	36159	24 ABN85329	Human kinase gene.
26	9	9.1	82938	24 ABV72623	Human transporter
27	8	8.1	45	17 AAT42481	Human transp
28	8	8.1	263	22 ABA75510	Human foetal liver
29	8	8.1	263	22 ABA40130	Probe #18596 for g
30	8	8.1	263	22 AAK24082	Human brain expres
31	8	8.1	263	22 AAK50145	Human bone marrow
32	8	8.1	263	22 AAI27228	Probe #17161 for g
33	8	8.1	263	22 AAI56085	Probe #24771 used
34	8	8.1	263	23 ABS49777	Human liver single
35	8	8.1	263	24 ABS23621	Human genome-deriv
36	8	8.1	278	25 ABX82738	Corn ear-derived p
37	8	8.1	307	22 ABA47823	Human breast cell
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40	8	8.1	307	22 AAK14115	Human brain expres
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ALIGNMENTS

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DT 21-MAR-2001 (first entry)	
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KW antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;	
KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;	
KW antiallergic; antiasthmatic; immune related disorder;	
KW hepatobiliary disease; autoimmune disease; allergy; ss.	
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OS Homo sapiens.	



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PD 07-DEC-2000.  
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PF 02-JUN-2000; 2000WO-US15264.  
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PR 20-JUL-1999; 99US-0144732.  
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PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 29-OCT-1999; 99US-0162506.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28634.  
PR 09-DEC-1999; 99US-0170262.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
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PR 22-MAY-2000; 2000WO-US14042.  
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PA (GETH ) GENENTECH INC.  
PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AJ;  
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;  
PI Wood WI;  
XX  
XX WPI; 2001-025253/03.  
DR P-PSDB; AAB50916.  
DR  
XX  
XX Thirty three nucleic acids encoding PRO polypeptides which are useful  
PT in the diagnosis and treatment of immune related disorders, e.g.  
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
PT thyroiditis and diabetes mellitus -  
XX  
XX Claim 48; Fig 29; 218pp; English.  
PS  
XX The present sequence is one of thirty three nucleic acids encoding PRO  
CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and  
CC antagonists are useful for treating and diagnosing immune related  
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis,  
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
CC demyelinating polynuropathy or Guillain-Barre syndrome, and chronic  
CC inflammatory demyelinating polynuropathy), hepatobiliary diseases  
CC (such as infectious, autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
CC food hypersensitivity and urticaria), immunological diseases of the  
CC lung (such as eosinophilic pneumonitis, idiopathic pulmonary fibrosis  
CC and hypersensitivity pneumonitis), transplantation associated diseases  
CC including graft rejection and graft-versus-host diseases.  
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XX Sequence 414 BP; 98 A; 126 C; 92 G; 98 T; 0 other;  
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Db 193 GATGAGTTCCTGAACCTGGCACGCCCCTTTGAGTCTATCAAAAGAAACTTCTTCTC 252  
QY 81 AsnTrpAspAlaPheProLysLeuGIyGIyLeuArgSerAlaThrProAspAlaGIu 99  
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XX  
XX DT 09-APR-2002 (first entry)  
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XX DE Human DNA57694-1341 encoding PRO826.  
XX  
XX KW Human; ss; gene; PRO; antiinflammatory; ophthalmological; vasotropic;  
KW retinal cell injury; ocular disease; retinitis pigmentosa;  
KW macular degeneration; retinal detachment; retinal tear; retinopathy;  
KW retinal degenerative disease; macular hole; degenerative myopia;  
KW acute retinal necrosis syndrome; traumatic chorioretinopathy;  
KW Purtscher's retinopathy; oedema; ischaemic condition;  
KW retinal vision occlusion; collagen vascular disease;  
KW thrombocytopaenic purpura; uveitis; retinal vasculitis; Bales disease;  
KW systemic lupus erythematosus; environmental trauma.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200109327-A2.  
XX  
XX PD 08-FEB-2001.  
XX  
XX PF 28-JUL-2000; 2000WO-US20710.  
XX  
XX PR 28-JUL-1999; 99US-146222P.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.

PR -30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL,  
PI Kljavin IJ, Lafleur M, Mark MR, Marsters SA, Pitti RM;  
PI Watanabe CK, Wood WI;  
XX  
DR WPI; 2002-130120/17.  
DR P-PSDB; AAU81964.  
XX  
XX  
PT Promoting survival of retinal cells, or delaying or preventing retinal  
PT cell injury or death, by contacting retinal cells with PRO175, 220,  
PT 216, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132  
PT polypeptide -  
XX  
XX  
PS Claim 33; Fig 24; 152pp; English.  
XX  
CC The invention relates to promoting the survival of retinal cells, or  
CC delaying or preventing retinal cell injury or death, by contacting the  
CC retinal cells with the polypeptide such as PRO175, PRO220, PRO216,  
CC PRO243, PRO306, PRO346, PRO322, PRO536, PRO943, PRO840, PRO828, PRO826,  
CC PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids  
CC encoding the PRO proteins, a vector comprising the nucleic acid, a host  
CC cell comprising the vector, and anti-PRO antibody. The PRO proteins are  
CC useful for promoting survival of retinal cells (retinal neurons such as  
CC retinal ganglion cells, displaced retinal ganglion cells, amacrine  
CC cells, displaced amacrine cells, horizontal neurons or bipolar neurons,  
CC rod photoreceptors, or supportive cells such as Muller cells or pigment  
CC epithelial cells), or delaying or preventing retinal cell injury or  
CC death caused by ocular disease (which is or is associated with  
CC retinitis pigmentosa, macular degenerative disease, macular detachment, retinal  
CC tear, retinopathy, retinal degenerative disease, macular hole,  
CC degenerative myopia, acute retinal necrosis syndrome, traumatic  
CC chorioretinopathy or contusion, Purtscher's retinopathy, oedema, an  
CC ischaemic condition, central or branch retinal vision occlusion,  
CC collagen vascular disease, thrombocytopenic purpura, uveitis, retinal  
CC vasculitis, occlusion associated with Bales disease or systemic lupus  
CC erythematosus), retinal injury or environmental trauma. The retinal  
CC cell injury or death is delayed or prevented by substantially not  
CC causing angiogenesis or mitogenesis. The present sequence is a CDNA  
CC encoding a PRO protein.  
XX  
SQ Sequence 414 BP; 98 A; 126 C; 92 G; 98 T; 0 other;  
Alignment Scores:  
Pred. No.: 7.24e-88 Length: 414  
Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0  
US-10-059-395-142 (1-99) x ABK28600 (1-414)  
QY 1 MetLysIleProValIleuProAlaValIleuSerLeuLeuValIleuHisSerAla 20  
Db 13 ATGAAGATCCCGGCTCTCTCCGCGTGTCTCTCTCCCTCTGTCCTGCTCACTGACC 72  
QY 21 GInGIAlaThrLeuGIyGIYProGIuGIuGIuSerThrIleGIuAsnTYAlaSerArg 40  
Db 73 CAGGAGCCACCCTGGGTGCTCTGAGGAAGAACACCATTTAGAAATTAAGCTACGCA 132  
QY 41 ProGIuAlaPheAsnThrProPheLeuAsnIleAspIlyLeuArgSerAlaPheIysAla 60  
Db 133 CCCGAGGCTTTAACACCCCGTCTCTGAACATGCACAATTGCGATCTGCTTAAGGCT 192  
QY 61 AspGIuPheLeuAsnThrPheIleAlaLeuPheGIuSerIleIysArgIlyLeuProPheLeu 80  
Db 193 GATGAGTTCCTGAAGTGGACAGCCCTTTGAGTCTATCAAAAGAACTTCCTTCCCTC 252  
QY 81 AsnTrpAspAlaPheProIyIleuIyGIyLeuArgSerAlaThrProAspAlaGIu 99

DB 253 AACTGGATGCCTTCTCCTAAGCTGAAGAACTGAGAGCGCACTCCTGATGCCAG 309  
RESULT 3  
AAZ65018  
ID AAZ65018 standard; cDNA; 415 BP.  
XX  
AC AAZ65018;  
XX  
DT 05-APR-2000 (first entry)  
XX  
DE Membrane-bound protein PRO826 encoding cDNA.  
XX  
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9963088-A2.  
XX  
PD 09-DEC-1999.  
XX  
PF 02-JUN-1999; 99WO-US12252.  
XX  
PR 02-JUN-1998; 98US-0087607.  
PR 02-JUN-1998; 98US-0087609.  
PR 02-JUN-1998; 98US-0087759.  
PR 03-JUN-1998; 98US-0087827.  
PR 04-JUN-1998; 98US-0088021.  
PR 04-JUN-1998; 98US-0088025.  
PR 04-JUN-1998; 98US-0088028.  
PR 04-JUN-1998; 98US-0088029.  
PR 04-JUN-1998; 98US-0088030.  
PR 04-JUN-1998; 98US-0088033.  
PR 04-JUN-1998; 98US-0088326.  
PR 05-JUN-1998; 98US-0088167.  
PR 05-JUN-1998; 98US-0088202.  
PR 05-JUN-1998; 98US-0088212.  
PR 05-JUN-1998; 98US-0088217.  
PR 09-JUN-1998; 98US-0088655.  
PR 10-JUN-1998; 98US-0088722.  
PR 10-JUN-1998; 98US-0088730.  
PR 10-JUN-1998; 98US-0088734.  
PR 10-JUN-1998; 98US-0088738.  
PR 10-JUN-1998; 98US-0088740.  
PR 10-JUN-1998; 98US-0088741.  
PR 10-JUN-1998; 98US-0088742.  
PR 10-JUN-1998; 98US-0088810.  
PR 10-JUN-1998; 98US-0088811.  
PR 10-JUN-1998; 98US-0088824.  
PR 10-JUN-1998; 98US-0088825.  
PR 10-JUN-1998; 98US-0088826.  
PR 11-JUN-1998; 98US-0088858.  
PR 11-JUN-1998; 98US-0088861.  
PR 11-JUN-1998; 98US-0088863.  
PR 11-JUN-1998; 98US-0088876.  
PR 12-JUN-1998; 98US-0089090.  
PR 12-JUN-1998; 98US-0089105.  
PR 16-JUN-1998; 98US-0089440.  
PR 16-JUN-1998; 98US-0089512.  
PR 16-JUN-1998; 98US-0089514.  
PR 17-JUN-1998; 98US-0089532.  
PR 17-JUN-1998; 98US-0089538.  
PR 17-JUN-1998; 98US-0089598.  
PR 17-JUN-1998; 98US-0089599.  
PR 17-JUN-1998; 98US-0089600.  
PR 17-JUN-1998; 98US-0089653.  
PR 18-JUN-1998; 98US-0089801.  
PR 18-JUN-1998; 98US-0089907.  
PR 18-JUN-1998; 98US-0089908.  
PR 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089948.  
PR 19-JUN-1998; 98US-0089952.

PR 22-JUN-1998; 98US-0090246.  
PR 22-JUN-1998; 98US-0090252.  
PR 22-JUN-1998; 98US-0090254.  
PR 23-JUN-1998; 98US-0090349.  
PR 23-JUN-1998; 98US-0090355.  
PR 24-JUN-1998; 98US-0090429.  
PR 24-JUN-1998; 98US-0090431.  
PR 24-JUN-1998; 98US-0090435.  
PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090445.  
PR 24-JUN-1998; 98US-0090461.  
PR 24-JUN-1998; 98US-0090472.  
PR 24-JUN-1998; 98US-0090535.  
PR 24-JUN-1998; 98US-0090538.  
PR 24-JUN-1998; 98US-0090540.  
PR 24-JUN-1998; 98US-0090557.  
PR 25-JUN-1998; 98US-0090676.  
PR 25-JUN-1998; 98US-0090678.  
PR 25-JUN-1998; 98US-0090688.  
PR 25-JUN-1998; 98US-0090690.  
PR 25-JUN-1998; 98US-0090691.  
PR 25-JUN-1998; 98US-0090694.  
PR 25-JUN-1998; 98US-0090695.  
PR 25-JUN-1998; 98US-0090696.  
PR 26-JUN-1998; 98US-0090862.  
PR 26-JUN-1998; 98US-0090863.  
PR 01-JUL-1998; 98US-0091358.  
PR 01-JUL-1998; 98US-0091360.  
PR 01-JUL-1998; 98US-0091544.  
PR 02-JUL-1998; 98US-0091478.  
PR 02-JUL-1998; 98US-0091486.  
PR 02-JUL-1998; 98US-0091519.  
PR 02-JUL-1998; 98US-0091626.  
PR 02-JUL-1998; 98US-0091628.  
PR 02-JUL-1998; 98US-0091633.  
PR 02-JUL-1998; 98US-0091646.  
PR 02-JUL-1998; 98US-0091673.  
PR 07-JUL-1998; 98US-0091978.  
PR 07-JUL-1998; 98US-0091982.  
PR 09-JUL-1998; 98US-0092182.  
PR 10-JUL-1998; 98US-0092472.  
PR 20-JUL-1998; 98US-0093339.  
PR 30-JUL-1998; 98US-0094651.  
PR 04-AUG-1998; 98US-0095282.  
PR 04-AUG-1998; 98US-0095285.  
PR 04-AUG-1998; 98US-0095301.  
PR 04-AUG-1998; 98US-0095302.  
PR 04-AUG-1998; 98US-0095318.  
PR 04-AUG-1998; 98US-0095321.  
PR 04-AUG-1998; 98US-0095325.  
PR 10-AUG-1998; 98US-0095916.  
PR 10-AUG-1998; 98US-0095929.  
PR 10-AUG-1998; 98US-0096012.  
PR 11-AUG-1998; 98US-0096143.  
PR 11-AUG-1998; 98US-0096146.  
PR 12-AUG-1998; 98US-0096329.  
PR 17-AUG-1998; 98US-0096757.  
PR 17-AUG-1998; 98US-0096766.  
PR 17-AUG-1998; 98US-0096768.  
PR 17-AUG-1998; 98US-0096773.  
PR 17-AUG-1998; 98US-0096791.  
PR 17-AUG-1998; 98US-0096867.  
PR 17-AUG-1998; 98US-0096891.  
PR 17-AUG-1998; 98US-0096894.  
PR 17-AUG-1998; 98US-0096895.  
PR 17-AUG-1998; 98US-0096897.  
PR 18-AUG-1998; 98US-0096949.  
PR 18-AUG-1998; 98US-0096950.  
PR 18-AUG-1998; 98US-0096959.  
PR 18-AUG-1998; 98US-0096960.  
PR 18-AUG-1998; 98US-0097022.  
PR 19-AUG-1998; 98US-0097141.  
PR 20-AUG-1998; 98US-0097218.

PR 24-AUG-1998; 98US-0097661.  
PR 26-AUG-1998; 98US-0097951.  
PR 26-AUG-1998; 98US-0097952.  
PR 26-AUG-1998; 98US-0097954.  
PR 26-AUG-1998; 98US-0097955.  
PR 26-AUG-1998; 98US-0097971.  
PR 26-AUG-1998; 98US-0097974.  
PR 26-AUG-1998; 98US-0097978.  
PR 26-AUG-1998; 98US-0097979.  
PR 26-AUG-1998; 98US-0097986.  
PR 26-AUG-1998; 98US-0098014.  
PR 31-AUG-1998; 98US-0098525.  
PR 16-SEP-1998; 98US-0100634.  
PR 12-JAN-1999; 99US-0115565.  
XX  
XX (GETH ) GENENTECH INC.  
XX PA  
XX PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK,  
PI Wood WI, Yuan J;  
XX  
XX WPI, 2000-072883/06.  
DR P-PSDB; AAY66681.  
XX  
PT Membrane-bound proteins and related nucleotide sequences -  
XX  
XX PS Claim 2; Fig 128; 822pp; English.  
XX  
CC The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIE  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
CC will also be useful for the preparation of PRO polypeptides, especially  
CC by recombinant techniques.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
Alignment Scores:  
Pred. No.: 7,26e-88 Length: 415  
Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
DB: 21  
US-10-059-395-142 (1-99) x AAZ65018 (1-415)  
QY 1 MetlyslleProvalleuProAlaValleuSerleuValleuHisSera 20  
Db 13 ATGAAGATCCCGGTCTTCTGCGGTGCTCTCTCCCTGCTGCTCACTG 72  
QY 21 GlnGlyAlaThrleuGlyGlyProGluGluSerThrIleGluAsnTyra 40  
Db 73 CAGGAGCCACCTGGGTGCTCTGAGGAAGAACCAATTGAGATTATGCGT 132  
QY 41 ProGluAlaPheAsnThrProPheleuAsnIleAspLySleuArgSera 60  
Db 133 CCGGAGGCTTTAAACACCCCGTTCTGACATGACAAATTGCGATCTGCTT 192  
QY 61 AspGluPheleuAsnTrpHisAlaIleuPheGluSerIleLySArgLyS 80  
Db 193 GATGAGTTCTCGAACTGGACAGCCCTCTTGAATATCAAAAGGAAC 252  
QY 81 AsnTrpAspAlaPheProLySleuLySArgSeraIaThrProAspAla 99  
Db 253 AACTGGATGCTTCTCTAAGCTGAAGGACTGAGAGCGCAACTCTGATGCC 309

RESULT 4  
AAF30059  
ID AAF30059 standard; cDNA; 415 BP.  
XX  
XX AAF30059;  
AC  
XX 30-APR-2001 (first entry)  
DT  
XX Human cDNA encoding PRO826.  
DE  
XX  
XX PRO826; UNQ467; human; immune disease; autoimmune disease;  
KM antirheumatic; antiarthritic; antiinflammatory; antianaemic;  
KM immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
KM hepatocarcinoma; virucide; dermatological; antipsoriatic;  
KM antiaesthetic; antiallergic; immunostimulant; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FH CDS 13..312  
FT /\*tag= a  
FT sig\_peptide 13..78  
FT /\*tag= b  
FT mat\_peptide 79..309  
FT /\*tag= c  
XX  
XX WO200105972-A1.  
XX PD 25-JAN-2001.  
XX  
XX 15-MAR-2000; 2000WO-US06884.  
XX PR 20-JUL-1999; 99US-0144758.  
XX  
XX (GETH ) GENENTECH INC.  
PA  
XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;  
PI Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK;  
PI Wood WI;  
XX WPI; 2001-103149/11.  
DR P-PSDB; AAB20117.  
XX  
XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
PT diagnosing and treating immune-related disorders, such as multiple  
PT sclerosis, rheumatoid arthritis and diabetes -  
PT  
XX Claim 21; Fig 19; 127pp; English.  
PS  
XX The present sequence is that of cDNA clone DNA57694-1341 (ATCC 203017)  
CC encoding novel human immunomodulator protein PRO826 (UNQ467) (see  
CC AAB20117). The clone was isolated following a database search by  
CC applying a signal sequence algorithm. The predicted protein has a  
CC mol.wt. of 11 kDa and a pI of 7.47. The invention provides  
CC polynucleotides (see AAF30050-62) encoding novel human PRO proteins  
CC (see AAB20108-20) including PRO826. Claimed compositions  
CC comprising these proteins or their agonists are useful for increasing  
CC infiltration of inflammatory cells into a tissue of a mammal,  
CC stimulating or enhancing an immune response in a mammal, or  
CC increasing the proliferation of T-lymphocytes in a mammal in response  
CC to an antigen. Claimed compositions comprising the PRO polypeptide  
CC or its antagonist have the opposite effect. A claimed method for  
CC treating an immune related disorder, such as a T cell disorder,  
CC involves administering the PRO polypeptide, an agonist antibody or  
CC an antagonist antibody. The disorder is selected from systemic  
CC lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
CC juvenile chronic arthritis, spondyloarthropathy, systemic  
CC sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome,  
CC autoimmune vasculitis, sarcoidosis, autoimmune haemolytic anaemia,  
CC autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinated diseases (such as  
CC multiple sclerosis), autoimmune chronic active hepatitis, primary

CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
CC inflammatory bowel disease (ulcerative colitis and Crohn's disease),  
CC gluten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated  
CC skin diseases (such as bullous skin disease, erythema multiforme and  
CC psoriasis), allergic diseases (such as asthma, allergic rhinitis,  
CC atopic dermatitis, food hypersensitivity and urticaria), immunologic  
CC diseases of the lung and transplantation associated diseases (such  
CC as graft rejection and graft-versus-host disease) (all claimed).  
CC Claimed methods of diagnosing these disorders comprise detecting  
CC the level of expression of the PRO gene. Also claimed are a method  
CC of identifying a compound capable of inhibiting the expression or  
CC activity of the PRO polypeptide, vectors, host cells, antibodies  
CC and a method of stimulating the proliferation of T-lymphocytes  
CC using PRO826.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
Alignment Scores:  
Pred. No.: 7,266-88 Length: 415  
Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0  
US-10-059-395-142 (1-99) x AAF30059 (1-415)  
QY 1 MetLysIleProValIleuProAlaValIleuSerLeuIleuValIleuHisSerAla 20  
Db 13 ATGAAGATCCCGGTCTTCCCTGCGGTGCTCTCTCCCTCGTGTCACTCTGCC 72  
QY 21 GInGlyAlaThrIleuGlyGlyProGluGluGluSerThrIleGluAsnTYAlaSerArg 40  
Db 73 CAGGAGCCACCCTGGGTGCTCTGAGGAGAAAGCAACCATTTGAGATTTGCGTCAAGA 132  
QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
Db 133 CCCGAGGCTTTTAAACACCCCGTTCTCGAATCGACAAATTGCGATCTGCTTAAGGCT 192  
QY 61 AspGluPheLeuAsnThrPheAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
Db 193 GATGAGTTCCTGAACCTGGACGCGCCCTTTGAGTCTATCAAAAGGAACCTTCTTCCTC 252  
QY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
Db 253 AACTGGATGCTTCTCTTAAGCTGAAGAGACTGAGAGCGCAACTCTGATGCCAG 309  
RESULT 5  
AAF44164  
ID AAF44164 standard; cDNA; 415 BP.  
XX  
XX AAF44164;  
AC  
XX 02-APR-2001 (first entry)  
DT  
XX Human PRO826 (UNQ467) nucleotide sequence SEQ ID NO:200.  
DE  
XX Human; secreted and transmembrane protein; PRO; cytosstatic;  
KM cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
KM diagnostic assay; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200073454-A1.  
PN  
XX 07-DEC-2000.  
PD  
XX  
XX 30-MAR-2000; 2000WO-US08439.  
PF  
XX 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 07-JUL-1999; 99US-0143048.  
PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146222.  
PR 17-AUG-1999; 99US-0149396.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 08-OCT-1999; 99US-0158663.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.

XX (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,  
PI Grimaldi CJ, Gurney AL, Kijavir IU, Napier MA, Pan J, Paoni NF,  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
PI Zhang Z;

XX MPI; 2001-032160/04.

DR P-PSDB; AAB65204.

XX PRO polynucleotides used to produce polypeptides used to target  
PT bioactive molecules such as toxins, radiolabels or antibodies, to  
PT specific cells, to cause targeted cell death -

XX Claim 2; Fig 128; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytosolic activity. The PRO proteins  
CC can be used for targeted delivery of bioactive molecules, such as  
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridisation probes, in  
CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
CC and DNA. They may also be used to produce transgenic animals which are  
CC used to develop and screen therapeutically useful reagents. The PRO  
CC nucleotide and protein sequence can be used for tissue typing and in  
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.

XX Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

XX Alignment Scores:

Pred. No.: 7.26e-88 Length: 415  
Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0

US-10-059-395-142 (1-99) X AAF44164 (1-415)

QY 1 MetLysIleProValIeuProAlaValIleuSerIeuValIleuHisSerAla 20  
Db 13 ATGAAGATCCCGTCTCTGCGGTGTGCTCTCTCTCTGCTCCACTCTGCC 72  
QY 21 GlnGlyAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAsnTyrAlaSerArg 40  
Db 73 CAGGAGCCACCCTGGGTGTCTGAGGAAGAACCATTTGAGATTATGCGTACGA 132

QY 41 ProGluAlaPheAsnThrProPheIleuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
Db 133 CCCGAGGCCCTTAACACCCCGTCTCTGACATCGACAATTCGATCTGCGTTAAGGCT 192  
QY 61 AspGluPheIleuAsnTrpHisAlaIleuPheGluSerIleLysArgLysLeuProPheIleu 80  
Db 193 GATGAGTCTCTGAACTGGCAGCCCTCTTGTAGCTATCAAAAGAACTCTTCTCCTC 252  
QY 81 AsnTrpAspAlaPheProLysLeuLysGlyIleuArgSerAlaThrProAspAlaGln 99  
Db 253 AACTGGATGCTTCTCTTAAGCTGAAGACTGAGAGCGCAACTCTGATGCCAG 309

RESULT 6  
AAC97491  
ID AAC97491 standard; cDNA, 415 BP.

XX AAC97491;

DT 28-FEB-2001 (first entry)

XX Human angiogenesis-associated protein PRO826 cDNA, SEQ ID NO:157.

XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
KW gene therapy; transgenic animal; ss.

XX Homo sapiens.

XX WO200053753-A2.

XX 14-SEP-2000.

PF 05-JAN-2000; 2000WO-US00219.

XX 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.

XX (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;

DR MPI; 2001-090793/10.  
DR P-PSDB; AAB53094.

PT New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -

PS Claim 58; Fig 61; 293pp; English.

XX The invention relates to novel human angiogenesis-associated proteins  
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
CC PRO proteins. The invention also relates to vectors and host cells



comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion proteins comprising a PRO protein, agonists or antagonists of a PRO protein, and compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying modulators of PRO expression or activity; diagnosing a cardiovascular, endothelial or angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid, or PRO agonist or antagonist; a retroviral gene therapy vector comprising a cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the administration of a PRO protein, or an agonist or antagonist thereof. PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO agonists and PRO antagonists may be used as therapeutic agents to treat cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, osteoporosis, myocardial infarction, hypertension, diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis, endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to screen libraries to isolate cDNAs with sequence identity to PRO proteins, to map genes encoding PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the development and screening of potential therapeutic agents. The present sequence represents a cDNA encoding a PRO protein of the invention.

Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

#### Alignment Scores:

Pred. No.:	7.26e-88	Length:	415
Score:	99.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-10-059-395-142 (1-99) x AAC97491 (1-415)

```
OY 1 MetLysIleProValIleuProAlaValIleuSerLeuLeuValIleuHisSeraIa 20
    |||||
Db 13 ATGAAGATCCCGGCTCTCTCCGTCGTCTCTCCCTCTGCTGCTCCACTGCGC 72

OY 21 GlnGlyAlaThrLeuGlyGlyProGluGluSerThrIleGluAsnTyraIaSerArg 40
    |||||
Db 73 CAGGGAGCCACCCTGGGTGCTCTGAGGAAGAAAGCATTGAGAAATATGCGTCACGA 132

OY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60
    |||||
Db 133 CCCGAGGCTTTTACACCCCGTCTCTGAAACATGCACAAATTGCGATCGCTTAAAGGCT 192

OY 61 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80
    |||||
Db 193 GATGAGTTCCTGAACTGGCAGCCCTCTTGAAGTATCAAAAGAACTTCCTTCCTC 252

OY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99
    |||||
Db 253 AACTGGATGCTTCTCTTAAGCTGAAGAGACTGAGAGCGCAACTCTGATGCCAG 309
```

#### RESULT 7

ABL95626 standard; cDNA, 415 BP.

ABL95626;

19-JUL-2002 (first entry)

Human angiogenesis related cDNA PRO826 SEQ ID NO: 131.

Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;

KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;  
antiartherosclerotic; gene; ss.

OS Homo sapiens.

PN WO200208284-A2.

PD 31-JAN-2002.

PF 09-JUL-2001; 2001WO-US21735.

PR 20-JUL-2000; 2000US-219556P.

PR 25-JUL-2000; 2000US-220624P.

PR 25-JUL-2000; 2000US-220664P.

PR 28-JUL-2000; 2000WO-US20710.

PR 02-AUG-2000; 2000US-222695P.

PR 17-AUG-2000; 2000US-0643657.

PR 23-AUG-2000; 2000WO-US23522.

PR 24-AUG-2000; 2000WO-US23328.

PR 07-SEP-2000; 2000US-230978P.

PR 15-SEP-2000; 2000US-000000P.

PR 18-SEP-2000; 2000US-0664610.

PR 18-SEP-2000; 2000US-0665350.

PR 24-OCT-2000; 2000US-242922P.

PR 08-NOV-2000; 2000US-0709238.

PR 08-NOV-2000; 2000WO-US30952.

PR 10-NOV-2000; 2000WO-US30873.

PR 01-DEC-2000; 2000WO-US32678.

PR 20-DEC-2000; 2000US-0747259.

PR 20-DEC-2000; 2000WO-US34956.

PR 22-JAN-2001; 2001US-0767609.

PR 28-FEB-2001; 2001US-0796498.

PR 01-MAR-2001; 2001WO-US06666.

PR 09-MAR-2001; 2001US-0802706.

PR 14-MAR-2001; 2001US-0808689.

PR 22-MAR-2001; 2001US-0816744.

PR 05-APR-2001; 2001US-0828366.

PR 10-MAY-2001; 2001US-0854208.

PR 10-MAY-2001; 2001US-0854280.

PR 25-MAY-2001; 2001US-0866028.

PR 25-MAY-2001; 2001US-0866034.

PR 30-MAY-2001; 2001US-0870574.

PR 30-MAY-2001; 2001WO-US17443.

PR 01-JUN-2001; 2001WO-US17800.

PR 20-JUN-2001; 2001WO-US19692.

PR 28-JUN-2001; 2001WO-US00000.

XX (GETH ) GENENTECH INC.

PA (BAKE/) BAKER K P.

PA (FERR/) FERRARA N.

PA (GERB/) GERBER H.

PA (GERR/) GERRITSEN M E.

PA (GODD/) GODDARD A.

PA (GODO/) GODOWSKI P J.

PA (GURN/) GURNEY A L.

PA (HILL/) HILLAN K J.

PA (MARS/) MARSTERS S A.

PA (PANJ/) PAN J.

PA (PAON/) PAONI N F.

PA (STEP/) STEPHAN J F.

PA (WATA/) WATANABE C K.

PA (WILL/) WILLIAMS P M.

PA (WOOD/) WOOD W I.

Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

WPI; 2002-171999/22.

P-PSDB; ABB95488.

DR

XX

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal -

PS Claim 1; Fig 131; 567bp; English.

XX  
CC The present invention provides the protein and coding sequences of human  
CC PRO proteins. These are useful for treating or diagnosing a  
CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
CC hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The present sequence is a coding sequence of the invention.

XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

#### Alignment Scores:

Pred. No.:	7.26e-88	Length:	415
Score:	99.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-10-059-395-142 (1-99) x ABL95626 (1-415)

```

QY      1 MetLysIleProValLeuProAlaValValLeuSerLeuLeuValLeuHisSerAla 20
Db      13 ATGAAGATCCCGGTCCTTCCCTCCGCGTGCTCCTCCTCCTGCTGCTCCACTCTGCC 72

QY      21 GInGIyAlaThrLeuGIyGIyProGIuGIuGIuSerThrIleGIuAsnTyraIaSerArg 40
Db      73 CAGGAGGCCACCCCTGGGTGCTCTGAGGAGAAAGCACCAATTGAGAAATTATGCTCAGCA 132

QY      41 ProGIuAlaPheAsnThrProPheLeuAsnIleAspIyLeuArgSerAlaPheIySAla 60
Db      133 CCCGAGGCTTTAAACACCCCGCTCTGAAACATGCAAAATGCGATCTGCGTTAAGGCT 192

QY      61 AspGIuPheLeuAsnTrpHisAlaLeuPheGIuSerIleIySArgIyLeuProPheLeu 80
Db      193 GATGAGTTCCTGAAGCTGCGCCCTCTTGAAGTCTATCAAAAGAACTCTTCTTCCTC 252

QY      81 AsnTrpAspAlaPheProIySLeuIyGIyLeuArgSerAlaThrProAspAlaGln 99
Db      253 AACTGGATGCTTCTTCTTAAGCTGAAGACTGAGAGCGCACTCCTGATGCCAG 309

```

#### RESULT 8

ABK69971 standard; DNA; 415 BP.

XX  
AC ABK69971;

XX  
DT 15-JUL-2002 (first entry)

XX  
DE cDNA encoding human Pro peptide #11.

XX  
KW Human; ss; gene; PRO; secreted protein; transmembrane protein;

XX  
KW genetic disorder; tumour; cancer.

XX  
OS Homo sapiens.

XX  
PN WO200224888-A2.

XX  
PD 28-MAR-2002.

XX  
PF 29-AUG-2001; 2001WO-US27099.

XX  
PR 01-SEP-2000; 2000US-229896P.

PR 05-SEP-2000; 2000US-230621P.

PR 22-SEP-2000; 2000US-235147P.

PR 10-NOV-2000; 2000WO-US30873.

PR 12-JAN-2001; 2001US-261878P.

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PR      16-JAN-2001; 2001US-261910P.
PR      16-JAN-2001; 2001US-261939P.
PR      16-JAN-2001; 2001US-262150P.
PR      25-JAN-2001; 2001US-264395P.
PR      02-FEB-2001; 2001US-266421P.
PR      09-FEB-2001; 2001US-267623P.
PR      28-FEB-2001; 2001WO-US06520.
PR      09-MAR-2001; 2001US-274399P.
PR      03-APR-2001; 2001US-280982P.
PR      04-APR-2001; 2001US-282129P.
PR      04-APR-2001; 2001US-282199P.
PR      09-MAY-2001; 2001US-290589P.
PR      25-MAY-2001; 2001WO-US17092.
PR      01-JUN-2001; 2001WO-US17800.
PR      20-JUN-2001; 2001WO-US19692.
PR      29-JUN-2001; 2001WO-US21066.
PR      09-JUL-2001; 2001WO-US21735.
XX
XX      (GETH ) GENENTECH INC.
XX
PI      Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI      Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z,
PI      Fong S,
XX
XX      WPI; 2002-362426/39.
DR      P-PSDB; ABG34040.
XX
XX
XX      New PRO polypeptides and polynucleotides encoding the polypeptides,
PT      useful in gene therapy, chromosome identification, tissue typing, or
PT      for genetic analysis of individuals with genetic disorders -
XX
XX
PS      Claim 2; Figure 21; 218bp; English.
XX
XX
CC      This invention relates to the cDNA and protein sequences of novel
CC      secreted and transmembrane polypeptides PRO polypeptides. The
CC      invention also comprises a method for producing the proteins of the
CC      invention by recombinant means and antibodies specific for the protein
CC      of the invention. The antibody may be used for detecting the PRO
CC      proteins of the invention and may be used to modify their activity.
CC      polynucleotides may be used as hybridisation probes for a cDNA library
CC      to isolate the full-length PRO cDNA or to isolate other cDNAs, to
CC      construct hybridisation probes for mapping the gene which encodes that
CC      PRO and for genetic analysis of individuals with genetic disorders, in
CC      assays to identify other proteins or molecules involved in binding
CC      reaction, to generate transgenic animals or knock-out animals which in
CC      turn are useful in the development and screening of therapeutically
CC      useful reagents, for chromosome identification, and tissue typing. The
CC      PRO polypeptides are useful in gene therapy, and as molecular weight
CC      markers for protein electrophoresis purposes. The sequences may
CC      also be used to detect overexpression on PRO polypeptides in cancerous
CC      tumours and for screening for differentially expressed genes using
CC      microarray technology. The present sequence represents a cDNA encoding
CC      a human PRO protein of the invention.
XX
XX      Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;
SQ

```

#### Alignment Scores:

Pred. No.:	7.26e-88	Length:	415
Score:	99.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-10-059-395-142 (1-99) x ABK69971 (1-415)

```

QY      1 MetLysIleProValLeuProAlaValValLeuSerLeuLeuValLeuHisSerAla 20
Db      13 ATGAAGATCCCGGTCCTTCCCTGCGGTGCTCCTCCTCCTGCTGCTCCACTCTGCC 72

QY      21 GInGIyAlaThrLeuGIyGIyProGIuGIuGIuSerThrIleGIuAsnTyraIaSerArg 40
Db      73 CAGGAGGCCACCCCTGGGTGCTCCTGAGGAGAAAGCACCAATTGAGAAATTATGCTCAGCA 132

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```
OY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60
DB 133 CCGAGGCGCTTTAAACACCCCGTCTCTGAACATCGACAATTGGATCTCGCTTTAAGGCT 192
OY 61 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80
DB 193 GATGAGTTCCTGAACCTGGACGCGCCCTTTGAGTCTATCAAAAGGAACTTCTTCCCTC 252
OY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99
DB 253 AACTGGATGCTTCTCTAAGCTGAAGAGACTGAGAGCGCAACTCCTGATGCCAG 309
RESULT 9
ABL88137
ID ABL88137 standard; cDNA; 415 BP.
XX AC ABL88137;
XX DT 16-MAY-2002 (first entry)
DE Human PRO826 cDNA sequence SEQ ID NO:131.
XX
KW Human; angiogenesis; cardiact; cytostatic; antiangiogenic; hypotensive;
KW vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping; gene; ss.
XX OS Homo sapiens.
XX PN WO200200690-A2.
XX PD 03-JAN-2002.
XX PF 20-JUN-2001; 2001WO-US19692.
XX
PR 23-JUN-2000; 2000US-213637P.
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
```

```
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gunney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
XX
DR WPI: 2002-090516/12.
DR P-PSDB; ABB84882.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 2; Fig 131; 565pp; English.
XX
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiact, cytostatic,
CC antiangiogenic, hypotensive, vulnerable and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC degeneration, atherosclerosis, hypertension, arterial restenosis,
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC carcinoma) and wound healing. The PRO polynucleotides have applications
CC in molecular biology, including use as hybridisation probes, and in
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC probes used in the exemplification of the present invention.
XX
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;
XX
Alignment Scores:
Pred. No.: 7.26e-88 Length: 415
Score: 99.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
US-10-059-395-142 (1-99) x ABL88137 (1-415)
OY 1 MetLysIleProValLeuProAlaValLeuLeuSerLeuValLeuHisSerAla 20
DB 13 ATGAAGATCCCGGTCTTCTGCGCGGTGTCTCTCTCCCTCTGCTCCACTCTGCC 72
OY 21 GInGlyAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAsnTyrAlaSerArg 40
DB 73 CAGGAGCCACCCCTGGGTGCTCTGAGGAAGAAAGCACCATTTGAATATATGCGTCACGA 132
OY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60
DB 133 CCGAGGCGCTTTAAACACCCCGTCTCTGAACATCGACAATTGGATCTGCGTTAAGCT 192
OY 61 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80
DB 193 GATGAGTTCCTGAACCTGGACGCGCCCTTTGAGTCTATCAAAAGGAACTTCTTCCCTC 252
OY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99
DB 253 AACTGGATGCTTCTCTAAGCTGAAGAGACTGAGAGCGCAACTCCTGATGCCAG 309
RESULT 10
ABL88137
ID ABL88137 standard; cDNA; 415 BP.
XX AC ABL88137;
XX DT 08-MAY-2002 (first entry)
XX
```

DE cDNA encoding human PRO protein, Seq ID No 145.  
XX  
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
KW pericyte cell proliferation; chondrocyte cell proliferation;  
KW tumour necrosis factor-alpha; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200208288-A2.  
XX  
PD 31-JAN-2002.  
XX  
PF 29-JUN-2001; 2001WO-US21066.  
XX  
PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220585P.  
PR 25-JUL-2000; 2000US-220605P.  
PR 25-JUL-2000; 2000US-220607P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220638P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 25-JUL-2000; 2000US-220666P.  
PR 26-JUL-2000; 2000US-220893P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 15-SEP-2000; 2000US-000000P.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 28-NOV-2000; 2000US-253646P.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001WO-US17092.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,  
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
XX  
XX WPI; 2002-172001/22.  
DR P-PSDB; AAU83664.  
XX  
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,  
PT useful for treating a PRO related disorder and for diagnosing tumours  
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal  
PT tumour or liver tumour -  
XX  
XX  
PS Claim 2; Figure 145; 359pp; English.  
XX  
XX The invention relates to one hundred and twenty two nucleic acids  
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
CC agonists and antagonists are useful for treating a PRO related disorder.  
CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
CC liver tumour. The PRO polypeptides are useful for stimulating the  
CC proliferation of, or gene expression, in pericyte cells, for stimulating  
CC the proliferation or differentiation of chondrocyte cells, for  
CC stimulating the release of tumour necrosis factor-alpha from human blood,  
CC for stimulating or inhibiting the proliferation of normal human dermal  
CC fibroblast cells. The PRO polypeptide may also be used as molecular  
CC weight markers and for tissue typing. The PRO nucleic acids have  
CC applications in molecular biology, including use as hybridisation probes,  
CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human  
CC PRO protein coding sequences of the invention.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

Alignment Scores: 7.26e-88 Length: 415  
Pred. No.:

Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0  
US-10-059-395-142 (1-99) x ABK33608 (1-415)  
QY 1 MetLysIleProValLeuProAlaValLeuLeuSerLeuLeuValLeuHisSerAla 20  
DB 13 ATGAGATCCCGGCTCTCCGCGTGTGCTCTCTCCCTCCGTGTGCTCCACTGCC 72  
QY 21 GlnGlyAlaThrLeuGlyGlyProGlnGlnGlnSerThrIleGluAsnTyrAlaSerArg 40  
DB 73 CAGGAGCCACCCCTGGGTGCTCGAGGAGAGAACCATTTGAGATTATGCGTACGA 132  
QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
DB 133 CCCGAGGCTTTACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTAAGGCT 192  
QY 61 AspGluPheLeuAsnThrHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
DB 193 GATGAGTTCCTGAACCTGGACCGCTCTTGAGTCTATCAAAAGAACTTCCTTCCTC 252  
QY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
DB 253 AACTGGATGCCTTCTTAAGCTGAAGAGACTGAGAGCGCAACTCCTGATGCCAG 309  
RESULT 11  
ID ABX80255 standard; DNA; 415 BP.  
XX  
XX AC ABX80255;  
XX  
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DE Novel human secreted or transmembrane protein PRO819 DNA.  
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KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosum; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
XX  
XX  
OS Homo sapiens.  
XX  
XX US2002132252-A1.  
XX  
XX PD 19-SEP-2002.  
XX  
PF 14-NOV-2001; 2001US-0990442.  
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XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
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PR 08-MAR-1999; 99WO-US05028.  
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PR 15-SEP-1999; 99WO-US21090.  
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PR 20-DEC-1999; 99WO-US30911.  
PR 06-JAN-2000; 2000WO-US00219.







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Db 193 GATGAGTTCCTGAAGCTGGCAGCCCTCTTGTAGTCTATCAAAAGGAACTTCTTCTC 252  
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Db 253 AACTGGATGCTTTCCTTAAGCTGAAGGACTGAGGAGCGCAACTCTGATGCCAG 309  
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ID ABX80759 standard; cDNA; 415 BP.  
XX  
AC ABX80759;  
XX  
DT 22-APR-2003 (first entry)  
XX  
DE Human secreted/transmembrane protein cDNA, #78.  
XX  
KW Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;  
KW diagnostic; biosensor; bioreactor; tumour; therapeutic;  
KW gene therapy; tumour-associated antigenic target; TAT; ADEPT;  
KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN US2003027162-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 15-NOV-2001; 2001US-0997428.  
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PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
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PR 26-AUG-1998; 98US-098014P.

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RESULT 14

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XX AC ABX90232;

XX DT 01-MAY-2003 (first entry)

XX DE Human secreted/transmembrane protein cDNA, #78.

XX KM Human; gene; ss; PRO; secreted; transmembrane; signal peptide;

XX KM pharmaceutical; diagnostic; therapeutic; gene therapy.

XX OS Homo sapiens.

XX PN US2002160384-A1.

XX PD 31-OCT-2002.

XX PF 14-NOV-2001; 2001US-0992598.

XX 05-NOV-1997; 97WO-US20069.  
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XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen MB, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;

XX WPI; 2003-288106/28.  
DR P-PSDB; ABU60528.

PT New transmembrane polypeptides and nucleic acids encoding the  
PT polypeptides, useful in gene therapy, in chromosome identification, as  
PT chromosome markers, or in generating probes -

PS Claim 2; Fig 128; 650pp; English.

XX The invention discloses isolated PRO secreted/transmembrane polypeptides  
CC comprising a sequence without signal peptide and the nucleic acid  
CC encoding them. The polypeptides can be used to raise antibodies that  
CC specifically bind to the PRO polypeptide, for linking a bioactive  
CC molecule to a cell expressing a PRO protein and for modulating at least  
CC one biological activity of a cell. The PRO polypeptides or  
CC polynucleotides are also useful in gene therapy, in chromosome  
CC identification, as chromosome markers, or in generating probes. The PRO  
CC polypeptides are useful as molecular markers for protein  
CC electrophoresis, and the isolated nucleic acids may be used for  
CC recombinantly expressing those markers. The PRO polypeptides and nucleic  
CC acids may also be used in tissue typing. Anti-PRO antibodies are useful  
CC in diagnostic assays for PRO, and in affinity purification of PRO from  
CC recombinant cell culture or natural sources. The sequences presented in  
CC ABX90083-ABX90468 are the genes encoding, the primers amplifying and the  
CC probes detecting the PRO polynucleotides of the invention.  
CC Note: The sequence data for this patent is also available in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

Alignment Scores:

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US-10-059-395-142 (1-99) x ABX90232 (1-415)

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QY 41 ProGlnAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
DB 133 CCCGAGGCTTTAACACCCCGTCTCGAACAATCGACAATTCGATCTGCGTTAAGGCT 192  
QY 61 AspGluPheLeuAsnTyrPheIleAlaLeuPheGlnSerIleLysArgLysLeuProPheLeu 80  
DB 193 GATGAGTTCCTGAACCTGGACCGCCCTCTTGAGTCTATCAAAAGAAACTTCTTCTC 252

QY 81 AsnTyrPheAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
DB 253 AACTGGATGCTTTCCTAAGCTGAAGAGACTGAGAGCGCAACTCCTGATGCCAG 309

RESULT 15  
ABX77843  
ID ABX77843 standard; cDNA; 415 BP.

XX AC ABX77843;

DT 14-APR-2003 (first entry)

XX Human PRO polynucleotide #51.

XX Human; PRO; gene; ss; cytosstatic; tumour; cancer; breast; lung; stomach;  
KW liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;  
KW antibody-dependent enzyme mediated prodnug therapy.

XX Homo sapiens.

PN US2003027163-A1.

PD 06-FEB-2003.

XX 15-NOV-2001; 2001US-0997666.

XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
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PR 01-DEC-1998; 98WO-US25108.  
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PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.



PR 24-NOV-1997; 97US-066770P.  
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US-10-059-395-142 (1-99) X ABX77843 (1-415)

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

SUMMARIES

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9	99	100.0	415	10	US-09-991-163-200	Sequence 200, App
10	99	100.0	415	10	US-09-993-604-200	Sequence 200, App
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ALIGNMENTS

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Sequence 200, Application US/09989722  
Patent No. US20020072067A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Aubin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC63  
CURRENT APPLICATION NUMBER: US/09/989,722  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
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PRIOR FILING DATE: 1998-05-07  
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PRIOR APPLICATION NUMBER: 60/087607  
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;; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

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US-10-059-395-142 (1-99) x US-09-989-722-200 (1-415)

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## RESULT 2

US-09-989-723-200

; Sequence 200, Application US/09989723

; Patent No. US20020072092A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Geritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
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;; APPLICANT: Napier, Mary A.  
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;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730P1C62  
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;; PRIOR FILING DATE: 1998-07-09

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Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

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## RESULT 3

US-09-989-279-200

; Sequence 200, Application US/09989279

; Patent No. US20020072496A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

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; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tamas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C56

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RESULT 4
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C65
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## RESULT 6

US-09-989-732-200

; Sequence 200, Application US/09989732

; Patent No. US20020123463A1

## ; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
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;; APPLICANT: Pan, James  
;; APPLICANT: Paont, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin  
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Acids Encoding the Same  
FILE REFERENCE: P2730P1C57  
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PRIOR APPLICATION NUMBER: 60/049787  
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US-10-059-395-142 (1-99) x US-09-989-732-200 (1-415)

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; APPLICANT: Zhang, Zemin
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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US-10-059-395-142 (1-99) x US-09-993-604-200 (1-415)

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QY      81 AsnTrpASpAlaPheProLYsLeuLYSGlyLeuArgSerAlaThrProASPAlaGln 99
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; Sequence 200, Application US/09990456
; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

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Db 133 CCCGAGGCTTTAAACACCCCGTCTCTGAACATCGACAAATTGCGATCTCGCTTAAGCT 192  
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Db 193 GATGAGTCTCTGAACCTGGACGCGCTCTTGAAGTCTATCAAAAGAAACTTCTTCTC 252  
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RESULT 13  
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Patent No. US20020160384A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C20  
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;; PRIOR FILING DATE: 1998-07-09

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; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
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64	PRIOR APPLICATION NUMBER: 60/091982
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66	PRIOR APPLICATION NUMBER: 60/092182
67	PRIOR FILING DATE: 1998-07-09

Alignment Scores:	
Pred. No.:	5.22e-92
Score:	99.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
	length: 415
	Matches: 99
	Conservative: 0
	Mismatches: 0





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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.:	5,22e-92	Length:	415
Score:	99.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-059-395-142 (1-99) x US-09-989-735-200 (1-415)

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DB 13 ATGAAGATCCCGGCTTCCTGCGGTGCTCTCCCTCCTGCTGCTCACTCTGCC 72  
QY 21 GInGlyAlaThrIeuGlyGlyProGluGluSerThrIleGluAsnTYrAlaSerArg 40  
DB 73 CAGGAGCCACCCTGGGTGGTCTGAGGAGAAAGCACCATTTGAAATTATGCGTCACGA 132  
QY 41 ProGluAlaPheAsnThrProPheIleuAsnIleAspLysIleuArgSerAlaPheLysAla 60  
DB 133 CCCGAGGCTTTAACAACCCCGTTCTGAACTGACAAATTGCGATCGCTTTAAGGCT 192  
QY 61 AspGluPheIleuAsnTrpHisAlaIleuPheGluSerIleLysArgLysIleuProPheIleu 80  
DB 193 GATGAGTTCCTGAACCTGGCACGCGCTTGTGAGTCTATCAAAAGGAACCTTCCTCCTC 252  
QY 81 AsnTrpAspAlaPheProLysIleuLysGlyIleuArgSerAlaThrProAspAlaGln 99  
DB 253 AACTGGATGCTTCTTAAGCTGAAGGACTGAGAGCGCACTCCTGATGCCAG 309

Search completed: November 28, 2003, 10:58:01  
Job time : 266 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2003, 05:59:39 ; Search time 48 Seconds  
(without alignments)  
327.374 Million cell updates/sec

Title: US-10-059-395-142  
Perfect score: 510  
Sequence: 1 MKIPVLPAVLLSLVLHSA.....LWDAFPKLGKRSATPPAQ 99

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	510	100.0	99	20	AAW67828
2	510	100.0	99	21	AAV66681
3	510	100.0	99	22	AAAB20117
4	510	100.0	99	22	AAAB65204
5	510	100.0	99	22	AAAB50916
6	510	100.0	99	22	AAAB53094
7	510	100.0	99	23	ABP69586
8	510	100.0	99	23	ABB95488
9	510	100.0	99	23	ABG34040

10	510	100.0	99	23	ABB84882	Human PRO826 prote
11	510	100.0	99	23	AAU83664	Human PRO protein,
12	510	100.0	99	23	AAU81964	Human PRO826. Hom
13	510	100.0	99	24	ABU59097	Novel human secret
14	510	100.0	99	24	ABU59244	Human secreted/tr
15	510	100.0	99	24	ABU59323	Novel human secret
16	510	100.0	99	24	ABU60528	Human secreted/tr
17	510	100.0	99	24	ABU58019	Human PRO polypept
18	510	100.0	99	24	ABU58950	Human secreted/tr
19	510	100.0	99	24	ABU13910	Human PRO826 polyp
20	510	100.0	99	24	ABU10865	Human PRO polypept
21	421	82.5	85	23	ABP69669	Human polypeptide
22	278	54.5	96	23	ABP69669	Human polypeptide
23	255.5	50.1	88	23	ABB72393	Murine protein iso
24	77.5	15.2	1544	22	ABB69002	Drosophila melanog
25	72.5	14.2	500	21	AAG40462	Arabidopsis thalia
26	72.5	14.2	505	21	AAG40461	Arabidopsis thalia
27	72.5	14.2	612	21	AAG40460	Arabidopsis thalia
28	72.5	14.2	629	21	AAG31693	Arabidopsis thalia
29	72.5	14.2	634	21	AAG31692	Arabidopsis thalia
30	72.5	14.2	741	21	AAG31691	Arabidopsis thalia
31	71	13.9	749	21	AAG52606	Arabidopsis thalia
32	71	13.9	758	21	AAG51789	Arabidopsis thalia
33	71	13.9	842	21	AAG52605	Arabidopsis thalia
34	71	13.9	851	21	AAG51788	Arabidopsis thalia
35	71	13.9	876	21	AAG52604	Arabidopsis thalia
36	71	13.9	885	21	AAG51787	Arabidopsis thalia
37	70.5	13.8	731	22	AAB95828	Human protein sequ
38	69.5	13.6	116	22	AAW94219	Human reproductive
39	69.5	13.6	230	20	AAV60056	Human endometrium
40	69.5	13.6	479	21	AAV50941	Human adult skin c
41	68.5	13.4	96	22	AAW06384	Human foetal prote
42	68.5	13.4	601	22	ABB66854	Drosophila melanog
43	66.5	13.0	531	22	ABB63846	Drosophila melanog
44	66.5	13.0	692	20	AAV35548	C. pneumoniae prot
45	65.5	12.8	361	24	ABU11576	Human MDR polypep

ALIGNMENTS

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ID	AAW67828	standard; Protein; 99	AA.		
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AC	AAW67828;				
XX					
DT	25-MAR-1999	(first entry)			
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DE	Human secreted protein encoded by gene 22 clone HFEAF41.				
XX					
KW	Human; secreted protein; fusion protein; gene therapy; protein therapy;				
KW	diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;				
KW	developmental abnormality; foetal deficiency; blood; allergy; renal;				
KW	immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;				
KW	inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;				
KW	cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;				
KW	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;				
KW	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.				
OS	Homo sapiens.				
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PN	WO9842738-A1.				
XX					
PD	01-OCT-1998.				
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PF	19-MAR-1998;	98WO-US05311.			
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PR	30-MAY-1997;	97US-0050937.			
PR	21-MAR-1997;	97US-0041276.			
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PR	21-MAR-1997;	97US-0042344.			

PR 30-MAY-1997; 97US-0048069.  
PR 30-MAY-1997; 97US-0048094.  
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PR 30-MAY-1997; 97US-0048099.  
PR 30-MAY-1997; 97US-0048131.  
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PR 30-MAY-1997; 97US-0048188.  
PR 30-MAY-1997; 97US-0048350.  
PR 30-MAY-1997; 97US-0048351.  
PR 30-MAY-1997; 97US-0048352..  
PR 30-MAY-1997; 97US-0048355.  
PR 05-AUG-1997; 97US-0054804.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA;  
PI Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS;  
PI Rosen CA, Ruben SM, Shi Y, Young P;  
XX  
DR WPI; 1999-070066/06.  
DR N-PSDB; AAX00632.  
XX  
PT New isolated human genes and the secreted polypeptides they encode -  
PT useful for diagnosis and treatment of e.g. cancer, neurological  
PT disorders, immune diseases, inflammation or blood disorders  
XX  
PS Claim 11; Page 285; 385pp; English.  
XX  
CC This sequence represents a secreted human protein encoded by the gene  
CC clone detailed in the descriptor line. The gene can be used to generate  
CC fusion proteins by linking to the gene to a human immunoglobulin Fc  
CC portion (e.g. AAX00602) for increasing the stability of the fused  
CC protein as compared to the human protein only.  
CC The invention relates to 87 novel genes and their fragments (nucleic  
CC acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004)  
CC which are useful for preventing, treating or ameliorating medical  
CC conditions e.g. by protein or gene therapy. Also, pathological  
CC conditions can be diagnosed by determining the amount of the new  
CC polypeptides in a sample or by determining the presence of mutations in  
CC the new polynucleotides. Specific uses are described for each of the 87  
CC polynucleotides, based on which tissues they are most highly expressed in  
CC (see AAX00611 for described uses).  
XX  
SQ Sequence 99 AA;  
Query Match 100.0%; Score 510; DB 20; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4.6e-57;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKIPVLPAYVLLSLVLSAOGATLGPPEESTIENYASRPEAFNTPLNIDKLSAFKA 60  
Db 1 MKIPVLPAYVLLSLVLSAOGATLGPPEESTIENYASRPEAFNTPLNIDKLSAFKA 60  
QY 61 DEFLNMHALFESIKRKLPLNWDAPFKLKGIRSATPDAQ 99  
Db 61 DEFLNMHALFESIKRKLPLNWDAPFKLKGIRSATPDAQ 99  
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ID AAY66681 standard; protein; 99 AA.  
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AC AAY66681;  
XX  
DT 05-APR-2000 (first entry)  
XX  
DE Membrane-bound protein PRO826.  
XX

KM Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KM pharmaceutical; receptor immunoadhesin; gene mapping.  
XX  
OS Homo sapiens.  
XX  
PN WO963088-A2.  
XX  
PD 09-DEC-1999.  
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PF 02-JUN-1999; 99WO-US12252.  
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PR 02-JUN-1998; 98US-0087607.  
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PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.

PR 12-JAN-1999; 99US-0115565.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK,
PI Wood WT, Yuan J;
XX
XX WPI; 2000-072883/06.
DR N-PSDB; AAZ65018.
XX
XX Membrane-bound proteins and related nucleotide sequences
PT
XX
XX claim 12; Fig 129; 822pp; English.
PS
XX
XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including ldl receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
SQ Sequence 99 AA;

Query Match 100.0%; Score 510; DB 21; Length 99;
Best Local Similarity 100.0%; Pred. No. 4,6e-57;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVLPAVVLSTLVLSAQGATLGGPEESTTENYASRPEAFNTPLNIDKLSAFKA 60
Db 1 MKIPVLPAVVLSTLVLSAQGATLGGPEESTTENYASRPEAFNTPLNIDKLSAFKA 60
QY 61 DEFLNHALFESIKRKLPFLNWDAPFKLGLRSATPDDAQ 99
Db 61 DEFLNHALFESIKRKLPFLNWDAPFKLGLRSATPDDAQ 99

RESULT 3
AAB20117
ID AAB20117 standard; Protein; 99 AA.
XX
AC AAB20117;
XX
DT 30-APR-2001 (first entry)
XX
DE Human immunostimulant PRO826.
XX
KW PRO826; UNQ467; human; immune disease; autoimmune disease;
KW antirheumatic; antiarthritic; antiinflammatory; antianaemic;
KW immunosuppressive; antidiabetic; antidiabetic; neuroprotective;
KW hepatotropic; virucide; dermatological; antipsoriatic;
KW antiasthmatic; antiallergic; immunostimulant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Peptide 1..22
FT /label= Signal_peptide
FT Protein 23..99
FT /label= Mature_protein
FT Modified-site 22..28
FT /note= "N-myristoylation site"
FT Modified-site 90..96
FT /note= "N-myristoylation site"
FT Region 16..48
FT /note= "homology to peroxidase"
```



```
XX PN WO200105972-A1.
XX PD 25-JAN-2001.
XX PF 15-MAR-2000; 2000WO-US06884.
XX PR 20-JUL-1999; 99US-0144758.
XX PA (GETH ) GENENTECH INC.
XX PI Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL,
PI Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK,
PI Wood WI;
XX DR WPI; 2001-103149/11.
XX DR N-PSDB; AAF30059.
XX PT New PRO polypeptides, nucleic acids and (ant)agonists, useful for
PT diagnosing and treating immune-related disorders, such as multiple
PT sclerosis, rheumatoid arthritis and diabetes -
XX PS Claim 20; Fig 20; 127pp; English.
XX CC The present sequence is that of novel human immunomodulator PRO826
CC (UNQ467), as deduced from cDNA (see AAF30059) isolated from a
CC database screening. PRO826 has a mol.wt. of 11 kDa and a pI of
CC 7.47. The invention provides polynucleotides (see AAF30050-62)
CC encoding novel human PRO proteins (see AAB20108-20) including PRO826.
CC Claimed compositions comprising these proteins or their agonists
CC are useful for increasing infiltration of inflammatory cells into
CC a tissue of a mammal, stimulating or enhancing an immune
CC response, or increasing the proliferation of T-lymphocytes in a
CC mammal in response to an antigen. Claimed compositions comprising
CC a PRO polypeptide or its antagonist have the opposite effect. A
CC claimed method for treating an immune related disorder, such as a T
CC cell disorder, involves administering a PRO polypeptide, an agonist
CC antibody or an antagonist antibody. The disorder is selected from
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, spondyloarthritis, systemic sclerosis,
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated
CC renal disease, demyelinating diseases (such as multiple sclerosis),
CC autoimmune chronic active hepatitis, primary biliary cirrhosis,
CC granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel
CC disease (ulcerative colitis and Crohn's disease), gluten-sensitive
CC enteropathy, Whipple's disease, (auto)immune-mediated skin diseases
CC (such as bullous skin disease, erythema multiforme and psoriasis),
CC allergic diseases (such as asthma, allergic rhinitis, atopic
CC dermatitis, food hypersensitivity and urticaria), immunologic
CC diseases of the lung and transplantation associated diseases (such
CC as graft rejection and graft-versus-host disease) (all claimed).
CC Claimed methods of diagnosing these disorders comprise detecting
CC the level of expression of the PRO gene. Also claimed are a method
CC of identifying a compound capable of inhibiting the expression or
CC activity of the PRO polypeptide, vectors, host cells, antibodies,
CC and a method of stimulating the proliferation of T lymphocytes
CC using PRO826.
XX SQ Sequence 99 AA;
Query Match 100.0%; Score 510; DB 22; Length 99;
Best Local Similarity 100.0%; Pred. No. 4.6e-57;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy ' 1 MKIPVLPVAVLISLVLSAOGATLGPPEESTIENYASRBEAFNTPFLNIDKLSAFKA 60
Db 1 MKIPVLPVAVLISLVLSAOGATLGPPEESTIENYASRBEAFNTPFLNIDKLSAFKA 60
Qy 61 DEFILNHALFESIKRKLPLINWDAPFKLGLRSATPDAQ 99
Db 61 DEFILNHALFESIKRKLPLINWDAPFKLGLRSATPDAQ 99
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RESULT 4
AAB65204
ID AAB65204 standard; Protein; 99 AA.
XX AC AAB65204;
XX DT 02-APR-2001 (first entry)
XX DE Human PRO826 (UNQ467) protein sequence SEQ ID NO:201.
XX KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
XX OS Homo sapiens.
XX PN WO200073454-A1.
XX PD 07-DEC-2000.
XX PF 30-MAR-2000; 2000WO-US08439.
XX PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
XX PA (GETH ) GENENTECH INC.
XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
PI Zhang Z;
XX DR WPI; 2001-032160/04.
XX DR N-PSDB; AAF44164.
XX PT PRO polynucleotides used to produce polypeptides used to target
PT bioactive molecules such as toxins, radiolabels or antibodies, to
PT specific cells, to cause targeted cell death -
XX PS Claim 12; Fig 129; 935pp; English.
XX CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA
CC and DNA. They may also be used to produce transgenic animals which are
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CC used to develop and screen therapeutically useful reagents. The PRO  
CC nucleotide and protein sequence can be used for tissue typing and in  
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.

XX  
SQ Sequence 99 AA;

Query Match 100.0%; Score 510; DB 22; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4.6e-57;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVLPVVLISLVLSHSAQATLGGPBEESTIENYASRPEAFNTPFLNIDKLSAFKA 60  
Db 1 MKIPVLPVVLISLVLSHSAQATLGGPBEESTIENYASRPEAFNTPFLNIDKLSAFKA 60

QY 61 DEFLNWHALFESIKRKLPLNWDAFPKLGKLSATPDAQ 99  
Db 61 DEFLNWHALFESIKRKLPLNWDAFPKLGKLSATPDAQ 99

RESULT 5  
AAB50916  
ID AAB50916 standard; Protein; 99 AA.

XX  
AC AAB50916;

XX  
DT 21-MAR-2001 (first entry)

XX  
DE Human PRO826 protein.

XX  
KW Human; PRO; antiinflammatory; dermatological; antiarthritic;  
KW antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;  
KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;  
KW antiallergic; antiasthmatic; immune related disorder;  
KW hepatobiliary disease; autoimmune disease; allergy.

XX  
OS Homo sapiens.

XX  
PN WO200073452-A2.

XX  
PD 07-DEC-2000.

XX  
PF 02-JUN-2000; 2000WO-US15264.

XX  
PR 02-JUN-1999; 99WO-US12252.

XX  
PR 20-JUL-1999; 99US-0144732.

XX  
PR 20-JUL-1999; 99US-0144758.

XX  
PR 28-JUL-1999; 99US-0146222.

XX  
PR 01-SEP-1999; 99WO-US20111.

XX  
PR 15-SEP-1999; 99WO-US21090.

XX  
PR 15-SEP-1999; 99WO-US21547.

XX  
PR 29-OCT-1999; 99US-0162506.

XX  
PR 30-NOV-1999; 99WO-US28313.

XX  
PR 01-DEC-1999; 99WO-US28634.

XX  
PR 09-DEC-1999; 99US-0170262.

XX  
PR 20-DEC-1999; 99WO-US30911.

XX  
PR 05-JAN-2000; 2000WO-US00219.

XX  
PR 06-JAN-2000; 2000WO-US00376.

XX  
PR 11-FEB-2000; 2000WO-US03565.

XX  
PR 18-FEB-2000; 2000WO-US04341.

XX  
PR 18-FEB-2000; 2000WO-US04342.

XX  
PR 22-FEB-2000; 2000WO-US04414.

XX  
PR 24-FEB-2000; 2000WO-US04914.

XX  
PR 15-MAR-2000; 2000WO-US06884.

XX  
PR 20-MAR-2000; 2000WO-US07377.

XX  
PR 21-MAR-2000; 2000WO-US07532.

XX  
PR 30-MAR-2000; 2000WO-US08439.

XX  
PR 17-MAY-2000; 2000WO-US13705.

XX  
PR 22-MAY-2000; 2000WO-US14042.

PA (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;

PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;

PI Wood WI;

XX WPI; 2001-025253/03.

DR N-PSDB; AAC91475.

XX Thirty three nucleic acids encoding PRO polypeptides which are useful

PT in the diagnosis and treatment of immune related disorders, e.g.

PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,

PT thyroiditis and diabetes mellitus -

XX Claim 58, Fig 30; 218pp; English.

XX The present sequence is one of thirty three novel PRO polypeptides.

CC The PRO polypeptides, anti-PRO antibodies, agonists and

CC antagonists are useful for treating and diagnosing immune related

CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,

CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,

CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's

CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic

CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,

CC immune-mediated renal disease, demyelinating diseases of the central

CC and peripheral nervous systems (such as multiple sclerosis, idiopathic

CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic

CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases

CC (such as infectious, autoimmune chronic active hepatitis, primary

CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),

CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's

CC disease, autoimmune or immune-mediated skin diseases (such as bullous

CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),

CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,

CC food hypersensitivity and urticaria), immunological diseases of the

CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis

CC and hypersensitivity pneumonitis), transplantation associated diseases

CC including graft rejection and graft-versus-host diseases.

XX  
SQ Sequence 99 AA;

Query Match 100.0%; Score 510; DB 22; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4.6e-57;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVLPVVLISLVLSHSAQATLGGPBEESTIENYASRPEAFNTPFLNIDKLSAFKA 60  
Db 1 MKIPVLPVVLISLVLSHSAQATLGGPBEESTIENYASRPEAFNTPFLNIDKLSAFKA 60

QY 61 DEFLNWHALFESIKRKLPLNWDAFPKLGKLSATPDAQ 99  
Db 61 DEFLNWHALFESIKRKLPLNWDAFPKLGKLSATPDAQ 99

RESULT 6  
AAB53094  
ID AAB53094 standard; Protein; 99 AA.

XX  
AC AAB53094;

XX  
DT 28-FEB-2001 (first entry)

XX  
DE Human angiogenesis-associated protein PRO826, SEQ ID NO:158.

XX  
KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;

XX  
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;

XX  
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;

XX  
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;

XX  
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;

XX  
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;

XX  
KW gene therapy; transgenic animal.

XX  
OS Homo sapiens.

XX WO200053753-A2.  
PN  
XX  
PD 14-SEP-2000.  
XX  
PF 05-JAN-2000; 2000WO-US00219.  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
XX  
XX (GETH ) GENENTECH INC.  
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NF, Picti RM, Watanabe CK, Williams PM, Wood WI;  
XX  
DR WPI; 2001-090793/10.  
DR N-PSDB; AAC97491.  
XX  
PT New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
XX  
XX  
PS Claim 69; Fig 62; 293pp; English.  
XX  
XX The invention relates to novel human angiogenesis-associated proteins  
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
CC PRO proteins. The invention also relates to vectors and host cells  
CC comprising a PRO nucleic acid, the recombinant production of a PRO  
CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
CC compounds which inhibit the expression of a PRO gene. The invention  
CC additionally encompasses methods of identifying modulators of PRO  
CC expression or activity; diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
CC mutations in a PRO gene, or the expression level of a PRO gene within a  
CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
CC administration of a PRO protein, or an agonist or antagonist thereof.  
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
CC agonists and PRO antagonists may be used as therapeutic agents to treat  
CC cardiovascular, endothelial or angiogenic disorders, such as  
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
CC disease, or stroke. PRO nucleic acids are additionally useful in the  
CC recombinant production of PRO proteins, as hybridisation probes to  
CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
CC animals useful for the development and screening of potential  
CC therapeutic agents. The present sequence represents a PRO protein of the  
CC invention.  
XX  
XX Sequence 99 AA;

Query Match 100.0%; Score 510; DB 22; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4.6e-57;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKIPVLPVAVVLSLVLSAOGATLGGPEESTIENTYASRPEAFNTPFLNIDKLSAFKA 60  
Db 1 MKIPVLPVAVVLSLVLSAOGATLGGPEESTIENTYASRPEAFNTPFLNIDKLSAFKA 60  
QY 61 DEFLNWHALFESI KRKL PFLNWDAPFKLGKLSATPDAQ 99  
Db 61 DEFLNWHALFESI KRKL PFLNWDAPFKLGKLSATPDAQ 99  
RESULT 7  
ABP69586  
ID ABP69586 standard; Protein; 99 AA.  
XX  
AC ABP69586;  
XX  
DT 20-JAN-2003 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 1633.  
XX  
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;  
KW cell-proliferative disorder; neurodegenerative disease; bacterial;  
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;  
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;  
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;  
KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;  
KW antiarthritic.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO200270539-A2.  
XX  
PD 12-SEP-2002.  
XX  
PF 05-MAR-2002; 2002WO-US05095.  
XX  
PR 05-MAR-2001; 2001US-0799451.  
XX  
PA (HYSE-) HYSEQ INC.  
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;  
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
PI Wehrman T, Wang J, Wang D, Drmanac RT;  
XX  
DR WPI; 2002-759812/82.  
DR N-PSDB; ABZ11803.  
XX  
PT New polynucleotides comprising sequences assembled from expressed  
PT sequence tags (ESTs), useful for treating cell-proliferative,  
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or  
PT platelet or coagulation disorders -  
XX  
PS Claim 9; SEQ ID NO 1633; 1012pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated polynucleotide (I) comprising a  
CC nucleotide sequence selected from any of 948 sequences  
CC (ABZ1119-ABZ12066) or their mature protein coding portion, active domain  
CC coding protein or complementary sequences. The polynucleotides are useful  
CC for identifying expressed genes or for physical mapping of human genome.  
CC The encoded polypeptides (ABP68902-ABP69849) are useful as molecular  
CC weight markers, as a food supplement, for generating antibodies, in  
CC medical imaging, screening and diagnostic assays and for treating  
CC cell-proliferative disorders (cancer), neurodegenerative diseases  
CC (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple  
CC sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid  
CC disorders, platelet or coagulation disorders, wound, burns, incision,  
CC ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal,  
CC parasitic), arthritis, etc.  
CC  
CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 99 AA;

Query Match 100.0%; Score 510; DB 23; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-57;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKIPVLPVAVLLSLVLSAAGATLGGPEESTIENYASRPEAFNTPFLNIDKLSAFKA 60  
 |||||  
 DB 1 MKIPVLPVAVLLSLVLSAAGATLGGPEESTIENYASRPEAFNTPFLNIDKLSAFKA 60

OY 61 DEFLNMHALFESIKRKLPLNWDAPFKLKGSRATPDQAQ 99  
 |||||  
 DB 61 DEFLNMHALFESIKRKLPLNWDAPFKLKGSRATPDQAQ 99

RESULT 8  
 ABB95488  
 ID ABB95488 standard; Protein; 99 AA.  
 XX  
 AC ABB95488;

DT 19-JUL-2002 (first entry)  
 XX

DB Human angiogenesis related protein PRO826 SEQ ID NO: 132.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 KM atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KM cardiac; cytosolic; antiangiogenic; hypotensive; vulnerary;  
 KM antiarteriosclerotic.

OS Homo sapiens.

XX WO200208284-A2.

PN 31-JAN-2002.

PD 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220664P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 02-AUG-2000; 2000US-222695P.  
 PR 17-AUG-2000; 2000US-0643657.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 07-SEP-2000; 2000US-230978P.  
 PR 15-SEP-2000; 2000US-000000P.  
 PR 18-SEP-2000; 2000US-0664610.  
 PR 18-SEP-2000; 2000US-0665350.  
 PR 24-OCT-2000; 2000US-242922P.  
 PR 08-NOV-2000; 2000US-0709238.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 22-JAN-2001; 2001US-0767609.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001US-0802706.  
 PR 09-MAR-2001; 2001US-0808689.  
 PR 14-MAR-2001; 2001US-0816744.  
 PR 22-MAR-2001; 2001US-0828366.  
 PR 05-APR-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001WO-US17092.

PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001WO-US17443.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 28-JUN-2001; 2001WO-US00000.

XX (GETH ) GENENTECH INC.

PA (BAKE/) BAKER K P.

PA (FERR/) FERRARA N.

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PA (GODD/) GODDARD A.

PA (GODO/) GODOWSKI P J.

PA (GURN/) GURNEY A L.

PA (HILL/) HILLAN K J.

PA (MARS/) MARSTERS S A.

PA (PANU/) PAN J.

PA (PAON/) PAONI N F.

PA (STEP/) STEPHAN J F.

PA (WATA/) WATANABE C K.

PA (WILL/) WILLIAMS P M.

PA (WOOD/) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI; 2002-171999/22.

DR N-PSDB; ABL95626.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -

XX Claim 11; Fig 132; 567bp; English.

XX The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
 CC hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a PRO protein of the invention.

XX Sequence 99 AA;

Query Match 100.0%; Score 510; DB 23; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-57;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKIPVLPVAVLLSLVLSAAGATLGGPEESTIENYASRPEAFNTPFLNIDKLSAFKA 60  
 |||||  
 DB 1 MKIPVLPVAVLLSLVLSAAGATLGGPEESTIENYASRPEAFNTPFLNIDKLSAFKA 60

OY 61 DEFLNMHALFESIKRKLPLNWDAPFKLKGSRATPDQAQ 99  
 |||||  
 DB 61 DEFLNMHALFESIKRKLPLNWDAPFKLKGSRATPDQAQ 99

RESULT 9  
 ABG34040  
 ID ABG34040 standard; Protein; 99 AA.  
 XX  
 AC ABG34040;

DT 15-JUL-2002 (first entry)  
 XX

XX Human Pro peptide #11.

KM Human; PRO; secreted protein; transmembrane protein;  
 KM genetic disorder; tumour; cancer.

OS Homo sapiens.  
XX  
PN WO200224888-A2.  
XX  
PD 28-MAR-2002.  
XX  
PF 29-AUG-2001; 2001WO-US27099.  
XX  
PR 01-SEP-2000; 2000US-229896P.  
PR 05-SEP-2000; 2000US-230621P.  
PR 22-SEP-2000; 2000US-235147P.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 12-JAN-2001; 2001US-261878P.  
PR 16-JAN-2001; 2001US-261910P.  
PR 16-JAN-2001; 2001US-261939P.  
PR 16-JAN-2001; 2001US-262150P.  
PR 25-JAN-2001; 2001US-264395P.  
PR 02-FEB-2001; 2001US-266421P.  
PR 09-FEB-2001; 2001US-267623P.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 09-MAR-2001; 2001US-274399P.  
PR 03-APR-2001; 2001US-280982P.  
PR 04-APR-2001; 2001US-282129P.  
PR 04-APR-2001; 2001US-282199P.  
PR 09-MAY-2001; 2001US-290589P.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,  
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z,  
PI Fong S;  
XX  
DR WPI; 2002-362426/39.  
XX  
DR N-PSDB; ABK69971.  
XX  
PT New PRO polypeptides and polynucleotides encoding the polypeptides,  
PT useful in gene therapy, chromosome identification, tissue typing, or  
PT for genetic analysis of individuals with genetic disorders -  
XX  
XX  
PS Claim 11; Figure 22; 218pp; English.  
XX  
CC This invention relates to the cDNA and protein sequences of novel  
CC secreted and transmembrane polypeptides PRO polypeptides. The  
CC invention also comprises a method for producing the proteins of the  
CC invention by recombinant means and antibodies specific for the protein  
CC of the invention. The antibody may be used for detecting the PRO  
CC proteins of the invention and may be used to modify their activity.  
CC polynucleotides may be used as hybridisation probes for a cDNA library  
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, to  
CC construct hybridisation probes for mapping the gene which encodes that  
CC PRO and for genetic analysis of individuals with genetic disorders, in  
CC assays to identify other proteins or molecules involved in binding  
CC reaction, to generate transgenic animals or knock-out animals which in  
CC turn are useful in the development and screening of therapeutically  
CC useful reagents, for chromosome identification, and tissue typing. The  
CC PRO polypeptides are useful in gene therapy, and as molecular weight  
CC markers for protein electrophoresis purposes. The sequences may  
CC also be used to detect overexpression on PRO polypeptides in cancerous  
CC tumours and for screening for differentially expressed genes using  
CC microarray technology. The present sequence represents a human PRO  
CC protein of the invention.  
XX  
XX  
SQ Sequence 99 AA;

Query Match 100.0%; Score 510; DB 23; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4.6e-57;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVLPVLLISLVLSAOGATLGGPEESTIENTYASRPEAFNTPLNIDKLSAFKA 60  
|||  
Db 1 MKIPVLPVAVLLISLVLSAOGATLGGPEESTIENTYASRPEAFNTPLNIDKLSAFKA 60  
QY 61 DEFLNWHALFESIKRKLPEFLNWDAPPKLGLRSATPDAQ 99  
|||  
Db 61 DEFLNWHALFESIKRKLPEFLNWDAPPKLGLRSATPDAQ 99  
RESULT 10  
ABB84882  
ID ABB84882 standard; Protein; 99 AA.  
XX  
AC ABB84882;  
XX  
DT 16-MAY-2002 (first entry)  
XX  
DE Human PRO826 protein sequence SEQ ID NO:132.  
XX  
KW Human; angiogenesis; cardiant; cyostatic; antiangiogenic; hypotensive;  
KW vulnerable; arteriosclerotic; PRO agonist; PRO antagonist; trauma;  
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
KW age-related macular degeneration; arterial restenosis; angina;  
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
KW wound healing; chromosome mapping; gene mapping.  
XX  
OS Homo sapiens.  
XX  
PN WO200200690-A2.  
XX  
XX  
PD 03-JAN-2002.  
XX  
PF 20-JUN-2001; 2001WO-US19692.  
XX  
XX  
PR 23-JUN-2000; 2000US-213637P.  
PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 02-AUG-2000; 2000US-222695P.  
PR 17-AUG-2000; 2000US-0643657.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 07-SEP-2000; 2000US-230978P.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-0709238.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0808744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
XX  
PA (GETH ) GENENTECH INC.



```
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CX, Williams PM, Wood WI, Ye W;
XX
DR WPI: 2002-090516/12.
DR N-PSDB; ABL88137.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
PS Claim 11; Fig 132; 565pp; English.
XX
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC degeneration, atherosclerosis, hypertension, arterial restenosis,
CC rheumatoid arthritis, tumour angiogenesis (such as breast carcinoma and liver
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC carcinoma) and wound healing. The PRO polynucleotides have applications
CC in molecular biology, including use as hybridisation probes, and in
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC probes used in the exemplification of the present invention.
XX
SQ Sequence 99 AA;

Query Match 100.0%; Score 510; DB 23; Length 99;
Best Local Similarity 100.0%; Pred. No. 4.6e-57;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKIPVLPVAVLLSLVLSAQAQATLGGPEESTIENYASRPEAFNTPFLNIDKLSAFKA 60
DB 1 MKIPVLPVAVLLSLVLSAQAQATLGGPEESTIENYASRPEAFNTPFLNIDKLSAFKA 60
OY 61 DEFLNWHALFESIKRKLPLNWDAPFKLKGLSATPDAQ 99
DB 61 DEFLNWHALFESIKRKLPLNWDAPFKLKGLSATPDAQ 99

RESULT 11
AAU83664
ID AAU83664 standard; Protein; 99 AA.
XX
AC AAU83664;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human PRO protein, Seq ID No 146.
XX
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha.
XX
OS Homo sapiens.
XX
PN WO200208288-A2.
XX
PD 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US21066.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220585P.
PR 25-JUL-2000; 2000US-220605P.
PR 25-JUL-2000; 2000US-220607P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220638P.
XX
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PR 25-JUL-2000; 2000US-220664P.
PR 25-JUL-2000; 2000US-220666P.
PR 26-JUL-2000; 2000US-220893P.
PR 28-JUL-2000; 2000WO-US20710.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 15-SEP-2000; 2000US-000000P.
PR 10-NOV-2000; 2000WO-US30873.
PR 28-NOV-2000; 2000US-253646P.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001WO-US17092.
XX
PA (GENT ) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CX, Wood WI;
XX
DR WPI: 2002-172001/22.
DR N-PSDB; ABK33608.
XX
PS Claim 11; Figure 146; 359pp; English.
XX
CC The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC protein sequences of the invention.
XX
SQ Sequence 99 AA;

Query Match 100.0%; Score 510; DB 23; Length 99;
Best Local Similarity 100.0%; Pred. No. 4.6e-57;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKIPVLPVAVLLSLVLSAQAQATLGGPEESTIENYASRPEAFNTPFLNIDKLSAFKA 60
DB 1 MKIPVLPVAVLLSLVLSAQAQATLGGPEESTIENYASRPEAFNTPFLNIDKLSAFKA 60
OY 61 DEFLNWHALFESIKRKLPLNWDAPFKLKGLSATPDAQ 99
DB 61 DEFLNWHALFESIKRKLPLNWDAPFKLKGLSATPDAQ 99

RESULT 12
AAU81964
ID AAU81964 standard; Protein; 99 AA.
XX
AC AAU81964;
XX
DT 09-APR-2002 (first entry)
XX
DE Human PRO826.
XX
```

KW Human; PRO; antiinflammatory; ophthalmological; vasotropic;  
KW retinal cell injury; ocular disease; retinitis pigmentosa;  
KW macular degeneration; retinal detachment; retinal tear; retinopathy;  
KW retinal degenerative disease; macular hole; degenerative myopia;  
KW acute retinal necrosis syndrome; traumatic chorioretinopathy;  
KW Purtscher's retinopathy; oedema; ischaemic condition;  
KW retinal vision occlusion; collagen vascular disease;  
KW thrombocytopaenic purpura; uveitis; retinal vasculitis; Bales disease;  
KW systemic lupus erythematosus; environmental trauma.  
XX  
OS Homo sapiens.  
XX WO200109327-A2.  
PD 08-FEB-2001.  
XX  
PF 28-JUL-2000; 2000WO-US20710.  
XX  
PR 28-JUL-1999; 99US-146222P.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;  
PI Kijavini IJ, Lafleur M, Mark MR, Marsters SA, Pitti RM;  
PI Watanabe CK, Wood WI;  
XX  
DR WPI; 2002-130120/17.  
DR N-PSDB; ABK28600.  
XX  
PT Promoting survival of retinal cells, or delaying or preventing retinal  
PT cell injury or death, by contacting retinal cells with PRO175, 220,  
PT 216, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132  
PT polypeptide -  
XX  
PS Claim 44; Fig 25; 152pp; English.  
XX  
XX The invention relates to promoting the survival of retinal cells, or  
CC delaying or preventing retinal cell injury or death, by contacting the  
CC retinal cells with the polypeptide such as PRO175, PRO220, PRO216,  
CC PRO243, PRO306, PRO346, PRO322, PRO536, PRO943, PRO840, PRO828, PRO826,  
CC PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids  
CC encoding the PRO proteins, a vector comprising the nucleic acid, a host  
CC cell comprising the vector, and anti-PRO antibody. The PRO proteins are  
CC useful for promoting survival of retinal cells (retinal neurons such as  
CC retinal ganglion cells, displaced retinal ganglion cells, amacrine  
CC cells, displaced amacrine cells, horizontal neurons or bipolar neurons,  
CC rod photoreceptors, or supportive cells such as Muller cells or pigment  
CC epithelial cells), or delaying or preventing retinal cell injury or  
CC death caused by ocular disease (which is or is associated with  
CC retinitis pigmentosa, macular degeneration, retinal detachment, retinal  
CC tear, retinopathy, acute retinal necrosis syndrome, traumatic  
CC degenerative myopia, acute retinal necrosis syndrome, traumatic  
CC chorioretinopathy or contusion, Purtscher's retinopathy, oedema, an  
CC ischaemic condition, central or branch retinal vision occlusion,  
CC collagen vascular disease, thrombocytopaenic purpura, uveitis, retinal  
CC vasculitis, occlusion associated with Bales disease or systemic lupus  
CC erythematosus), retinal injury or environmental trauma. The retinal  
CC cell injury or death is delayed or prevented by substantially not

CC causing angiogenesis or mitogenesis. The present sequence represents  
CC a PRO protein.  
XX  
SQ Sequence 99 AA;  
Query Match 100.0%; Score 510; DB 23; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4.6e-57;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MKIPVPAVLLSLVLHSAQATLGGPEESTIENTYASRPEAFNTPLNIDKLSAFKA 60  
DB 1 MKIPVPAVLLSLVLHSAQATLGGPEESTIENTYASRPEAFNTPLNIDKLSAFKA 60  
OY 61 DEFLNTHALFESIKRKLPLFNWDAPFKLGLRSATPDAQ 99  
DB 61 DEFLNTHALFESIKRKLPLFNWDAPFKLGLRSATPDAQ 99  
RESULT 13  
ABUS9097  
ID ABUS9097 standard; Protein; 99 AA.  
XX  
AC ABUS9097;  
XX  
DT 28-APR-2003 (first entry)  
XX  
DE Novel human secreted or transmembrane protein PRO826.  
XX  
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosum; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis.  
XX  
OS Homo sapiens.  
XX  
PN US2002132252-A1.  
XX  
PD 19-SEP-2002.  
XX  
PF 14-NOV-2001; 2001US-0990442.  
XX  
PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 06-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.

PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
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PR 04-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
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PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
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PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
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PR 18-JUN-1998; 98US-089907P.  
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PR 28-AUG-2001; 2001US-0941992.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
PI Ferrara N, Fong S, Gerber H, Gerlitsen ME, Goddard A, Godowski PJ,  
PI Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF,

PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX WPI; 2003-247083/24.  
DR N-PSDB; ABX80254.  
XX  
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
PT are therapeutically useful for enhancing immune response and in cancer  
PT treatments -  
XX  
PS Claim 12; Fig 129; 648pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO  
CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
CC in modulating at least one biological activity of a cell expressing a PRO  
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
CC useful for treating conditions or disorders where angiogenesis would be  
CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
CC useful for treating cancerous tumours. PRO812 inhibits vascular  
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
CC cells and is thus useful for inhibiting endothelial cell growth in  
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
CC rod photoreceptor cells) and therefore are useful for treating retinal  
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813  
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
CC and therefore are useful for treating kidney disorders associated with  
CC decreased mesangial cell function such as Berger disease or other  
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
CC proliferation and/or redifferentiation of chondrocytes in culture and  
CC are thus useful for treating sports injuries, and arthritis. This  
CC is the amino acid sequence of a novel human PRO protein.

XX SQ Sequence 99 AA;

Query Match 100.0%; Score 510; DB 24; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4.6e-57;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVPAVVLISLVLSAOGATLGPEESTIENTYASRPEAFNTPFLNIDKLSAFKA 60  
DB 1 MKIPVPAVVLISLVLSAOGATLGPEESTIENTYASRPEAFNTPFLNIDKLSAFKA 60

QY 61 DEFLNWHALFESIKRKLPLFNWDAFPKLGKRSATPDQAQ 99  
DB 61 DEFLNWHALFESIKRKLPLFNWDAFPKLGKRSATPDQAQ 99

RESULT 14

ABU59244  
ID ABU59244 standard; Protein; 99 AA.

XX AC ABU59244;

XX DT 22-APR-2003 (first entry)

XX DE Human secreted/transmembrane protein, #78.

XX KW Human; PRO; secreted; transmembrane; pharmaceutical;  
KW diagnostic; biosensor; bioreactor; tumour; therapeutic;  
KW gene therapy; tumour-associated antigenic target; TAT; ADAPT;  
KW antibody-dependent enzyme mediated produg therapy; cytostatic.

OS Homo sapiens.  
XX  
PN US2003027162-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 15-NOV-2001; 2001US-0997428.  
XX  
05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
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PR 11-AUG-1998; 98US-096143P.  
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PR 26-AUG-1998; 98US-097978P.  
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PR 26-AUG-1998; 98US-098014P.  
PR 31-AUG-1998; 98US-098525P.  
PR 16-SEP-1998; 98US-100634P.  
PR 17-SEP-1998; 98US-100858P.  
PR 22-DEC-1998; 98US-113296P.  
PR 12-MAR-1999; 99US-123957P.  
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Query Match 100.0%; Score 510; DB 24; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4.6e-57;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKIPVLPVAVLISLVLSHSAQATLGGPEESTIENTYASRPEAFNTPFNLIDKLSAFKA 60  
QY 61 DEFLNWHALFESIKRKLPEFLNWDAPFKLGLRSATPDAQ 99  
61 DEFLNWHALFESIKRKLPEFLNWDAPFKLGLRSATPDAQ 99  
Db 61 DEFLNWHALFESIKRKLPEFLNWDAPFKLGLRSATPDAQ 99

RESULT 15  
ABUS9393  
ID ABUS9393 standard; Protein; 99 AA.  
XX  
AC ABUS9393;  
XX  
DT 22-APR-2003 (first entry)  
XX  
DE Novel human secreted or transmembrane protein PRO819.

XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;

KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis.  
XX Homo sapiens.  
XX US2003027985-A1.  
XX 06-FEB-2003.  
XX 14-NOV-2001; 2001US-0990562.  
XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
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PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
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PR 22-MAY-2000; 2000WO-US14042.  
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PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
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PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
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PR 16-JUN-1997; 97US-049787P.  
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PR 03-JUN-1998; 98US-087827P.  
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PR 12-JUN-1998; 98US-089105P.  
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Search completed: November 28, 2003, 07:55:09  
Job time : 50 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 07:55:42 ; Search time 315 Seconds

(without alignments)  
57.968 Million cell updates/sec

Title: US-10-059-395-142

Perfect score: 510  
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Searched: 673684 seqs, 184443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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#### ALIGNMENTS

RESULT 1

US-09-989-722-201

Sequence 201, Application US/09989722

Patent No. US20020072067A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Geritsen, Mary B.

APPLICANT: Goddard, Audrey

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730P1C63

CURRENT APPLICATION NUMBER: US/09/989,722

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

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## RESULT 2

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 510; DB 9; Length 99;  
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; Patent No. US20020072496A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
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; APPLICANT: Gurney, Austin L.  
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; APPLICANT: Napier, Mary A.  
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; APPLICANT: Roy, Margaret Ann  
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; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC56  
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US-09-989-727-201  
; Sequence 201, Application US/09989727  
; Patent No. US20020072497A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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; APPLICANT: Ashkenazi, Avi J.  
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; APPLICANT: Williams, P. Mickey  
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; APPLICANT: Zhang, Zemin  
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; TITLE OF INVENTION: Acids Encoding the Same  
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US-09-989-732-201  
; Sequence 201, Application US/09989732  
; Patent No. US20020123463A1

## GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnovers, Luc  
;; APPLICANT: Eaton, Dan L.  
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;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730P1C57  
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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
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; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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; Patent No. US20020132252A1
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1  APPLICANT: Ashkenazi, Avi J.
2  APPLICANT: Baker, Kevin P.
3  APPLICANT: Botstein, David
4  APPLICANT: Desnoyers, Luc
5  APPLICANT: Baton, Dan L.
6  APPLICANT: Ferrara, Napoleone
7  APPLICANT: Fong, Sherman
8  APPLICANT: Gerber, Hanspeter
9  APPLICANT: Gerritsen, Mary E.
10 APPLICANT: Goddard, Audrey
11 APPLICANT: Godowski, Paul J.
12 APPLICANT: Grimaldi, J. Christopher
13 APPLICANT: Gurney, Austin L.
14 APPLICANT: Kljavin, Ivar J.
15 APPLICANT: Napier, Mary A.
16 APPLICANT: Pan, James
17 APPLICANT: Paoni, Nicholas F.
18 APPLICANT: Roy, Margaret Ann
19 APPLICANT: Stewart, Timothy A.
20 APPLICANT: Tumas, Daniel
21 APPLICANT: Watanabe, Colin K.
22 APPLICANT: Williams, P. Mickey
23 APPLICANT: Wood, William I.
24 APPLICANT: Zhang, Zemin
25 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
26 TITLE OF INVENTION: Acids Encoding the Same
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; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Williams, P. Mickey  
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; APPLICANT: Zhang, Zemin  
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Db 1 MKIPVLPAVLTLVLHSAQATLGPEESTIENTYASRPEAFNTPLNIDKLSAPKA 60

QY 61 DEFLNMHALFESIKRKLPELNWDAFPKLKGLRSATPDAQ 99

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## RESULT 10

US-09-993-604-201

; Sequence 201, Application US/09993604

; Patent No. US20020137075A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C25

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Db 61 DEFLNHALFESIKRKLPLFNWDAPFKLGLSATPDQ 99

## RESULT 11

US-09-990-456-201

; Sequence 201, Application US/09990456  
; Patent No. US20020137890A1

## GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC22

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;; PRIOR FILING DATE: 1998-07-09
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Query Match 100.0%; Score 510; DB 10; Length 99;  
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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
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; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
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; APPLICANT: Paoni, Nicholas F.  
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; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C55  
; CURRENT APPLICATION NUMBER: US/09/989,721  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
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; APPLICANT: Botstein, David
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; APPLICANT: Eaton, Dan L.
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Query Match 100.0%; Score 510; DB 10; Length 99;  
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Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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; Sequence 142, Application US/09984245  
; Patent No. US20020165374A1

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; FILE REFERENCE: P2004P1
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Db      61 DEFLNHALFESIKRKLPLFNWDAFPKLGKLSATPDAQ 99

RESULT 15
US-09-989-293A-201
; Sequence 201, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottlieb, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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Best Local Similarity 100.0%; Pred. No. 1,4e-55;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKIPVLPVAVLSTLVLSAAGATLGSPBEESTIENYASRPEAFNTPLNTDKLSAFKA 60  
QY 61 DEFLNHALFESIKKLPFLNWDAPFKLKGURSATPDAQ 99  
|||||

Db 61 DEFINWHLFESIKRKLPLINWDAPPKLGSRATPDAQ 99

Search completed: November 28, 2003, 08:03:02  
Job time : 319 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 08:04:48 ; Search time 230 Seconds

(without alignments)  
1161.932 Million cell updates/sec

Title: US-10-059-395-142

Perfect score: 510

Sequence: 1 MKIPVLPAVVLSSLVLHSA.....LNWDAPFKLGLRSATPDQ 99

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO.spool/US10059395/runat\_25112003\_140711\_7093/app.query.fasta\_1.263  
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_19Jun03:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	510	100.0	414	22 AAC91475	Human PRO826 cDNA.
2	510	100.0	414	24 ABK28600	Human DNA57694-134
3	510	100.0	415	21 AAZ65018	Membrane-bound pro
4	510	100.0	415	22 AAF30059	Human cDNA encodin
5	510	100.0	415	22 AAF44164	Human PRO826 (UNQ4
6	510	100.0	415	22 AAC97491	Human angiogenesis
7	510	100.0	415	24 ABL95626	Human encoding huma
8	510	100.0	415	24 ABK69971	Human PRO826 cDNA
9	510	100.0	415	24 ABK33608	CDNA encoding huma
10	510	100.0	415	24 ABK33608	Novel human secret
11	510	100.0	415	25 ABX80255	Human secreted/tr
12	510	100.0	415	25 ABX80759	Novel human secret
13	510	100.0	415	25 ABX81142	Human secreted/tr
14	510	100.0	415	25 ABX90232	Human PRO polynuc
15	510	100.0	415	25 ABX77843	Human PRO polynuc
16	510	100.0	415	25 ABX79439	Human secreted/tr
17	510	100.0	415	25 ABX64078	CDNA encoding huma
18	510	100.0	415	25 ABX17042	Human PRO polynuc
19	510	100.0	428	24 ABZ11803	Human polynucleoti
20	510	100.0	456	20 AAX00632	Human secreted pro
21	504	98.8	518	22 ABA09519	Human secreted pro
22	421	82.5	386	24 ABZ11804	Human polynucleoti
23	308	60.4	278	21 AAC68806	Human head/neck tu
24	278	54.5	305	24 ABZ11886	Human polynucleoti
25	267.5	52.5	288	25 ABX85674	Corn ear-derived p
26	255.5	50.1	413	24 ABL35083	Murine cDNA isolat
27	82.5	16.2	530	21 AAC01489	Human secreted pro
28	78.5	15.4	437	24 ABV96116	Human pancreatic c
29	78.5	15.4	686	21 AAZ80280	Human colon cancer
30	78.5	15.4	700	22 AAH23810	Human transferrase
31	78.5	15.4	2583	22 AAK80169	Human immune/haema
32	78.5	15.4	2583	22 AAK82168	Human immune/haema
33	78	15.3	3525	23 ABL23024	Drosophila melanog
34	78	15.3	5397	23 ABL08196	Drosophila melanog
35	77.5	15.2	2267	23 ABL25420	Drosophila melanog
36	77.5	15.2	4635	23 ABL24371	Drosophila melanog
37	77.5	15.2	7544	23 ABL24370	Drosophila melanog
38	73.5	14.4	2116	20 AAZ07515	Human RAP-2 clone
39	73.5	14.4	13868	22 AAK77131	Human immune/haema
40	72.5	14.2	1839	21 AAC46455	Arabidopsis thalia
41	72.5	14.2	2226	21 AAC43120	Arabidopsis thalia
42	72.5	14.2	2226	24 ABZ12478	Arabidopsis thalia
43	72	14.1	606	24 ABA92962	Human cDNA clone D
44	71	13.9	2631	21 AAC50996	Arabidopsis thalia
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# ALIGNMENTS

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ID AAC91475 standard; cDNA; 414 BP.  
XX AAC91475;  
AC  
XX 21-MAR-2001 (first entry)  
XX  
DE Human PRO826 cDNA.  
XX Human; PRO; antiinflammatory; dermatological; antiarthritic;  
KW antiinflammatory; cardiant; antihaemic; immunosuppressive; antithyroid;  
KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;  
KW antiallergic; antiaesthetic; immune related disorder;  
KW hepatobiliary disease; autoimmune disease; allergy; ss.  
XX  
OS Homo sapiens.



XX WO200073452-A2.  
PN  
XX  
PD 07-DEC-2000.  
XX  
PF 02-JUN-2000; 2000WO-US15264.  
XX  
PR 02-JUN-1999; 99WO-US12252.  
PR 20-JUL-1999; 99US-0144732.  
PR 20-JUL-1999; 99US-0144758.  
PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 29-OCT-1999; 99US-0162506.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28634.  
PR 09-DEC-1999; 99US-0170262.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;  
PI Wood WI;  
XX  
DR WPI; 2001-025253/03.  
DR P-PSDB; AAB50916.  
XX  
XX Thirty three nucleic acids encoding PRO polypeptides which are useful  
PT in the diagnosis and treatment of immune related disorders, e.g.  
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
PT thyroiditis and diabetes mellitus -  
XX  
PS Claim 48; Fig 29; 218bp; English.  
XX  
XX The present sequence is one of thirty three nucleic acids encoding PRO  
CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and  
CC antagonists are useful for treating and diagnosing immune related  
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
CC osteoarthritis, juvenile chronic inflammatory myopathies, Sjogren's  
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
CC demyelinating polynuropathy or Guillain-Barre syndrome, and chronic  
CC inflammatory demyelinating polynuropathy), hepatobiliary diseases  
CC (such as infectious, autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
CC food hypersensitivity and urticaria), immunological diseases of the  
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
CC and hypersensitivity pneumonitis), transplantation associated diseases  
CC including graft rejection and graft-versus-host diseases.  
XX  
XX Sequence 414 BP; 98 A; 126 C; 92 G; 98 T; 0 other;

Alignment Scores:		1.57e-60	Length:	414
Pred. No.:	Score:	510.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
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US-10-059-395-142 (1-99) x AAC91475 (1-414)

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DB	13	ATGAGATCCCGGTCCTTCCTGCCGTGGTGCTCTCTCCCTCGGTGCTCACTGCC	72
QY	21	GIingIAlaThrIeuGIyGIyProGIuGIuGIuSerThrIleGIuAsnIyAlaSerArg	40
DB	73	CAGGAGCCACCCCTGGGTGCTCTGAGGAAGAAGCACCATTTAGATATATGCCCTCACGA	132
QY	41	ProGIuAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla	60
DB	133	CCCGAGGCTTTAACACCCCGTTCTCTGAACATCGACAAATTGGATCTGCGTTTAAAGCT	192
QY	61	AspGIuPheLeuAsnTrpHisAlaLeuPheGIuSerIleLysArgLysLeuProPheLeu	80
DB	193	GATGAGTTCCTGAAGCTGACGCGCTCTTTGAGTCTATCAAAAGGAACCTTCTTCCTC	252
QY	81	AsnTrpAspAlaPheProLysLeuLysGIyLeuArgSerAlaThrProAspAlaGln	99
DB	253	AACTGGGATGCTTCTTCTTAAGCTGAAGAAGACTGAGAGCGCACTCCTGATGCCAG	309

RESULT 2

ABK28600

ABK28600 standard; cDNA; 414 BP.

XX AC ABK28600;

XX DT 09-APR-2002 (first entry)

XX DE Human DNA57694-1341 encoding PRO826.

XX KW Human; ss; gene; PRO; antiinflammatory; ophthalmological; vasotropic; retinal cell injury; ocular disease; retinitis pigmentosa; macular degeneration; retinal detachment; retinal tear; retinopathy; retinal degenerative disease; macular hole; degenerative myopia; acute retinal necrosis syndrome; traumatic chorioretinopathy; Purtscher's retinopathy; oedema; ischaemic condition; retinal vision occlusion; collagen vascular disease; thrombocytopaenic purpura; uveitis; retinal vasculitis; Eales disease; systemic lupus erythematosus; environmental trauma.

XX OS Homo sapiens.

XX WO200109327-A2.

XX PD 08-FEB-2001.

XX PF 28-JUL-2000; 2000WO-US20710.

XX PR 28-JUL-1999; 99US-146222P.

PR 13-SEP-1999; 99WO-US20944.

PR 15-SEP-1999; 99WO-US21090.

PR 29-NOV-1999; 99WO-US28214.

PR 30-NOV-1999; 99WO-US28313.

PR 01-DEC-1999; 99WO-US28301.

PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US05004.

PR 02-MAR-2000; 2000WO-US05841.

PR 15-MAR-2000; 2000WO-US06884.

PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;  
PI Kljavin IJ, Lafleur M, Mark MR, Marsters SA, Plichi RM,  
PI Watanabe CK, Wood WI;  
XX  
DR WPI; 2002-130120/17.  
DR P-PSDB; AAU81964.  
XX  
PT Promoting survival of retinal cells, or delaying or preventing retinal  
PT cell injury or death, by contacting retinal cells with PRO175, 220,  
PT 216, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132  
PT polypeptide -  
XX  
PS Claim 33; Fig 24; 152pp; English.  
XX  
CC The invention relates to promoting the survival of retinal cells, or  
CC delaying or preventing retinal cell injury or death, by contacting the  
CC retinal cells with the polypeptide such as PRO175, PRO220, PRO216,  
CC PRO243, PRO306, PRO346, PRO322, PRO536, PRO943, PRO840, PRO828, PRO826,  
CC PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids  
CC encoding the PRO proteins, a vector comprising the nucleic acid, a host  
CC cell comprising the vector, and anti-PRO antibody. The PRO proteins are  
CC useful for promoting survival of retinal cells (retinal neurons such as  
CC retinal ganglion cells, displaced retinal ganglion cells, amacrine  
CC cells, displaced amacrine cells, horizontal neurons or bipolar neurons,  
CC rod photoreceptors, or supportive cells such as Muller cells or pigment  
CC epithelial cells), or delaying or preventing retinal cell injury or  
CC death caused by ocular disease (which is or is associated with  
CC retinitis pigmentosa, macular degenerative disease, macular detachment, retinal  
CC tear, retinopathy, retinal degenerative disease, traumatic  
CC degenerative myopia, acute retinal necrosis syndrome, traumatic  
CC chorioretinopathy or contusion, Purtscher's retinopathy, oedema, an  
CC ischaemic condition, central or branch retinal vision occlusion,  
CC collagen vascular disease, thrombocytopaenic purpura, uveitis, retinal  
CC vasculitis, occlusion associated with Eales disease or systemic lupus  
CC erythematosus), retinal injury or environmental trauma. The retinal  
CC cell injury or death is delayed or prevented by substantially not  
CC causing angiogenesis or mitogenesis. The present sequence is a cDNA  
CC encoding a PRO protein.  
XX  
SQ Sequence 414 BP; 98 A; 126 C; 92 G; 98 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 1.57e-60 Length: 414  
Score: 510.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0  
  
US-10-059-395-142 (1-99) x ABK28600 (1-414)  
QY 1 MetLySileProValLeuProAlaValLeuLeuSerLeuLeuValLeuHisSerAla 20  
Db 13 ATGAAGATCCCGGTCTTCCTGCGGTGCTCTCTCCCTCTGCTGCTCCACTTGC 72  
QY 21 GlnGlyAlaThrLeuGlyGlyProGlnGlnGlnSerThrIleGluAsnTyrAlaSerArg 40  
Db 73 CAGGAGCCACCCCTGGTGTCTGAGAAAGAACACCATGAGAAATTATGCGTACGA 132  
QY 41 ProGlnAlaPheAsnThrProPheLeuAsnIleAspIleLeuArgSerAlaPheIleAla 60  
Db 133 CCGAGGCTTTAACAACCCGTTCTCGAACAATGCAATGCGTAAAGCT 192  
QY 61 AspGlnPheLeuAsnTrpHisAlaLeuPheGluSerIleLeuArgIleLeuProPheLeu 80  
Db 193 GATGAGTTCCTGAACGACGCGCTCTTGTAGTCTATCAAAAGAAACTTCTTCTC 252  
QY 81 AsnTrpAspAlaPheProIleLeuGlyLeuArgSerAlaThrProAspAlaGln 99

Db 253 AACTGGATGCTTTCCTTAAGCTGAAGAGACTGAGAGCGCAACTCCTGATGCCAG 309  
RESULT 3  
AAZ65018  
ID AAZ65018 standard; cDNA; 415 BP.  
XX  
AC AAZ65018;  
XX  
DT 05-APR-2000 (first entry)  
XX  
DE Membrane-bound protein PRO826 encoding cDNA.  
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9963088-A2.  
XX  
PD 09-DEC-1999.  
XX  
PF 02-JUN-1999; 99WO-US12252.  
XX  
PR 02-JUN-1998; 98US-0087607.  
PR 02-JUN-1998; 98US-0087609.  
PR 02-JUN-1998; 98US-0087759.  
PR 03-JUN-1998; 98US-0087827.  
PR 04-JUN-1998; 98US-0088021.  
PR 04-JUN-1998; 98US-0088025.  
PR 04-JUN-1998; 98US-0088028.  
PR 04-JUN-1998; 98US-0088029.  
PR 04-JUN-1998; 98US-0088030.  
PR 04-JUN-1998; 98US-0088033.  
PR 04-JUN-1998; 98US-0088326.  
PR 05-JUN-1998; 98US-0088167.  
PR 05-JUN-1998; 98US-0088202.  
PR 05-JUN-1998; 98US-0088212.  
PR 05-JUN-1998; 98US-0088217.  
PR 09-JUN-1998; 98US-0088655.  
PR 10-JUN-1998; 98US-0088722.  
PR 10-JUN-1998; 98US-0088730.  
PR 10-JUN-1998; 98US-0088734.  
PR 10-JUN-1998; 98US-0088738.  
PR 10-JUN-1998; 98US-0088740.  
PR 10-JUN-1998; 98US-0088741.  
PR 10-JUN-1998; 98US-0088742.  
PR 10-JUN-1998; 98US-0088810.  
PR 10-JUN-1998; 98US-0088811.  
PR 10-JUN-1998; 98US-0088824.  
PR 10-JUN-1998; 98US-0088825.  
PR 10-JUN-1998; 98US-0088826.  
PR 11-JUN-1998; 98US-0088858.  
PR 11-JUN-1998; 98US-0088861.  
PR 11-JUN-1998; 98US-0088863.  
PR 11-JUN-1998; 98US-0088876.  
PR 12-JUN-1998; 98US-0089090.  
PR 12-JUN-1998; 98US-0089105.  
PR 16-JUN-1998; 98US-0089440.  
PR 16-JUN-1998; 98US-0089512.  
PR 16-JUN-1998; 98US-0089514.  
PR 17-JUN-1998; 98US-0089532.  
PR 17-JUN-1998; 98US-0089538.  
PR 17-JUN-1998; 98US-0089598.  
PR 17-JUN-1998; 98US-0089599.  
PR 17-JUN-1998; 98US-0089600.  
PR 17-JUN-1998; 98US-0089653.  
PR 18-JUN-1998; 98US-0089801.  
PR 18-JUN-1998; 98US-0089907.  
PR 18-JUN-1998; 98US-0089908.  
PR 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089948.  
PR 19-JUN-1998; 98US-0089952.

PR 22-JUN-1998; 98US-0090246.  
PR 22-JUN-1998; 98US-0090252.  
PR 22-JUN-1998; 98US-0090254.  
PR 23-JUN-1998; 98US-0090349.  
PR 23-JUN-1998; 98US-0090355.  
PR 24-JUN-1998; 98US-0090429.  
PR 24-JUN-1998; 98US-0090431.  
PR 24-JUN-1998; 98US-0090435.  
PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090445.  
PR 24-JUN-1998; 98US-0090472.  
PR 24-JUN-1998; 98US-0090535.  
PR 24-JUN-1998; 98US-0090538.  
PR 24-JUN-1998; 98US-0090540.  
PR 24-JUN-1998; 98US-0090557.  
PR 25-JUN-1998; 98US-0090678.  
PR 25-JUN-1998; 98US-0090688.  
PR 25-JUN-1998; 98US-0090690.  
PR 25-JUN-1998; 98US-0090691.  
PR 25-JUN-1998; 98US-0090694.  
PR 25-JUN-1998; 98US-0090695.  
PR 25-JUN-1998; 98US-0090696.  
PR 26-JUN-1998; 98US-0090862.  
PR 26-JUN-1998; 98US-0090863.  
PR 01-JUL-1998; 98US-0091358.  
PR 01-JUL-1998; 98US-0091360.  
PR 01-JUL-1998; 98US-0091544.  
PR 02-JUL-1998; 98US-0091478.  
PR 02-JUL-1998; 98US-0091486.  
PR 02-JUL-1998; 98US-0091519.  
PR 02-JUL-1998; 98US-0091626.  
PR 02-JUL-1998; 98US-0091628.  
PR 02-JUL-1998; 98US-0091633.  
PR 02-JUL-1998; 98US-0091646.  
PR 02-JUL-1998; 98US-0091673.  
PR 07-JUL-1998; 98US-0091978.  
PR 07-JUL-1998; 98US-0091982.  
PR 09-JUL-1998; 98US-0092182.  
PR 10-JUL-1998; 98US-0092472.  
PR 20-JUL-1998; 98US-0093339.  
PR 30-JUL-1998; 98US-0094651.  
PR 04-AUG-1998; 98US-0095282.  
PR 04-AUG-1998; 98US-0095285.  
PR 04-AUG-1998; 98US-0095301.  
PR 04-AUG-1998; 98US-0095302.  
PR 04-AUG-1998; 98US-0095318.  
PR 04-AUG-1998; 98US-0095321.  
PR 04-AUG-1998; 98US-0095325.  
PR 10-AUG-1998; 98US-0095916.  
PR 10-AUG-1998; 98US-0095929.  
PR 10-AUG-1998; 98US-0096012.  
PR 11-AUG-1998; 98US-0096143.  
PR 11-AUG-1998; 98US-0096146.  
PR 12-AUG-1998; 98US-0096329.  
PR 17-AUG-1998; 98US-0096757.  
PR 17-AUG-1998; 98US-0096766.  
PR 17-AUG-1998; 98US-0096768.  
PR 17-AUG-1998; 98US-0096773.  
PR 17-AUG-1998; 98US-0096791.  
PR 17-AUG-1998; 98US-0096867.  
PR 17-AUG-1998; 98US-0096891.  
PR 17-AUG-1998; 98US-0096894.  
PR 17-AUG-1998; 98US-0096895.  
PR 17-AUG-1998; 98US-0096897.  
PR 18-AUG-1998; 98US-0096949.  
PR 18-AUG-1998; 98US-0096950.  
PR 18-AUG-1998; 98US-0096959.  
PR 18-AUG-1998; 98US-0096960.  
PR 18-AUG-1998; 98US-0097022.  
PR 19-AUG-1998; 98US-0097141.  
PR 20-AUG-1998; 98US-0097218.

PR 24-AUG-1998; 98US-0097661.  
PR 26-AUG-1998; 98US-0097951.  
PR 26-AUG-1998; 98US-0097952.  
PR 26-AUG-1998; 98US-0097954.  
PR 26-AUG-1998; 98US-0097955.  
PR 26-AUG-1998; 98US-0097971.  
PR 26-AUG-1998; 98US-0097974.  
PR 26-AUG-1998; 98US-0097978.  
PR 26-AUG-1998; 98US-0097979.  
PR 26-AUG-1998; 98US-0097986.  
PR 26-AUG-1998; 98US-0098014.  
PR 31-AUG-1998; 98US-0098525.  
PR 16-SEP-1998; 98US-0100634.  
PR 12-JAN-1999; 99US-0115565.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood WI, Yuan J;  
XX  
XX WPI; 2000-072883/06.  
DR P-PSDB; AAY66681.  
XX  
XX  
PT Membrane-bound proteins and related nucleotide sequences -  
XX  
XX Claim 2; Fig 128; 822pp; English.  
PS  
XX The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIE  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
CC will also be useful for the preparation of PRO polypeptides, especially  
CC by recombinant techniques.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 1.58e-60 Length: 415  
Score: 510.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 21 Gaps: 0  
  
US-10-059-395-142 (1-99) x AA265018 (1-415)  
  
QY 1 MetLysIleProValIleuProAlaValIleuLeuSerIleuLeuValIleuHisSerAla 20  
Db 13 ATGAAGATCCCGGTCTTCCTGCGGTGCTCTCTCCCTCGTGCTCCACTCTGCC 72  
  
QY 21 GInGIyAlaThrLeuGIyGIyProGIuGIuSerThrIleGIuAsnTYrAlaSerArg 40  
Db 73 CAGGAGCCACCCCTGGGTGCTCTGAGGAAGAAACCACTTGAGAAATTATGCGTCACGA 132  
  
QY 41 ProGIuAlaPheAsnThrProPheLeuAsnIleAspIlyLeuArgSerAlaPheIyAla 60  
Db 133 CCCGAGGCGCTTAAACACCCCGTTCCTGAACATGCAAAATTGCGATCTGCGTTTAAAGGCT 192  
  
QY 61 AspGIuPheLeuAsnTrpHisAlaLeuPheGluSerIleIySArgIlyLeuProPheLeu 80  
Db 193 GATGAGTTCCTGAACTGGACACGCCCTCTTGAGTCTATCAAAAGAAACTTCCTTCCTC 252  
  
QY 81 AsnTrpAspAlaPheProIySleuIySgIlyLeuArgSerAlaThrProAspAlaGln 99  
Db 253 AACTGGAGATGCCCTTCTCTAAGCTGAAGACTGAGAGCGCACTCCTGATGCCAG 309

RESULT 4  
AAF30059  
ID AAF30059 standard; cDNA; 415 BP.  
XX  
AC AAF30059;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Human cDNA encoding PRO826.  
XX  
KW PRO826; UNQ467; human; immune disease; autoimmune disease;  
KW antirheumatic; antiarthritic; antiinflammatory; antianaemic;  
KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
KW hepatotropic; virucide; dermatological; antipneumatic;  
KW antiaesthetic; antiallergic; immunostimulant; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 13..312  
FT sig\_peptide /+tag= a  
FT /+tag= b  
FT mat\_peptide /+tag= c  
FT /+tag= c  
XX  
PN WO200105972-A1.  
XX  
PD 25-JAN-2001.  
XX  
PF 15-MAR-2000; 2000WO-US06884.  
XX  
PR 20-JUL-1999; 99US-0144758.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;  
PI Hillan KJ, Mark MR, Masters SA, Pitti RM, Tumas D, Watanabe CK;  
PI Wood WJ;  
XX  
DR WPI; 2001-103149/11.  
DR P-PSDB; AAB20117.  
XX  
PT New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
PT diagnosing and creating immune-related disorders, such as multiple  
PT sclerosis, rheumatoid arthritis and diabetes -  
XX  
PS Claim 21; Fig 19; 127pp; English.  
XX  
CC The present sequence is that of cDNA clone DNA57694-1341 (ATCC 203017)  
CC encoding novel human immunomodulator protein PRO826 (UNQ467) (see  
CC AAB20117). The clone was isolated following a database search by  
CC applying a signal sequence algorithm. The predicted protein has a  
CC mol.wt. of 11 kDa and a pI of 7.47. The invention provides  
CC polynucleotides (see AAF30050-62) encoding novel human PRO proteins  
CC (see AAB20108-20) including PRO826. Claimed compositions  
CC comprising these proteins or their agonists are useful for increasing  
CC infiltration of inflammatory cells into a tissue of a mammal,  
CC stimulating or enhancing an immune response in a mammal, or  
CC increasing the proliferation of T-lymphocytes in a mammal in response  
CC to an antigen. Claimed compositions comprising the PRO polypeptide  
CC or its antagonist have the opposite effect. A claimed method for  
CC treating an immune related disorder, such as a T cell disorder,  
CC involves administering the PRO polypeptide, an agonist antibody or  
CC an antagonist antibody. The disorder is selected from systemic  
CC lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
CC juvenile chronic arthritis, spondyloarthritis, Sjogren's syndrome,  
CC sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome,  
CC systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia,  
CC autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinated diseases (such as  
CC multiple sclerosis), autoimmune chronic active hepatitis, primary

CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
CC inflammatory bowel disease (ulcerative colitis and Crohn's disease),  
CC gluten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated  
CC skin diseases (such as bullous skin disease, erythema multiforme and  
CC psoriasis), allergic diseases (such as asthma, allergic rhinitis,  
CC atopic dermatitis, food hypersensitivity and urticaria), immunologic  
CC diseases of the lung and transplantation associated diseases (such  
CC as graft rejection and graft-versus-host disease) (all claimed).  
CC Claimed methods of diagnosing these disorders comprise detecting  
CC the level of expression of the PRO gene. Also claimed are a method  
CC of identifying a compound capable of inhibiting the expression or  
CC activity of the PRO polypeptide, vectors, host cells, antibodies  
CC and a method of stimulating the proliferation of T-lymphocytes  
CC using PRO826.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
XX  
Alignment Scores:  
Pred. No.: 1,58e-60 Length: 415  
Score: 510.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0  
US-10-059-395-142 (1-99) x AAF30059 (1-415)  
QY 1 MetLysIleProValIleuProAlaValIleuSerLeuLeuValIleuHisSerAla 20  
Db 13 ATGAAGATCCCGGCTCTCCTGCGCTGCTCCTCCTCCTGCTGCTCACTGCTGCC 72  
QY 21 GlnGlyAlaThrLeuGlyGlyProGlnGlnGlnSerThrIleGlnAsnTyrAlaSerArg 40  
Db 73 CAGGAGCCACCCTGGTGTCTCTGAGGAGAGAGACCATTTGAGATTAATGCGTCAAGA 132  
QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
Db 133 CCCGAGGCTTTAAACACCCCGCTTCTGACATGACAAATTGCGATCTGCTTAAAGCT 192  
QY 61 AspGluPheLeuAsnTyrHisAlaLeuPheGlnSerIleLysArgLysLeuProPheLeu 80  
Db 193 GATGAGTCTCTGAACCTGGACGCGCCCTCTTGAAGTATCAAAAGGAACCTTCTTCTC 252  
QY 81 AsnTyrAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
Db 253 AACTGGATGCTTCTCTTAAGCTGAAGAGACTGAGAGCGCACTCTGATGCCAG 309  
RESULT 5  
AAF44164  
ID AAF44164 standard; cDNA; 415 BP.  
XX  
AC AAF44164;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Human PRO826 (UNQ467) nucleotide sequence SEQ ID NO:200.  
XX  
KW Human; secreted and transmembrane protein; PRO; cytosstatic;  
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
KW diagnostic assay; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200073454-A1.  
PD 07-DEC-2000.  
XX  
PF 30-MAR-2000; 2000WO-US08439.  
XX  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 07-JUL-1999; 99US-0143048.  
PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 17-AUG-1999; 99US-0149396.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 08-OCT-1999; 99US-0158663.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.

XX (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi CJ, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;

XX WPI; 2001-032160/04.

DR P-PSDB; AAB65204.

PT PRO polynucleotides used to produce polypeptides used to target  
 PT bioactive molecules such as toxins, radiolabels or antibodies, to  
 PT specific cells, to cause targeted cell death -

XX Claim 2; Fig 128; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO  
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins  
 CC can be used for targeted delivery of bioactive molecules, such as  
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
 CC sequences, and their fragments, can be used as hybridisation probes, in  
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
 CC and DNA. They may also be used to produce transgenic animals which are  
 CC used to develop and screen therapeutically useful reagents. The PRO  
 CC nucleotide and protein sequence can be used for tissue typing and in  
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.

XX Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

XX Alignment Scores:

Pred. No.: 1.58e-60 Length: 415  
 Score: 510.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0

US-10-059-395-142 (1-99) x AAF44164 (1-415)

OY 1 MetlyetleProValleuProAlaValleuLeuSerleuLeuValleuHisSerAla 20  
 DB 13 ATGAAGATCCCGGCTCTCCTGCGGTGCTCTCTCCCTCTGCTGCTCCACTGCGC 72  
 OY 21 GlnGlyAlaThrleuGlyGlyProGluGluGluSerThrIleGluValentYrAlaSerArg 40  
 DB 73 CAGGGAGCCACCTGGGTGCTCTGAGGAGAAAGACACCATGAGATATATGCTCAGCA 132

OY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
 DB 133 CCCGAGGCCCTTTAAACACCCCGTCTGAAATCATGCACAAATTCGATCTGCGTTAAGGCT 192  
 OY 61 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
 DB 193 GATGAGTTCCTGAAGTGGACGCGCCCTCTTGAAGTATCAAAAGAACTCTTCCTC 252  
 OY 81 AsnTrpAspAlaPheProLysLeuYsgLysLeuArgSerAlaThrProAspAlaGln 99  
 DB 253 AACTGGATGCTTTCCTAAGCTGAAGAGACTGAGAGCGCAACTCTGATGCCAG 309

RESULT 6

AAC97491

ID AAC97491 standard; cDNA; 415 BP.

XX AAC97491;

DT 28-FEB-2001 (first entry)

DE Human angiogenesis-associated protein PRO826 cDNA, SEQ ID NO:157.

XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
 KW gene therapy; transgenic animal; ss.

XX Homo sapiens.

XX WO200053753-A2.

XX 14-SEP-2000.

PF 05-JAN-2000; 2000WO-US00219.

XX 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.

XX (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Ferrera N, Gerber H, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
 PI Paoni NF, Platt RM, Watanabe CK, Williams PM, Wood WI;

DR WPI; 2001-090793/10.

DR P-PSDB; AAB53094.

PT New isolated nucleic acid for producing a PRO polypeptide, analyzing  
 PT genetic disorders and treating cardiovascular, endothelial or  
 PT angiogenic disorders, such as atherosclerosis, wounds or cancer -

PS Claim 58; Fig 61; 293pp; English.

XX The invention relates to novel human angiogenesis-associated proteins  
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
 CC PRO proteins. The invention also relates to vectors and host cells



CC comprising a PRO nucleic acid, the recombinant production of a PRO  
CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
CC compounds which inhibit the expression of a PRO gene. The invention  
CC additionally encompasses methods of identifying modulators of PRO  
CC expression or activity; diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
CC mutations in a PRO gene, or the expression level of a PRO gene within a  
CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
CC administration of a PRO protein, or an agonist or antagonist thereof.  
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
CC agonists and PRO antagonists may be used as therapeutic agents to treat  
CC cardiovascular, endothelial or angiogenic disorders, such as  
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
CC disease, or stroke. PRO nucleic acids are additionally useful in the  
CC recombinant production of PRO proteins, as hybridisation probes to  
CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
CC animals useful for the development and screening of potential  
CC therapeutic agents. The present sequence represents a cDNA encoding a PRO  
CC protein of the invention.

XX  
SQ Sequence 415 BP, 99 A; 126 C, 92 G, 98 T, 0 other;

Alignment Scores:

Pred. No.: 1.58e-60 Length: 415  
Score: 510.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0

US-10-059-395-142 (1-99) x AAC97491 (1-415)

QY 1 MetLySIIeProValLeuProAlaValValLeuLeuSerLeuLeuValLeuHisSerAla 20  
Db 13 ATGAAGATCCCGGTCCTTCCTGCGTGTCTCTCTCCTCTGCTCCACTCTGCT 72  
QY 21 GInGIyAlaThrLeuGIyGIyProGIyGIyLeuSerThrIleGIyAsnTYrAlaSerArg 40  
Db 73 CAGGAGCCACCCCTGGTGGTCTGAGGAAGAAAGCACCAATTGAGATTATGCGTCAGA 132  
QY 41 ProGIyAlaPheAsnThrProPheLeuAsnIleAspLySLeuArgSerAlaPheLySAla 60  
Db 133 CCCGAGGCTTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTAAGCT 192  
QY 61 AspGIyPheLeuAsnTrpHisAlaLeuPheGIySerIleLySArgLySLeuProPheLeu 80  
Db 193 GATGAGTTCCTGAAGTGCACGCGCTTTTGAGTCTATCAAAAGAACTTCTTCTC 252  
QY 81 AsnTrpAspAlaPheProLySLeuLySGLyLeuArgSerAlaThrProAspAlaGln 99  
Db 253 AACTGGATGCCCTTCTTAAGTGAAGAGACTGAGAGCGCACTCTGATGCCAG 309

RESULT 7

ABL95626  
ID ABL95626 standard; cDNA; 415 BP.

XX  
AC ABL95626;

XX  
DT 19-JUL-2002 (first entry)

DE Human angiogenesis related cDNA PRO826 SEQ ID NO: 131.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;

KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerable;  
KW antiarteriosclerotic; gene; ss.

OS Homo sapiens.

PN WO200208284-A2.

PD 31-JAN-2002.

PF 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 02-AUG-2000; 2000US-222695P.  
PR 17-AUG-2000; 2000US-0643657.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 07-SEP-2000; 2000US-230978P.  
PR 15-SEP-2000; 2000US-000000P.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-0709238.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 28-JUN-2001; 2001WO-US00000.

XX (GETH ) GENENTECH INC.  
PA (BAKE) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX WPI; 2002-171999/22.  
DR P-PSDB; ABB95488.

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal -  
XX  
XX  
PS Claim 1; Fig 131; 567pp; English.

CC The present invention provides the protein and coding sequences of human  
CC PRO proteins. These are useful for treating or diagnosing a  
CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
CC hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The present sequence is a coding sequence of the invention.

XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

## Alignment Scores:

Pred. No.:	1.58e-60	Length:	415
Score:	510.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-10-059-395-142 (1-99) x ABL95626 (1-415)

QY 1 MetLysileProValleuProAlaValleuLeuSerLeuLeuValleuHisSerAla 20  
|||  
Db 13 ATGAAGATCCCGGTCCTCTCCGCGGTGCTCCTCTCCCTCGGTGCTCCACTGTGCC 72  
QY 21 GlnGlyAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAsnTyrAlaSerArg 40  
|||  
Db 73 CAGGAGCCACCCTGGGTGCTCTGAGGAAGAAGACCAATTGAGAATTATGCTCAGCA 132  
QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
|||  
Db 133 CCCGAGCCTTTAACACCCCGTCTCTGAACATCGACAAATTGCGATCTGCGTTAAGGCT 192  
QY 61 AspGluPheLeuAsnTyrPheAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
|||  
Db 193 GATGAGTTCCTGAACCTGCGACCGCTCTTGAAGTCTATCAAAAGAACTTCTTCTC 252  
QY 81 AsnTyrAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
|||  
Db 253 AACTGGGATGCTTCTTCTTAAGCTGAAGAGACTGAGAGCGCACTCTGATGCCCAAG 309

RESULT 8  
ABK69971

ID ABK69971 standard; DNA; 415 BP.

AC ABK69971;

DT 15-JUL-2002 (first entry)

DE cDNA encoding human Pro peptide #11.

XX Human; ss; gene; PRO; secreted protein; transmembrane protein;

KW genetic disorder; tumour; cancer.

OS Homo sapiens.

PN WO200224888-A2.

PD 28-MAR-2002.

PF 29-AUG-2001; 2001WO-US27099.

PR 01-SEP-2000; 2000US-229896P.

PR 05-SEP-2000; 2000US-230621P.

PR 22-SEP-2000; 2000US-235147P.

PR 10-NOV-2000; 2000WO-US30873.

PR 12-JAN-2001; 2001US-261878P.

PR 16-JAN-2001; 2001US-261910P.  
PR 16-JAN-2001; 2001US-261939P.  
PR 16-JAN-2001; 2001US-262150P.  
PR 25-JAN-2001; 2001US-264395P.  
PR 02-FEB-2001; 2001US-266421P.  
PR 09-FEB-2001; 2001US-267623P.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 09-MAR-2001; 2001US-274399P.  
PR 03-APR-2001; 2001US-280982P.  
PR 04-APR-2001; 2001US-282129P.  
PR 04-APR-2001; 2001US-282199P.  
PR 09-MAY-2001; 2001US-290589P.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.

(GETH ) GENENTECH INC.

PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;

DR WPI; 2002-362426/39.  
DR P-PSDB; ABG34040.

PT New PRO polypeptides and polynucleotides encoding the polypeptides,  
PT useful in gene therapy, chromosome identification, tissue typing, or  
PT for genetic analysis of individuals with genetic disorders -

XX  
PS Claim 2; Figure 21; 218pp; English.

CC This invention relates to the cDNA and protein sequences of novel  
CC secreted and transmembrane polypeptides PRO polypeptides. The  
CC invention also comprises a method for producing the proteins of the  
CC invention by recombinant means and antibodies specific for the protein  
CC of the invention. The antibody may be used for detecting the PRO  
CC proteins of the invention and may be used to modify their activity.  
CC polynucleotides may be used as hybridisation probes for a cDNA library  
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, to  
CC construct hybridisation probes for mapping the gene which encodes that  
CC PRO and for genetic analysis of individuals with genetic disorders, in  
CC assays to identify other proteins or molecules involved in binding  
CC reaction, to generate transgenic animals or knock-out animals which in  
CC turn are useful in the development and screening of therapeutically  
CC useful reagents, for chromosome identification, and as molecular weight  
CC markers for protein electrophoresis purposes. The sequences may  
CC also be used to detect overexpression on PRO polypeptides in cancerous  
CC tumours and for screening for differentially expressed genes using  
CC microarray technology. The present sequence represents a cDNA encoding  
CC a human PRO protein of the invention.

XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

## Alignment Scores:

Pred. No.:	1.58e-60	Length:	415
Score:	510.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-10-059-395-142 (1-99) x ABK69971 (1-415)

QY 1 MetLysileProValleuProAlaValleuLeuSerLeuLeuValleuHisSerAla 20  
|||  
Db 13 ATGAAGATCCCGGTCCTCTGCGGTGCTCTCTCCCTCGGTGCTCCACTGTGCC 72  
QY 21 GlnGlyAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAsnTyrAlaSerArg 40  
|||  
Db 73 CAGGAGCCACCCTGGGTGCTCTGAGGAAGAAGACCAATTGAGAATTATGCTCAGCA 132

QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
DB 133 CCCGAGGCGCTTAACACCCCGTTCCTGACATCGACAAATTGCGATCTGCGTTAAGGCT 192  
QY 61 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
DB 193 GATGAGTTCCTGAACCTGCGACGCCCTCTTGAGTCTATCAAAAGAACTTCTTCCCTC 252  
QY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
DB 253 AACTGGATGCGCTTCTTAAGCTGAAGGAGGAGCGCAACTCTGATGCCAG 309  
RESULT 9  
ABL88137  
ID ABL88137 standard; cDNA; 415 BP.  
XX  
AC ABL88137;  
XX  
DT 16-MAY-2002 (first entry)  
XX  
DE Human PRO826 cDNA sequence SEQ ID NO:131.  
XX  
KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
KW vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
KW age-related macular degeneration; arterial restenosis; angina;  
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
KW wound healing; chromosome mapping; gene mapping; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200200690-A2.  
XX  
PD 03-JAN-2002.  
XX  
PF 20-JUN-2001; 2001WO-US19692.  
XX  
PR 23-JUN-2000; 2000US-213637P.  
PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 02-AUG-2000; 2000US-222695P.  
PR 17-AUG-2000; 2000US-0643657.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 07-SEP-2000; 2000US-230978P.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-0709238.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001US-0870574.

PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
XX  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX  
DR WPI; 2002-090516/12.  
DR P-PSDB; ABB84882.  
XX  
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal -  
XX  
PS Claim 2; Fig 131; 565pp; English.  
XX  
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
CC antiangiogenic, hypotensive, vulnerable and antiarteriosclerotic  
CC activities, and can be used in gene therapy. The PRO polynucleotides,  
CC proteins, agonists and antagonists are useful for treating or diagnosing  
CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
CC carcinoma) and wound healing. The PRO polynucleotides have applications  
CC in molecular biology, including use as hybridisation probes, and in  
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
CC probes used in the exemplification of the present invention.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

Alignment Scores:  
Pred. No.: 1.58e-60 Length: 415  
Score: 510.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0

US-10-059-395-142 (1-99) x ABL88137 (1-415)

QY 1 MetLysIleProValLeuProAlaValLeuLeuSerLeuLeuValLeuHisSerAla 20  
DB 13 ATGAAGATCCCGTCTTCTCCTGCGGTGCTCTCTCCCTCGTGTCTCACTCTGCC 72  
QY 21 GInGlyAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAsnTyraIaseArg 40  
DB 73 CAGGAGCCACCCCTGGTGGTCTCGAGGAAGAAGAACCATTTGAGATTTGCGTCACGA 132  
QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
DB 133 CCCGAGGCGCTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTAAGGCT 192  
QY 61 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
DB 193 GATGAGTTCCTGAACCTGCGACGCCCTCTTGAGTCTATCAAAAGAACTTCTTCCCTC 252  
QY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
DB 253 AACTGGATGCGCTTCTTAAGCTGAAGGAGGAGCGCAACTCTGATGCCAG 309  
RESULT 10  
ABK33608  
ID ABK33608 standard; cDNA; 415 BP.  
XX  
AC ABK33608;  
XX  
DT 08-MAY-2002 (first entry)  
XX

CDNA encoding human PRO protein, Seq ID No 145.

Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha; gene; ss.

Homo sapiens.

WO200208288-A2.

31-JAN-2002.

29-JUN-2001; 2001WO-US21066.

20-JUL-2000; 2000US-219556P.

25-JUL-2000; 2000US-220585P.

25-JUL-2000; 2000US-220605P.

25-JUL-2000; 2000US-220607P.

25-JUL-2000; 2000US-220624P.

25-JUL-2000; 2000US-220638P.

25-JUL-2000; 2000US-220664P.

25-JUL-2000; 2000US-220666P.

26-JUL-2000; 2000US-220893P.

28-JUL-2000; 2000WO-US20710.

23-AUG-2000; 2000WO-US23522.

24-AUG-2000; 2000WO-US23328.

15-SEP-2000; 2000US-000000P.

10-NOV-2000; 2000WO-US30873.

28-NOV-2000; 2000US-253646P.

01-DEC-2000; 2000WO-US32678.

20-DEC-2000; 2000US-0747259.

20-DEC-2000; 2000WO-US34956.

28-FEB-2001; 2001WO-US06520.

10-MAY-2001; 2001US-0854280.

25-MAY-2001; 2001WO-US17092.

(GETH ) GENENTECH INC.

Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI; WPI; 2002-172001/22.

P-PSDB; AAU83664.

One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour -

Claim 2; Figure 145; 359pp; English.

The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in pericyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the release of tumour necrosis factor-alpha from human dermal fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABK33536-ABK33657 represent human PRO protein coding sequences of the invention.

Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

Alignment Scores: 1.58e-60 Length: 415  
Pred. No.: 1

Score:	510.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0
US-10-059-395-142 (1-99) x ABK33608 (1-415)			
QY	1 MetLysIleProValIleuProAlaValIleuLeuSerLeuLeuValIleuHisSerAla 20		
Db	13 ATGAAGATCCCGGTCCTTCCTGCGGTGCTCTCCCTCTGGTGTCCACTCTGCC 72		
QY	21 GInGlyAlaThrIleuGlyGlyProGluGluGluSerThrIleGluAsnTyraSerArg 40		
Db	73 CAGGAGCCACCCTGGGTGTCTCTGAGGAAGAACACCATTTGAGATTATGCGTCACGA 13		
QY	41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60		
Db	133 CCCGAGCCCTTAAACACCCCGTTCCTGAACATGACAAATTGGATCTGCGTTAAAGCT 19		
QY	61 AspGluPheLeuAsnThrPHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80		
Db	193 GATGAGTTCCTGAACCTGGCAGCGCCCTTTGAGTCTATCAAAAGAACTCTTCCTC 25		
QY	81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99		
Db	253 AACTGGATGCTTCTCTAAGCTGAAGAGACTGAGAGCGCACTCCTGATGCCAG 309		
RESULT 11			
ID	ABX80255 standard; DNA; 415 BP.		
AC	ABX80255;		
XX	28-APR-2003 (first entry)		
DE	Novel human secreted or transmembrane protein PRO819 DNA.		
XX	Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;		
KW	cardiac insufficiency disorder; cancer; tumour; immune response;		
KW	adrenal cortical capillary endothelial growth; c-fos induction;		
KW	vascular endothelial growth factor inhibition; VEGF inhibition;		
KW	endothelial cell growth inhibitor; T-lymphocytes stimulation;		
KW	retinal neurons cell survival; rod photoreceptor cell survival;		
KW	retinal disorder; retinitis pigmentosa; kidney disorder;		
KW	mammalian kidney mesangial cell proliferation; Berger disease;		
KW	dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation;		
KW	chondrocyte redifferentiation; sports injury; arthritis; gene; ds.		
XX	Homo sapiens.		
OS	US2002132252-A1.		
PN	19-SEP-2002.		
XX	14-NOV-2001; 2001US-0990442.		
PF	05-NOV-1997; 97WO-US20069.		
XX	16-SEP-1998; 98WO-US19330.		
PR	17-SEP-1998; 98WO-US19437.		
PR	07-OCT-1998; 98WO-US21141.		
PR	01-DEC-1998; 98WO-US25108.		
PR	05-JAN-1999; 99WO-US00106.		
PR	08-MAR-1999; 99WO-US05028.		
PR	02-JUN-1999; 99WO-US12252.		
PR	15-SEP-1999; 99WO-US21090.		
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XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin LJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI: 2003-247083/24.
DR P-PSDB; ABUS9098.
XX
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments -
XX
PS Claim 2; Fig 130; 648pp; English.
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and
CC are thus useful for treating sports injuries, and arthritis. This
CC sequence represents a novel human PRO protein polynucleotide.
XX
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

Alignment Scores:
Pred. No.: 1,58e-60 Length: 415
Score: 510.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 25 Gaps: 0

US-10-059-395-142 (1-99) x ABX80255 (1-415)

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Db 13 ATGAAGATCCCGGTCTCTGCGGTGTGCTCTCCCTGCTGCTCACTGCC 72
QY 21 GlnGlyAlaThrIeuGlyGlyProGluGluGluSerThrIleGluAsnTyrlaSerArg 40.
Db 73 CAGGAGACCACTGCGGTGTGCTCTGAGGAAGAAGACCATTGAGATATATGCTCACGA 132
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QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
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QY 61 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
Db 193 GATGAGTTCCTGAACCTGGCAGCCCTCTTTGAGTCTATCAAAAGAAACTTCTTCTC 252  
QY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
Db 253 AACTGGATGCCCTTCTCTAAGCTGAAGACTGAGAGCGCAGCACTCCTGATGCCCAAG 309  
RESULT 12  
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ID ABX80759 standard; cDNA; 415 BP.  
XX ABX80759;  
AC  
XX 22-APR-2003 (first entry)  
DT  
XX Human secreted/transmembrane protein cDNA, #78.  
DE  
XX Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;  
KW diagnostic; biosensor; bioreactor; tumour; therapeutic;  
KW gene therapy; tumour-associated antigenic target; TAT; ADEPT;  
KW antibody-dependent enzyme mediated prodnug therapy; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN US2003027162-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 15-NOV-2001; 2001US-0997428.  
XX  
XX 05-NOV-1997; 97WO-US20069.  
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PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
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XX  
XX  
PA (GETH ) GENENTECH INC.

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PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NP;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;

XX WPI; 2003-288106/28.  
DR P-PSDB; ABU60528.  
XX

PT New transmembrane polypeptides and nucleic acids encoding the  
PT polypeptides, useful in gene therapy, in chromosome identification, as  
PT chromosome markers, or in generating probes -  
XX

PS Claim 2; Fig 128; 650pp; English.

XX  
CC The invention discloses isolated PRO secreted/transmembrane polypeptides  
CC comprising a sequence without signal peptide and the nucleic acid  
CC encoding them. The polypeptides can be used to raise antibodies that  
CC specifically bind to the PRO polypeptide, for linking a bioactive  
CC molecule to a cell expressing a PRO protein and for modulating at least  
CC one biological activity of a cell. The PRO polypeptides or  
CC polynucleotides are also useful in gene therapy, in chromosome  
CC identification, as chromosome markers, or in generating probes. The PRO  
CC polypeptides are useful as molecular markers for protein  
CC electrophoresis, and the isolated nucleic acids may be used for  
CC recombinantly expressing those markers. The PRO polypeptides and nucleic  
CC acids may also be used in tissue typing. Anti-PRO antibodies are useful  
CC in diagnostic assays for PRO, and in affinity purification of PRO from  
CC recombinant cell culture or natural sources. The sequences presented in  
CC ABX90083-ABX90468 are the genes encoding, the primers amplifying and the  
CC probes detecting the PRO polynucleotides of the invention.  
CC Note: The sequence data for this patent is also available in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX

SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

Alignment Scores:

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RESULT 15

ABX77843  
ID ABX77843 standard; cDNA; 415 BP.

XX  
AC ABX77843;

DT 14-APR-2003 (first entry)

DE Human PRO polynucleotide #51.

XX  
KW Human; PRO; gene; ss; cytosstatic; tumour; cancer; breast; lung; stomach;  
KW liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;  
KW antibody-dependent enzyme mediated prodrug therapy.

XX  
OS Homo sapiens.

XX  
PN US2003027163-A1.

XX  
PD 06-FEB-2003.

PF 15-NOV-2001; 2001US-0997666.

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PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
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PR 07-OCT-1998; 98WO-US21141.  
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US-10-059-395-142 (1-99) x ABX77843 (1-415)

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

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Title: US-10-059-395-142

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#### SUMMARIES

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#### ALIGNMENTS

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; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C63  
CURRENT APPLICATION NUMBER: US/09/989,722  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
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QY	61	AspGIuPheLeuAsnTrpHisAlaLeuPheGIuSerIleLysArgLysLeuProPheLeu	80
Db	193	GATGAGTTCCTGAACCTGGCACGCCCTCTTTGAGTCTATCAAAAGAAACTTCCTTCTC	252
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; GENERAL INFORMATION:  
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; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone

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: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
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: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
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: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
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;; PRIOR FILING DATE: 1998-07-09

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US-09-989-279-200

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; Patent No. US20020072496A1

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; APPLICANT: Desnoyers, Luc

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; APPLICANT: Zhang, Zemin

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; TITLE OF INVENTION: Acids Encoding the Same

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;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity: 100.00% Mismatches: 0  
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; Sequence 200, Application US/09989727  
; Patent No. US20020072497A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: KJavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C65  
; CURRENT APPLICATION NUMBER: US/09/989,727  
; PRIOR FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
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## Alignment Scores:

Pred. No.:	7.79e-67	Length:	415
Score:	510.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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US-10-059-395-142 (1-99) x US-09-989-727-200 (1-415)

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## RESULT 5

US-09-989-731-200

; Sequence 200, Application US/09989731

; Patent No. US20020103125A1

; GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C70
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Query Match:	100.00%	Indels:	0
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## RESULT 7

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US-09-991-073-200
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; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
Pred. No.: 7.79e-67 Length: 415  
Score: 510.00 Matches: 99  
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US-10-059-395-142 (1-99) x US-09-991-073-200 (1-415)

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; Sequence 200, Application US/09990442  
; Patent No. US20020132252A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavln, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tuma, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C8  
; CURRENT APPLICATION NUMBER: US/09/990,442  
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; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
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; APPLICANT: Goddard, Audrey J.  
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; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
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QY	61	AspGluPheIeuAsnTrpHisAlaIeuPheGluSerIleLysArgLysIeuProPheIeu	80
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US-09-993

US-09-993-604-200

; GENERAL INFORMATION:

1	APPLICANT:	Ashkenazi, Avi J.
2	APPLICANT:	Baker, Kevin P.
3	APPLICANT:	Botstein, David
4	APPLICANT:	Desnoyers, Luc
5	APPLICANT:	Eaton, Dan L.
6	APPLICANT:	Ferrara, Napoleone
7	APPLICANT:	Fong, Sherman
8	APPLICANT:	Gerber, Hanspeter
9	APPLICANT:	Gerritsen, Mary E.
10	APPLICANT:	Goddard, Audrey
11	APPLICANT:	Godowski, Paul J.
12	APPLICANT:	Grimaldi, J. Christopher
13	APPLICANT:	Gurney, Austin L.
14	APPLICANT:	Kl javin, Ivar J.
15	APPLICANT:	Napier, Mary A.
16	APPLICANT:	Pan, James
17	APPLICANT:	Paoni, Nicholas F.
18	APPLICANT:	Roy, Margaret Ann
19	APPLICANT:	Stewart, Timothy A.
20	APPLICANT:	Tumas, Daniel
21	APPLICANT:	Watanabe, Colin K.
22	APPLICANT:	Williams, P. Mickey
23	APPLICANT:	Wood, William I.

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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

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PRIOR FILING DATE:	1998-07-02
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PRIOR APPLICATION NUMBER:	60/091633
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091978
PRIOR FILING DATE:	1998-07-07
PRIOR APPLICATION NUMBER:	60/091982
PRIOR FILING DATE:	1998-07-07
PRIOR APPLICATION NUMBER:	60/092182
PRIOR FILING DATE:	1998-07-09

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US-09-990-456-200

; Sequence 200, Application US/09990456

; Patent No. US20020137890A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

[illegible]



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; PRIOR FILING DATE: 1998-06-25
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US-09-989-721-200
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

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Db 73 CAGGAGCCACCCTGGGTGCTCTGAGGAGAGAACCACTTGAGATTATGCGTCACGA 132  
QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
Db 133 CCCGAGGCCCTTTAACACCCCGTCTCTGACATCGAACAAATTGCGATCTGCTTTAAGGCT 192  
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; GENERAL INFORMATION:  
; APPLICANT: Aehkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
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; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.:	7.79e-67	Length:	415
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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-059-395-142 (1-99) X US-09-592-598-200 (1-415)

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Db 133 CCCGAGGCGCTTAAACACCCCGTCTCTGACATCGACAATTCGATCGCTTAAAGCT 192  
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Db 193 GATGAGTTCCTGAAGTGGACGCGCCCTCTTGAGTCTATCAAGAAGAACTTCTTCCTC 252  
QY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
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; Sequence 200, Application US/09989293A  
; Patent No. US20020177164A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Geritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PlC66  
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65	PRIOR FILING DATE: 1998-07-07
66	PRIOR APPLICATION NUMBER: 60/092182
67	PRIOR FILING DATE: 1998-07-09

Alignment Scores:	
Pred. No.:	7.79e-67
Score:	510.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Length:	415
Matches:	99
Conservative:	0
Mismatches:	0





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 ; PRIOR FILING DATE: 1998-07-09

Alignment Scores:	
Pred. No.:	7.79e-67
Score:	510.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	10
Length:	415
Matches:	99
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-059-395-142 (1-99) x US-09-989-735-200 (1-415)

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Job time : 270 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 13:39:58 ; Search time 35 Seconds

(without alignments)  
321.988 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Perfect score: 71

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	71	100.0	99	22	AAW65204
5	71	100.0	99	22	AAW50916
6	71	100.0	99	22	AAW53094
7	71	100.0	99	23	ABW6586
8	71	100.0	99	23	ABW95488
9	71	100.0	99	23	ABW34040

10	71	100.0	99	23	ABW84882	Human PRO826 prote
11	71	100.0	99	23	AAW83664	Human PRO protein,
12	71	100.0	99	23	AAW81964	Human PRO826. Hom
13	71	100.0	99	24	ABW59097	Novel human secret
14	71	100.0	99	24	ABW59244	Human secreted/tra
15	71	100.0	99	24	ABW59393	Novel human secret
16	71	100.0	99	24	ABW60528	Human secreted/tra
17	71	100.0	99	24	ABW58019	Human PRO polypept
18	71	100.0	99	24	ABW58950	Human secreted/tr
19	71	100.0	99	24	ABW13910	Human PRO826 polyp
20	71	100.0	99	24	ABW10865	Human PRO polypept
21	43	60.6	85	23	ABW69587	Human polypeptide
22	28	39.4	96	23	ABW69669	Human polypeptide
23	7	9.9	237	21	AAW60989	Arabidopsis thalia
24	7	9.9	238	21	AAW60988	Arabidopsis thalia
25	7	9.9	243	18	AAW09423	Banana polyphenol
26	7	9.9	246	21	AAW60987	Arabidopsis thalia
27	7	9.9	329	22	AAW38193	Salmonella typhi c
28	7	9.9	350	21	AAW96587	Glycine max isofla
29	7	9.9	351	21	AAW96585	Glycine max isofla
30	7	9.9	496	23	ABW93237	C. albicans BAX-as
31	7	9.9	1605	22	ABW70375	Drosophila melanog
32	6	8.5	18	17	AAW98980	Antimicrobial, cat
33	6	8.5	18	17	AAW98981	Antimicrobial, cat
34	6	8.5	18	17	AAW98982	Antimicrobial, cat
35	6	8.5	36	22	ABW50615	Human liver peptid
36	6	8.5	36	22	ABW30598	Peptide #3249 enco
37	6	8.5	36	22	ABW35762	Peptide #3268 enco
38	6	8.5	36	22	ABW21186	Protein #3185 enco
39	6	8.5	36	22	AAW56572	Human brain expres
40	6	8.5	36	22	AAW68952	Human bone marrow
41	6	8.5	36	22	AAW16778	Peptide #3212 enco
42	6	8.5	36	22	AAW29263	Peptide #3300 enco
43	6	8.5	36	22	AAW04495	Peptide #3177 enco
44	6	8.5	36	23	ABW38538	Human peptide enco
45	6	8.5	45	21	AAW09356	Hepatitis GB virus

ALIGNMENTS

RESULT 1	AAW67828	standard; Protein; 99 AA.
ID	AAW67828;	
XX	AAW67828;	
AC	AAW67828;	
XX	AAW67828;	
DT	25-MAR-1999	(first entry)
XX	25-MAR-1999	(first entry)
DE	Human secreted protein encoded by gene 22 clone HFEAF41.	
XX	Human; secreted protein; fusion protein; gene therapy; protein therapy;	
KW	diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;	
KW	developmental abnormality; foetal deficiency; blood; allergy; renal;	
KW	immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;	
KW	inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;	
KW	cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thyroid;	
KW	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;	
KW	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	Homo sapiens.	
PN	WO9842738-A1.	
XX	WO9842738-A1.	
PD	01-OCT-1998.	
XX	01-OCT-1998.	
PF	19-MAR-1998;	98WO-US05311.
XX	19-MAR-1998;	98WO-US05311.
PR	30-MAY-1997;	97US-0050937.
PR	21-MAR-1997;	97US-0041276.
PR	21-MAR-1997;	97US-0041277.
PR	21-MAR-1997;	97US-0041281.
PR	21-MAR-1997;	97US-0042344.

PR 30-MAY-1997; 97US-0048069.  
PR 30-MAY-1997; 97US-0048094.  
PR 30-MAY-1997; 97US-0048095.  
PR 30-MAY-1997; 97US-0048096.  
PR 30-MAY-1997; 97US-0048099.  
PR 30-MAY-1997; 97US-0048131.  
PR 30-MAY-1997; 97US-0048135.  
PR 30-MAY-1997; 97US-0048154.  
PR 30-MAY-1997; 97US-0048160.  
PR 30-MAY-1997; 97US-0048186.  
PR 30-MAY-1997; 97US-0048187.  
PR 30-MAY-1997; 97US-0048188.  
PR 30-MAY-1997; 97US-0048350.  
PR 30-MAY-1997; 97US-0048351.  
PR 30-MAY-1997; 97US-0048352.  
PR 30-MAY-1997; 97US-0048355.  
PR 05-AUG-1997; 97US-0054804.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA;  
PI Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS;  
PI Rosen CA, Ruben SM, Shi Y, Young P;  
XX  
DR WPI; 1999-070066/06.  
DR N-PSDB; AAX00632.  
XX  
PT New isolated human genes and the secreted polypeptides they encode -  
PT useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders  
XX  
PS Claim 11, Page 285; 385pp; English.  
XX  
CC This sequence represents a secreted human protein encoded by the gene  
CC clone detailed in the descriptor line. The gene can be used to generate  
CC fusion proteins by linking to the gene to a human immunoglobulin Fc  
CC portion (e.g. AAX00602) for increasing the stability of the fused  
CC protein as compared to the human protein only.  
CC The invention relates to 87 novel genes and their fragments (nucleic  
CC acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004)  
CC which are useful for preventing, treating or ameliorating medical  
CC conditions e.g. by protein or gene therapy. Also, pathological  
CC conditions can be diagnosed by determining the amount of the new  
CC polypeptides in a sample or by determining the presence of mutations in  
CC the new polynucleotides. Specific uses are described for each of the 87  
CC polynucleotides, based on which tissues they are most highly expressed in  
CC (see AAX00611 for described uses).  
XX  
SQ Sequence 99 AA;  
Query Match 100.0%; Score 71; DB 20; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.6e-69;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EEESTIENYASRPEAFNTPLNIDKLSAFKADDFLNWHLFESIKRKLPLFNWDAFPKL 60  
Db 29 EEESTIENYASRPEAFNTPLNIDKLSAFKADDFLNWHLFESIKRKLPLFNWDAFPKL 88  
QY 61 KGLRSATPDQAQ 71  
Db 89 KGLRSATPDQAQ 99  
RESULT 2  
ID AAY66681 standard; protein; 99 AA.  
XX  
AC AAY66681;  
XX  
DT 05-APR-2000 (first entry)  
XX  
DE Membrane-bound protein PRO826.  
XX

KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIR ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping.  
XX  
OS Homo sapiens.  
XX W09963088-A2.  
PN  
XX  
PD 09-DEC-1999.  
XX  
PF 02-JUN-1999; 99WO-US12252.  
XX  
PR 02-JUN-1998; 98US-0087607.  
PR 02-JUN-1998; 98US-0087609.  
PR 02-JUN-1998; 98US-0087759.  
PR 03-JUN-1998; 98US-0087827.  
PR 04-JUN-1998; 98US-0088021.  
PR 04-JUN-1998; 98US-0088025.  
PR 04-JUN-1998; 98US-0088028.  
PR 04-JUN-1998; 98US-0088029.  
PR 04-JUN-1998; 98US-0088030.  
PR 04-JUN-1998; 98US-0088033.  
PR 04-JUN-1998; 98US-0088326.  
PR 05-JUN-1998; 98US-0088167.  
PR 05-JUN-1998; 98US-0088202.  
PR 05-JUN-1998; 98US-0088212.  
PR 05-JUN-1998; 98US-0088217.  
PR 09-JUN-1998; 98US-0088655.  
PR 10-JUN-1998; 98US-0088722.  
PR 10-JUN-1998; 98US-0088730.  
PR 10-JUN-1998; 98US-0088734.  
PR 10-JUN-1998; 98US-0088738.  
PR 10-JUN-1998; 98US-0088740.  
PR 10-JUN-1998; 98US-0088741.  
PR 10-JUN-1998; 98US-0088742.  
PR 10-JUN-1998; 98US-0088810.  
PR 10-JUN-1998; 98US-0088811.  
PR 10-JUN-1998; 98US-0088824.  
PR 10-JUN-1998; 98US-0088825.  
PR 10-JUN-1998; 98US-0088826.  
PR 11-JUN-1998; 98US-0088828.  
PR 11-JUN-1998; 98US-0088861.  
PR 11-JUN-1998; 98US-0088863.  
PR 11-JUN-1998; 98US-0088876.  
PR 12-JUN-1998; 98US-0089090.  
PR 12-JUN-1998; 98US-0089105.  
PR 16-JUN-1998; 98US-0089440.  
PR 16-JUN-1998; 98US-0089512.  
PR 16-JUN-1998; 98US-0089514.  
PR 17-JUN-1998; 98US-0089532.  
PR 17-JUN-1998; 98US-0089538.  
PR 17-JUN-1998; 98US-0089598.  
PR 17-JUN-1998; 98US-0089599.  
PR 17-JUN-1998; 98US-0089600.  
PR 17-JUN-1998; 98US-0089653.  
PR 18-JUN-1998; 98US-0089801.  
PR 18-JUN-1998; 98US-0089907.  
PR 18-JUN-1998; 98US-0089908.  
PR 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089948.  
PR 19-JUN-1998; 98US-0089952.  
PR 22-JUN-1998; 98US-0090246.  
PR 22-JUN-1998; 98US-0090252.  
PR 22-JUN-1998; 98US-0090254.  
PR 23-JUN-1998; 98US-0090349.  
PR 23-JUN-1998; 98US-0090355.  
PR 24-JUN-1998; 98US-0090429.  
PR 24-JUN-1998; 98US-0090431.  
PR 24-JUN-1998; 98US-0090435.  
PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090445.  
PR 24-JUN-1998; 98US-0090461.  
PR 24-JUN-1998; 98US-0090472.  
PR 24-JUN-1998; 98US-0090535.

PR 24-JUN-1998; 98US-0090538.  
PR 24-JUN-1998; 98US-0090540.  
PR 24-JUN-1998; 98US-0090557.  
PR 25-JUN-1998; 98US-0090676.  
PR 25-JUN-1998; 98US-0090678.  
PR 25-JUN-1998; 98US-0090688.  
PR 25-JUN-1998; 98US-0090690.  
PR 25-JUN-1998; 98US-0090691.  
PR 25-JUN-1998; 98US-0090694.  
PR 25-JUN-1998; 98US-0090695.  
PR 25-JUN-1998; 98US-0090696.  
PR 26-JUN-1998; 98US-0090862.  
PR 26-JUN-1998; 98US-0090863.  
PR 01-JUL-1998; 98US-0091358.  
PR 01-JUL-1998; 98US-0091360.  
PR 01-JUL-1998; 98US-0091544.  
PR 02-JUL-1998; 98US-0091478.  
PR 02-JUL-1998; 98US-0091486.  
PR 02-JUL-1998; 98US-0091519.  
PR 02-JUL-1998; 98US-0091626.  
PR 02-JUL-1998; 98US-0091628.  
PR 02-JUL-1998; 98US-0091633.  
PR 02-JUL-1998; 98US-0091646.  
PR 02-JUL-1998; 98US-0091673.  
PR 07-JUL-1998; 98US-0091978.  
PR 07-JUL-1998; 98US-0091982.  
PR 09-JUL-1998; 98US-0092182.  
PR 10-JUL-1998; 98US-0092472.  
PR 20-JUL-1998; 98US-0093339.  
PR 30-JUL-1998; 98US-0094651.  
PR 04-AUG-1998; 98US-0095282.  
PR 04-AUG-1998; 98US-0095285.  
PR 04-AUG-1998; 98US-0095301.  
PR 04-AUG-1998; 98US-0095302.  
PR 04-AUG-1998; 98US-0095318.  
PR 04-AUG-1998; 98US-0095321.  
PR 04-AUG-1998; 98US-0095325.  
PR 10-AUG-1998; 98US-0095916.  
PR 10-AUG-1998; 98US-0095929.  
PR 10-AUG-1998; 98US-0096012.  
PR 11-AUG-1998; 98US-0096143.  
PR 11-AUG-1998; 98US-0096146.  
PR 12-AUG-1998; 98US-0096329.  
PR 17-AUG-1998; 98US-0096757.  
PR 17-AUG-1998; 98US-0096766.  
PR 17-AUG-1998; 98US-0096768.  
PR 17-AUG-1998; 98US-0096773.  
PR 17-AUG-1998; 98US-0096791.  
PR 17-AUG-1998; 98US-0096867.  
PR 17-AUG-1998; 98US-0096891.  
PR 17-AUG-1998; 98US-0096894.  
PR 17-AUG-1998; 98US-0096895.  
PR 17-AUG-1998; 98US-0096897.  
PR 18-AUG-1998; 98US-0096949.  
PR 18-AUG-1998; 98US-0096950.  
PR 18-AUG-1998; 98US-0096959.  
PR 18-AUG-1998; 98US-0096960.  
PR 18-AUG-1998; 98US-0097022.  
PR 19-AUG-1998; 98US-0097141.  
PR 20-AUG-1998; 98US-0097218.  
PR 24-AUG-1998; 98US-0097661.  
PR 26-AUG-1998; 98US-0097951.  
PR 26-AUG-1998; 98US-0097952.  
PR 26-AUG-1998; 98US-0097954.  
PR 26-AUG-1998; 98US-0097955.  
PR 26-AUG-1998; 98US-0097971.  
PR 26-AUG-1998; 98US-0097974.  
PR 26-AUG-1998; 98US-0097978.  
PR 26-AUG-1998; 98US-0097979.  
PR 26-AUG-1998; 98US-0097986.  
PR 26-AUG-1998; 98US-0098014.  
PR 31-AUG-1998; 98US-0098525.  
PR 16-SEP-1998; 98US-0100634.

PR 12-JAN-1999; 99US-0115565.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood WI, Yuan J;  
XX  
DR WPI; 2000-072883/06.  
DR N-PSDB; AA265018.  
XX  
PT Membrane-bound proteins and related nucleotide sequences -  
XX  
PS claim 12; Fig 129; 822pp; English.  
XX  
CC The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIE  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
CC will also be useful for the preparation of PRO polypeptides, especially  
CC by recombinant techniques.  
XX  
SQ Sequence 99 AA;  
  
Query Match 100.0%; Score 71; DB 21; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.6e-69;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 EESTIENYASRPEAFNTPLNIDKLSAFKADEFNLNWHALFESIKRKLPLNWDAPKX. 60  
Db 29 EESTIENYASRPEAFNTPLNIDKLSAFKADEFNLNWHALFESIKRKLPLNWDAPKX. 88  
QY 61 KGLRSATPDAQ 71  
Db 89 KGLRSATPDAQ 99  
  
RESULT 3  
ID AAB20117 standard; Protein; 99 AA.  
XX  
AC AAB20117;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Human immunostimulant PRO826.  
XX  
KW PRO826; UNQ467; human; immune disease; autoimmune disease;  
KW antirheumatic; antiarthritic; antiinflammatory; antianaemic;  
KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
KW hepatotropic; virucide; dermatological; antipsoriatic;  
KW antiasthmatic; antiallergic; immunostimulant.  
XX  
OS Homo sapiens.  
XX  
FH Key location/Qualifiers  
FH Peptide 1..22  
FT /label= signal\_peptide  
FT Protein 23..99  
FT /label= Mature\_protein  
FT Modified-site 22..28  
FT /note= "N-myristoylation site"  
FT Modified-site 90..96  
FT /note= "N-myristoylation site"  
FT Region 16..48  
FT /note= "homology to peroxidase"



```
XX PN WO200105972-A1.
XX PD 25-JAN-2001.
XX PF 15-MAR-2000; 2000WO-US06884.
XX PR 20-JUL-1999; 99US-0144758.
XX PA (GETH ) GENENTECH INC.
XX PI Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;
XX PI Hillan KJ, Mark MR, Masters SA, Pitti RM, Tumas D, Watanabe CK;
XX PI Wood WI;
XX DR WPI; 2001-103149/11.
XX DR N-PSDB; AAF30059.
XX PT New PRO polypeptides, nucleic acids and (ant)agonists, useful for
XX PT diagnosing and treating immune-related disorders, such as multiple
XX PT sclerosis, rheumatoid arthritis and diabetes -
XX PS Claim 20; Fig 20; 127pp; English.
XX CC The present sequence is that of novel human immunomodulator PRO826
XX CC (UNQ467), as deduced from cDNA (see AAF30059) isolated from a
XX CC database screening. PRO826 has a mol.wt. of 11 kDa and a pI of
XX CC 7.47. The invention provides polynucleotides (see AAF30050-62)
XX CC encoding novel human PRO proteins (see AAB20108-20) including PRO826.
XX CC Claimed compositions comprising these proteins or their agonists
XX CC are useful for increasing infiltration of inflammatory cells into
XX CC a tissue of a mammal, stimulating or enhancing an immune
XX CC response, or increasing the proliferation of T-lymphocytes in a
XX CC mammal in response to an antigen. Claimed compositions comprising
XX CC a PRO polypeptide or its antagonist have the opposite effect. A
XX CC claimed method for treating an immune related disorder, such as a T
XX CC cell disorder, involves administering a PRO polypeptide, an agonist
XX CC antibody or an antagonist antibody. The disorder is selected from
XX CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
XX CC juvenile chronic arthritis, spondyloarthritis, systemic sclerosis,
XX CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
XX CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
XX CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated
XX CC renal disease, demyelinated diseases (such as multiple sclerosis),
XX CC autoimmune chronic hepatitis, primary biliary cirrhosis,
XX CC granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel
XX CC disease (ulcerative colitis and Crohn's disease), gluten-sensitive
XX CC enteropathy, Whipple's disease, (auto)immune-mediated skin diseases
XX CC (such as bullous skin disease, erythema multiforme and psoriasis),
XX CC allergic diseases (such as asthma, allergic rhinitis, atopic
XX CC dermatitis, food hypersensitivity and urticaria), immunologic
XX CC diseases of the lung and transplantation associated diseases (such
XX CC as graft rejection and graft-versus-host disease) (all claimed).
XX CC Claimed methods of diagnosing these disorders comprise detecting
XX CC the level of expression of the PRO gene. Also claimed are a method
XX CC of identifying a compound capable of inhibiting the expression or
XX CC activity of the PRO polypeptide, vectors, host cells, antibodies,
XX CC and a method of stimulating the proliferation of T lymphocytes
XX CC using PRO826.
XX SQ Sequence 99 AA;
XX Query Match 100.0%; Score 71; DB 22; Length 99;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-69;
XX Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EESTIENYASRPEAFNTPLNIDKLSAFKADDFLNMWALFESIKRKLPLNWDAPFKL 60
Db 29 EESTIENYASRPEAFNTPLNIDKLSAFKADDFLNMWALFESIKRKLPLNWDAPFKL 88
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QY 61 KGLRSATPDAQ 71
Db 89 KGLRSATPDAQ 99
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RESULT 4
AAB65204
ID AAB65204 standard; Protein; 99 AA.
XX AC AAB65204;
XX DT 02-APR-2001 (first entry)
XX DE Human PRO826 (UNQ467) protein sequence SEQ ID NO:201.
XX KW Human; secreted and transmembrane protein; PRO; cytosstatic;
XX KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
XX KW diagnostic assay.
XX OS Homo sapiens.
XX PN WO200073454-A1.
XX PD 07-DEC-2000.
XX PF 30-MAR-2000; 2000WO-US08439.
XX PR 02-JUN-1999; 99WO-US12252.
XX PR 23-JUN-1999; 99US-0141037.
XX PR 07-JUL-1999; 99US-0143048.
XX PR 20-JUL-1999; 99US-0144758.
XX PR 26-JUL-1999; 99US-0145698.
XX PR 28-JUL-1999; 99US-0146222.
XX PR 17-AUG-1999; 99US-0149396.
XX PR 15-SEP-1999; 99WO-US21090.
XX PR 15-SEP-1999; 99WO-US21547.
XX PR 08-OCT-1999; 99US-0158663.
XX PR 30-NOV-1999; 99WO-US28313.
XX PR 01-DEC-1999; 99WO-US28301.
XX PR 16-DEC-1999; 99WO-US30095.
XX PR 20-DEC-1999; 99WO-US30911.
XX PR 05-JAN-2000; 2000WO-US00219.
XX PR 06-JAN-2000; 2000WO-US00376.
XX PR 11-FEB-2000; 2000WO-US03565.
XX PR 18-FEB-2000; 2000WO-US04341.
XX PR 22-FEB-2000; 2000WO-US04414.
XX PR 24-FEB-2000; 2000WO-US04914.
XX PR 24-FEB-2000; 2000WO-US05004.
XX PR 02-MAR-2000; 2000WO-US05841.
XX PR 15-MAR-2000; 2000WO-US06884.
XX PR 20-MAR-2000; 2000WO-US07377.
XX PA (GETH ) GENENTECH INC.
XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
XX PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoi NF;
XX PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
XX PI Zhang Z;
XX DR WPI; 2001-032160/04.
XX DR N-PSDB; AAF44164.
XX PT PRO polynucleotides used to produce polypeptides used to target
XX PT bioactive molecules such as toxins, radiolabels or antibodies, to
XX PT specific cells, to cause targeted cell death -
XX PS Claim 12; Fig 129; 935pp; English.
XX CC The present invention describes human secreted and transmembrane PRO
XX CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
XX CC can be used for targeted delivery of bioactive molecules, such as
XX CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
XX CC sequences, and their fragments, can be used as hybridisation probes, in
XX CC chromosomal and gene mapping, and in the generation of anti-sense RNA
XX CC and DNA. They may also be used to produce transgenic animals which are
```

CC used to develop and screen therapeutically useful reagents. The PRO  
CC nucleotide and protein sequence can be used for tissue typing and in  
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.

XX  
SQ Sequence 99 AA;

Query Match 100.0%; Score 71; DB 22; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.6e-69;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 60  
|||  
Db 29 EESTTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 88

QY 61 KGLRSATPDQAQ 71  
|||  
Db 89 KGLRSATPDQAQ 99

RESULT 5  
AAB50916  
ID AAB50916 standard; Protein; 99 AA.

XX  
AC AAB50916;

DT 21-MAR-2001 (first entry)

XX  
DE Human PRO826 protein.

XX  
KW Human; PRO; antiinflammatory; dermatological; antiarthritic;  
KW antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;  
KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;  
KW antiallergic; antiasthmatic; immune related disorder;  
KW hepatobiliary disease; autoimmune disease; allergy.

XX  
OS Homo sapiens.

XX  
PN WO200073452-A2.

XX  
PD 07-DEC-2000.

XX  
PF 02-JUN-2000; 2000WO-US15264.

XX  
PR 02-JUN-1999; 99WO-US12252.

XX  
PR 20-JUL-1999; 99US-0144732.

XX  
PR 20-JUL-1999; 99US-0144758.

XX  
PR 28-JUL-1999; 99US-0146222.

XX  
PR 01-SEP-1999; 99WO-US20111.

XX  
PR 15-SEP-1999; 99WO-US21090.

XX  
PR 15-SEP-1999; 99WO-US21547.

XX  
PR 29-OCT-1999; 99US-0162506.

XX  
PR 30-NOV-1999; 99WO-US28313.

XX  
PR 01-DEC-1999; 99WO-US28634.

XX  
PR 09-DEC-1999; 99US-0170262.

XX  
PR 20-DEC-1999; 99WO-US30911.

XX  
PR 05-JAN-2000; 2000WO-US00219.

XX  
PR 06-JAN-2000; 2000WO-US00376.

XX  
PR 11-FEB-2000; 2000WO-US03565.

XX  
PR 18-FEB-2000; 2000WO-US04341.

XX  
PR 22-FEB-2000; 2000WO-US04414.

XX  
PR 24-FEB-2000; 2000WO-US04914.

XX  
PR 15-MAR-2000; 2000WO-US06884.

XX  
PR 20-MAR-2000; 2000WO-US07377.

XX  
PR 21-MAR-2000; 2000WO-US07532.

XX  
PR 30-MAR-2000; 2000WO-US08439.

XX  
PR 17-MAY-2000; 2000WO-US13705.

XX  
PR 22-MAY-2000; 2000WO-US14042.

PA (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;

PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;

PI Wood WI;

XX WPI; 2001-025253/03.

DR N-PSDB; AAC91475.

XX Thirty three nucleic acids encoding PRO polypeptides which are useful

PT in the diagnosis and treatment of immune related disorders, e.g.

PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,

PT thyroiditis and diabetes mellitus -

XX Claim 58; Fig 30; 218pp; English.

XX The present sequence is one of thirty three novel PRO polypeptides.

CC The PRO polypeptides, anti-PRO antibodies, agonists and

CC antagonists are useful for treating and diagnosing immune related

CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,

CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,

CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's

CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic

CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,

CC immune-mediated renal disease, demyelinating diseases of the central

CC and peripheral nervous systems (such as multiple sclerosis, idiopathic

CC demyelinating polynuropathy or Guillain-Barre syndrome, and chronic

CC inflammatory demyelinating polynuropathy), hepatobiliary diseases

CC (such as infectious, autoimmune chronic active hepatitis, primary

CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),

CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's

CC disease, autoimmune or immune-mediated skin diseases (such as bullous

CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),

CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,

CC food hypersensitivity and urticaria), immunological diseases of the

CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis

CC and hypersensitivity pneumonitis), transplantation associated diseases

CC including graft rejection and graft-versus-host diseases.

XX  
SQ Sequence 99 AA;

Query Match 100.0%; Score 71; DB 22; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.6e-69;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 60  
|||  
Db 29 EESTTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 88

QY 61 KGLRSATPDQAQ 71  
|||  
Db 89 KGLRSATPDQAQ 99

RESULT 6  
AAB53094  
ID AAB53094 standard; Protein; 99 AA.

XX  
AC AAB53094;

DT 28-FEB-2001 (first entry)

XX  
DE Human angiogenesis-associated protein PRO826, SEQ ID NO:158.

XX  
KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;

KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;

KW angiotensin disorder; atherosclerosis; osteoporosis; hypertension;

KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;

KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;

KW Alzheimer's disease; Huntington's disease; stroke; drug screening;

XX  
KW gene therapy; transgenic animal.

XX  
OS Homo sapiens.

XX WO200053753-A2.  
PN  
XX 14-SEP-2000.  
PD  
XX 05-JAN-2000; 2000WO-US00219.  
PF  
XX 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
XX  
DR WPI; 2001-090793/10.  
DR N-PSDB; AAC97491.  
XX  
PT New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
PT  
XX  
PS Claim 69; Fig 62; 293pp; English.  
XX  
CC The invention relates to novel human angiogenesis-associated proteins  
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
CC PRO proteins. The invention also relates to vectors and host cells  
CC comprising a PRO nucleic acid, the recombinant production of a PRO  
CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
CC compounds which inhibit the expression of a PRO gene. The invention  
CC additionally encompasses methods of identifying modulators of PRO  
CC expression or activity; diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
CC mutations in a PRO gene, or the expression level of a PRO gene within a  
CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
CC administration of a PRO protein, or an agonist or antagonist thereof.  
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
CC agonists and PRO antagonists may be used as therapeutic agents to treat  
CC cardiovascular, endothelial or angiogenic disorders, such as  
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
CC disease, or stroke. PRO nucleic acids are additionally useful in the  
CC recombinant production of PRO proteins, as hybridisation probes to  
CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
CC animals useful for the development and screening of potential  
CC therapeutic agents. The present sequence represents a PRO protein of the  
CC invention.  
XX  
SQ Sequence 99 AA;

Query Match 100.0%; Score 71; DB 22; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.6e-69;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EEESTIENYASRPEAFNTPLINIDKLSAFKADFLNWHALFESIKRKLPLNWDAPPKL 60  
DB 29 EEESTIENYASRPEAFNTPLINIDKLSAFKADFLNWHALFESIKRKLPLNWDAPPKL 88  
QY 61 KGLRSATPDAQ 71  
DB 89 KGLRSATPDAQ 99  
RESULT 7  
ID ABP69586 standard; Protein; 99 AA.  
XX  
AC ABP69586;  
XX  
DT 20-JAN-2003 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 1633.  
XX  
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;  
KW cell-proliferative disorder; neurodegenerative disease; bacterial;  
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;  
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;  
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;  
KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;  
KW antiarthritic.  
XX  
OS Homo sapiens.  
XX  
PN WO200270539-A2.  
XX  
PD 12-SEP-2002.  
XX  
PF 05-MAR-2002; 2002WO-US05095.  
XX  
PR 05-MAR-2001; 2001US-0799451.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Zhou F, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;  
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
PI Wehrman T, Wang J, Wang D, Drmanac RT;  
XX  
DR WPI; 2002-759812/82.  
DR N-PSDB; ABZ11803.  
XX  
PS Claim 9; SEQ ID NO 1633; 1012pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated polynucleotide (I) comprising a  
CC nucleotide sequence selected from any of 948 sequences  
CC (ABZ1119-ABZ12066) or their mature protein coding portion, active domain  
CC coding protein or complementary sequences. The polynucleotides are useful  
CC for identifying expressed genes or for physical mapping of human genome.  
CC The encoded polypeptides (ABP69902-ABP69849) are useful as molecular  
CC weight markers, as a food supplement, for generating antibodies, in  
CC medical imaging, screening and diagnostic assays and for treating  
CC cell-proliferative disorders (cancer), neurodegenerative diseases  
CC (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple  
CC sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid  
CC disorders, platelet or coagulation disorders, wound, burns, incision,  
CC ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal,  
CC parasitic), arthritis, etc.  
CC  
CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 99 AA;

Query Match 100.0%; Score 71; DB 23; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.6e-69;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTIENYASRPEAFNTPFLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 60  
Db 29 EESTIENYASRPEAFNTPFLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 88

QY 61 KGLRSATPDQAQ 71  
Db 89 KGLRSATPDQAQ 99

RESULT 8  
ABB95488  
ID ABB95488 standard; Protein; 99 AA.  
XX  
AC ABB95488;

DT 19-JUL-2002 (first entry)

DE Human angiogenesis related protein PRO826 SEQ ID NO: 132.

KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
KW cardiant; cyostatic; antiangiogenic; hypotensive; vulnerary;  
KW antiarteriosclerotic.

OS Homo sapiens.

XX WO200208284-A2.

PD 31-JAN-2002.

PF 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 02-AUG-2000; 2000US-222695P.  
PR 17-AUG-2000; 2000US-0643657.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 07-SEP-2000; 2000US-230978P.  
PR 15-SEP-2000; 2000US-000000P.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-0709238.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.

PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 28-JUN-2001; 2001WO-US00000.

XX (GETH ) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN W E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODDOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANT/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX WPI; 2002-171999/22.  
DR N-PSDB; ABI95626.

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal -

PS Claim 11; Fig 132; 567pp; English.

XX The present invention provides the protein and coding sequences of human  
CC PRO proteins. These are useful for treating or diagnosing a  
CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
CC hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The present sequence is a PRO protein of the invention.

XX Sequence 99 AA;

Query Match 100.0%; Score 71; DB 23; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.6e-69;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTIENYASRPEAFNTPFLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 60  
Db 29 EESTIENYASRPEAFNTPFLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 88

QY 61 KGLRSATPDQAQ 71  
Db 89 KGLRSATPDQAQ 99

RESULT 9  
ABG34040  
ID ABG34040 standard; Protein; 99 AA.  
XX  
AC ABG34040;

DT 15-JUL-2002 (first entry)

DE Human Pro peptide #11.

KW Human; PRO; secreted protein; transmembrane protein;  
KW genetic disorder; tumour; cancer.

OS Homo sapiens.  
XX WO200224888-A2.  
PN  
XX  
PD 28-MAR-2002.  
XX  
PF 29-AUG-2001; 2001WO-US27099.  
XX  
PR 01-SEP-2000; 2000US-229896P.  
PR 05-SEP-2000; 2000US-230621P.  
PR 22-SEP-2000; 2000US-235147P.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 12-JAN-2001; 2001US-261878P.  
PR 16-JAN-2001; 2001US-261910P.  
PR 16-JAN-2001; 2001US-261939P.  
PR 16-JAN-2001; 2001US-262150P.  
PR 25-JAN-2001; 2001US-264395P.  
PR 02-FEB-2001; 2001US-266421P.  
PR 09-FEB-2001; 2001US-267623P.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 09-MAR-2001; 2001US-274399P.  
PR 03-APR-2001; 2001US-280982P.  
PR 04-APR-2001; 2001US-282129P.  
PR 04-APR-2001; 2001US-282199P.  
PR 09-MAY-2001; 2001US-290589P.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;  
XX  
DR WPI; 2002-362426/39.  
DR N-PSDB; ABK69971.  
XX  
PT New PRO polypeptides and polynucleotides encoding the polypeptides,  
PT useful in gene therapy, chromosome identification, tissue typing, or  
PT for genetic analysis of individuals with genetic disorders -  
XX  
PS Claim 11; Figure 22; 218bp; English.  
XX  
CC This invention relates to the cDNA and protein sequences of novel  
CC secreted and transmembrane polypeptides PRO polypeptides. The  
CC invention also comprises a method for producing the proteins of the  
CC invention by recombinant means and antibodies specific for the protein  
CC of the invention. The antibody may be used for detecting the PRO  
CC proteins of the invention and may be used to modify their activity.  
CC polynucleotides may be used as hybridisation probes for a cDNA library  
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, to  
CC construct hybridisation probes for mapping the gene which encodes that  
CC PRO and for genetic analysis of individuals with genetic disorders, in  
CC assays to identify other proteins or molecules involved in binding  
CC reaction, to generate transgenic animals or knock-out animals which in  
CC turn are useful in the development and screening of therapeutically  
CC useful reagents, for chromosome identification, and tissue typing. The  
CC PRO polypeptides are useful in gene therapy, and as molecular weight  
CC markers for protein electrophoresis purposes. The sequences may  
CC also be used to detect overexpression on PRO polypeptides in cancerous  
CC tumours and for screening for differentially expressed genes using  
CC microarray technology. The present sequence represents a human PRO  
CC protein of the invention.  
XX  
SQ Sequence 99 AA;

Query Match 100.0%; Score 71; DB 23; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.6e-69;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEESTIENYASRPEAFNTPELNIDKLSAFKADFLNWHALFESIKRKLPTLNWDAPPKL 60  
Db 29 EEESTIENYASRPEAFNTPELNIDKLSAFKADFLNWHALFESIKRKLPTLNWDAPPKL 88  
QY 61 KGLRSATPDAQ 71  
Db 89 KGLRSATPDAQ 99

RESULT 10  
ABB84882  
ID ABB84882 standard; Protein; 99 AA.  
XX  
AC ABB84882;  
XX  
DT 16-MAY-2002 (first entry)  
XX  
DE Human PRO826 protein sequence SEQ ID NO:132.  
XX  
KW Human; angiogenesis; cardiac; cytostatic; antiangiogenic; hypotensive;  
KW vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
KW age-related macular degeneration; arterial restenosis; angina;  
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
KW wound healing; chromosome mapping; gene mapping.  
XX  
OS Homo sapiens.  
XX  
PN WO200200690-A2.  
XX  
PD 03-JAN-2002.  
XX  
PF 20-JUN-2001; 2001WO-US19692.  
XX  
PR 23-JUN-2000; 2000US-213637P.  
PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 02-AUG-2000; 2000US-222695P.  
PR 17-AUG-2000; 2000US-0643657.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 07-SEP-2000; 2000US-230978P.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-0709238.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001US-0870574.  
PR 01-JUN-2001; 2001WO-US17800.  
XX  
PA (GETH ) GENENTECH INC.



XX Baker KP, Ferrara N, Gerber H, Gertlisen MB, Goddard A, Goddard PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF, Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX WPI; 2002-090516/12.  
DR N-PSDB; ABL88137.  
XX  
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -  
XX  
PS Claim 11; Fig 132; 565pp; English.  
XX  
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention.  
XX  
SQ Sequence 99 AA;  
Query Match 100.0%; Score 71; DB 23; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.6e-69;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EESTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 60  
DB 29 EESTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 88  
QY 61 KGLRSATPDAQ 71  
DB 89 KGLRSATPDAQ 99  
RESULT 11  
ID AAV83664 standard; Protein; 99 AA.  
XX  
AC AAV83664;  
DT 08-MAY-2002 (first entry)  
XX  
DE Human PRO protein, Seq ID No 146.  
XX  
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha.  
XX  
OS Homo sapiens.  
XX  
PN WO200208288-A2.  
PD 31-JAN-2002.  
XX  
PF 29-JUN-2001; 2001WO-US21066.  
XX  
PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220585P.  
PR 25-JUL-2000; 2000US-220605P.  
PR 25-JUL-2000; 2000US-220607P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220638P.  
XX

PR 25-JUL-2000; 2000US-220664P.  
PR 25-JUL-2000; 2000US-220666P.  
PR 26-JUL-2000; 2000US-220893P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 15-SEP-2000; 2000US-000000P.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 28-NOV-2000; 2000US-253646P.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001WO-US17092.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Goddard PJ, Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
XX WPI; 2002-172001/22.  
DR N-PSDB; ABK33608.  
XX  
PT One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour -  
XX  
PS Claim 11; Figure 146; 359pp; English.  
XX  
CC The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, CC agonists and antagonists are useful for treating a PRO related disorder. CC The PRO polypeptides are useful for diagnosing tumours, especially lung CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or CC liver tumour. The PRO polypeptides are useful for stimulating the CC proliferation of, or gene expression, in pericyte cells, for stimulating CC the proliferation or differentiation of chondrocyte cells, for CC stimulating the release of tumour necrosis factor-alpha from human blood, CC for stimulating or inhibiting the proliferation of normal human dermal CC fibroblast cells. The PRO polypeptide may also be used as molecular CC weight markers and for tissue typing. The PRO nucleic acids have CC applications in molecular biology, including use as hybridisation probes, CC and in chromosome and gene mapping. AAV83592-AAV83713 represent human PRO CC protein sequences of the invention.  
XX  
SQ Sequence 99 AA;  
Query Match 100.0%; Score 71; DB 23; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.6e-69;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EESTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 60  
DB 29 EESTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 88  
QY 61 KGLRSATPDAQ 71  
DB 89 KGLRSATPDAQ 99  
RESULT 12  
ID AAV81964 standard; Protein; 99 AA.  
XX  
AC AAV81964;  
DT 09-APR-2002 (first entry)  
XX  
DE Human PRO826.  
XX

KW Human; PRO; antiinflammatory; ophthalmological; vasotropic;  
KW retinal cell injury; ocular disease; retinitis pigmentosa;  
KW macular degeneration; retinal detachment; retinal tear; retinopathy;  
KW retinal degenerative disease; macular hole; degenerative myopia;  
KW acute retinal necrosis syndrome; traumatic chorioretinopathy;  
KW Purtscher's retinopathy; oedema; ischaemic condition;  
KW retinal vision occlusion; collagen vascular disease;  
KW thrombocytopenic purpura; uveitis; retinal vasculitis; Bales disease;  
KW systemic lupus erythematosus; environmental trauma.  
XX Homo sapiens.  
XX WO200109327-A2.  
XX 08-FEB-2001..  
XX 28-JUL-2000; 2000WO-US20710.  
XX 28-JUL-1999; 99US-146222P.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
XX (GETH ) GENENTECH INC.  
XX Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;  
PI Kljavin IJ, Lafleur M, Mark MR, Masters SA, Pitti RM;  
PI Watanabe CK, Wood WI;  
XX WPI; 2002-130120/17.  
DR N-PSDB; ABK28600.  
XX Promoting survival of retinal cells, or delaying or preventing retinal  
PT cell injury or death, by contacting retinal cells with PRO175, 220,  
PT 216, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132  
PT polypeptide -  
XX Claim 44; Fig 25; 152pp; English.  
PS The invention relates to promoting the survival of retinal cells, or  
XX delaying or preventing retinal cell injury or death, by contacting the  
CC retinal cells with the polypeptide such as PRO175, PRO220, PRO216,  
CC PRO243, PRO306, PRO346, PRO322, PRO536, PRO943, PRO840, PRO828, PRO826,  
CC PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids  
CC encoding the PRO proteins, a vector comprising the nucleic acid, a host  
CC cell comprising the vector, and anti-PRO antibody. The PRO proteins are  
CC useful for promoting survival of retinal cells (retinal neurons such as  
CC retinal ganglion cells, displaced retinal ganglion cells, amacrine  
CC cells, displaced amacrine cells, horizontal neurons or bipolar neurons,  
CC rod photoreceptors, or supportive cells such as Muller cells or pigment  
CC epithelial cells), or delaying or preventing retinal cell injury or  
CC death caused by ocular disease (which is or is associated with  
CC retinitis pigmentosa, macular degenerative disease, macular hole,  
CC tear, retinopathy, retinal degenerative disease, traumatic  
CC degenerative myopia, acute retinal necrosis syndrome, traumatic  
CC chorioretinopathy or contusion, Purtscher's retinopathy, oedema, an  
CC ischaemic condition, central or branch retinal vision occlusion,  
CC collagen vascular disease, thrombocytopenic purpura, uveitis, retinal  
CC vasculitis, occlusion associated with Bales disease or systemic lupus  
CC erythematosus), retinal injury or environmental trauma. The retinal  
CC cell injury or death is delayed or prevented by substantially not

CC causing angiogenesis or mitogenesis. The present sequence represents  
CC a PRO protein.  
XX  
SQ Sequence 99 AA;  
Query Match 100.0%; Score 71; DB 23; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.6e-69;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EESTIENYASRPEAFNTPLNIDKLSAFKADDFLNWHLFESIKRKLPLFNWDAPFKL 60  
DB 29 EESTIENYASRPEAFNTPLNIDKLSAFKADDFLNWHLFESIKRKLPLFNWDAPFKL 88  
QY 61 KGLRSATPDAQ 71  
DB 89 KGLRSATPDAQ 99  
RESULT 13  
ABUS9097  
ID ABUS9097 standard; Protein, 99 AA.  
XX  
AC ABUS9097;  
XX  
DT 28-APR-2003 (first entry)  
XX  
DE Novel human secreted or transmembrane protein PRO826.  
XX  
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis.  
XX Homo sapiens.  
XX  
OS  
XX  
PN US2002132252-A1.  
XX  
PD 19-SEP-2002.  
XX  
XX 14-NOV-2001; 2001US-0990442.  
PF 05-NOV-1997; 97WO-US20069.  
XX 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 30-NOV-1999; 99WO-US21547.  
PR 01-DEC-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 16-DEC-1999; 99WO-US28634.  
PR 20-DEC-1999; 99WO-US30095.  
PR 06-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.

PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089589P.  
PR 17-JUN-1998; 98US-089599P.  
PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 28-AUG-2001; 2001US-0941992.

XX  
PA (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gottlieb A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;

PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
DR WPI; 2003-247083/24.  
DR N-PSDB; ABX80254.  
XX  
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
PT are therapeutically useful for enhancing immune response and in cancer  
PT treatments -  
XX  
PS Claim 12; Fig 129; 648pp; English.

XX  
CC The invention describes an isolated human PRO polypeptide. The PRO  
CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
CC in modulating at least one biological activity of a cell expressing a PRO  
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
CC useful for treating conditions or disorders where angiogenesis would be  
CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
CC useful for treating cancerous tumours. PRO812 inhibits vascular  
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
CC cells and is thus useful for inhibiting endothelial cell growth in  
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
CC rod photoreceptor cells) and therefore are useful for treating retinal  
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
CC and therefore are useful for treating kidney disorders associated with  
CC decreased mesangial cell function such as Berger disease or other  
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
CC proliferation and/or redifferentiation of chondrocytes in culture and  
CC are thus useful for treating sports injuries, and arthritis. This  
CC is the amino acid sequence of a novel human PRO protein.

XX  
SQ Sequence 99 AA;

Query Match 100.0%; Score 71; DB 24; Length 99;  
Best Local Similarity 100.0%; Pred. NO. 1.6e-69;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTIENYASRPEAFNTPLNIDKLSAFKADFLNMHALFESIKRKLPLNWDAPFKL 60  
Db 29 EESTIENYASRPEAFNTPLNIDKLSAFKADFLNMHALFESIKRKLPLNWDAPFKL 88

QY 61 KGLRSATPDQAQ 71  
Db 89 KGLRSATPDQAQ 99

RESULT 14

ABUS9244

ID ABUS9244 standard; Protein; 99 AA.

XX

AC ABUS9244;

XX

DT 22-APR-2003 (first entry)

XX

DE Human secreted/transmembrane protein, #78.

XX

KW Human; PRO; secreted; transmembrane; pharmaceutical;

KW diagnostic; biosensor; bioreactor; tumour; therapeutic;

KW gene therapy; tumour-associated antigenic target; TAT; ADAPT;

KW antibody-dependent enzyme mediated prodrgug therapy; cytostatic.

XX

OS Homo sapiens.  
XX  
PN US2003027162-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 15-NOV-2001; 2001US-0997428.  
XX  
PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
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PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
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PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
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PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
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PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
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PR 04-JUN-1998; 98US-088030P.  
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PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
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PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089599P.  
PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
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PR 24-JUN-1998; 98US-090435P.  
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PR 24-JUN-1998; 98US-090445P.  
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PR 25-JUN-1998; 98US-090557P.  
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PR 11-AUG-1998; 98US-096146P.  
PR 12-AUG-1998; 98US-096329P.  
PR 17-AUG-1998; 98US-096757P.  
PR 17-AUG-1998; 98US-096766P.  
PR 17-AUG-1998; 98US-096773P.  
PR 17-AUG-1998; 98US-096791P.  
PR 17-AUG-1998; 98US-096867P.  
PR 17-AUG-1998; 98US-096891P.  
PR 17-AUG-1998; 98US-096894P.  
PR 17-AUG-1998; 98US-096895P.  
PR 17-AUG-1998; 98US-096897P.  
PR 18-AUG-1998; 98US-096949P.  
PR 18-AUG-1998; 98US-096950P.  
PR 18-AUG-1998; 98US-096959P.  
PR 18-AUG-1998; 98US-096960P.  
PR 18-AUG-1998; 98US-097022P.  
PR 19-AUG-1998; 98US-097141P.  
PR 20-AUG-1998; 98US-097218P.  
PR 24-AUG-1998; 98US-097661P.  
PR 26-AUG-1998; 98US-097952P.  
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ID ABU59393 standard; Protein; 99 AA.

XX ABU59393;  
DT 22-APR-2003 (first entry)

DE Novel human secreted or transmembrane protein PRO819.

XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;

KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis.  
XX Homo sapiens.  
XX US2003027985-A1.  
XX 06-FEB-2003.  
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#### ALIGNMENTS

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; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kjaavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC63  
; CURRENT APPLICATION NUMBER: US/09/989, 722  
; PRIOR FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
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; PRIOR APPLICATION NUMBER: 60/062250  
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; PRIOR FILING DATE: 1998-07-09
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Best Local Similarity 100.0%; Pred. No. 4.2e-66;
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## RESULT 2

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; Sequence 201, Application US/09989723
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC62
; CURRENT APPLICATION NUMBER: US/09/989,723
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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Patent No. US20020072496A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
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APPLICANT: Fong, Sherman  
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APPLICANT: Godowski, Paul J.  
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APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C56  
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Query Match 100.0%; Score 71; DB 9; Length 99;  
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QY 1 EEESTIENYASRPEAFNTPFLNIDKRSAPKADEFNLNWHALFESIKRKLPLNWDAPPKL 60  
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QY 61 KGLRSATPDQ 71  
Db 89 KGLRSATPDQ 99

#### RESULT 4

US-09-989-727-201  
; Sequence 201, Application US/09989727  
; Patent No. US20020072497A1

#### GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730PIC65

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; CURRENT FILING DATE: 2001-11-19

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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 71; DB 9; Length 99;  
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Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 29 EEESTIENYASRPEAFNTPEFLNIDKLSAFKADFLNTHALFESIKRKLPLFNWDAFPKL 88  
QY 61 KGLRSATPDAQ 71  
DB 89 KGLRSATPDAQ 99

## RESULT 5

US-09-989-731-201

Sequence 201, Application US/09989731

Patent No. US20020103125A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same

FILE REFERENCE: P2730P1C70

CURRENT APPLICATION NUMBER: US/09/989,731

CURRENT FILING DATE: 2001-11-20

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Query Match 100.0%; Score 71; DB 10; Length 99;  
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QY 61 KGLRSATPDQAQ 71  
Db 89 KGLRSATPDQAQ 99

## RESULT 6

US-09-989-732-201

;; Sequence 201, Application US/09989732  
;; Patent No. US20020123463A1

## GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
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;; APPLICANT: Grimaldi, J. Christopher  
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;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.

;; APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730P1C57

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US-09-991-073-201  
Sequence 201, Application US/09991073  
Patent No. US20020127576A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C15  
CURRENT APPLICATION NUMBER: US/09/991, 073  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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Query Match      100.0%; Score 71; DB 10; Length 99;
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
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Db 29 EESTIENYASRPEAFNTPLNIDKRSKFAKDEFLNWHALFESIKRKLPLNWDAPFKL 88  
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RESULT 10  
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Sequence 201, Application US/09993604  
Patent No. US20020137075A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C25  
CURRENT APPLICATION NUMBER: US/09/993, 604  
PRIOR FILING DATE: 2001-11-14  
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PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 71; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4.2e-66;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEESTIENTYASREAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPKLT 60  
DB 29 EEESTIENTYASREAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPKLT 88

QY 61 KGLRSATPDAQ 71  
DB 89 KGLRSATPDAQ 99

## RESULT 11

US-09-990-456-201

Sequence 201, Application US/09990456  
Patent No. US20020137890A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
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APPLICANT: Grimaldi, J. Christopher  
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APPLICANT: Kjaev, Ivar J.  
APPLICANT: Napier, Mary A.  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C22  
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Db 29 EEESTIENYASRPEAFNTPLNIDKLSAFKADEFNLNHALFESIKRKLPLNWDAPFKL 88  
OY 61 KGLRSATPDAQ 71  
Db 89 KGLRSATPDAQ 99

RESULT 12  
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: Patent No. US20020142961A1  
: GENERAL INFORMATION:  
: APPLICANT: Ashkenazi, Avi J.  
: APPLICANT: Baker, Kevin P.  
: APPLICANT: Botstein, David  
: APPLICANT: Desnoyers, Luc  
: APPLICANT: Eaton, Dan L.  
: APPLICANT: Ferrara, Napoleone  
: APPLICANT: Fong, Sherman  
: APPLICANT: Gerber, Hanspeter  
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: APPLICANT: Goddard, Audrey  
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: APPLICANT: Roy, Margaret Ann  
: APPLICANT: Stewart, Timothy A.  
: APPLICANT: Tuma, Daniel  
: APPLICANT: Watanabe, Colin K.  
: APPLICANT: Williams, P. Mickey  
: APPLICANT: Wood, William I.  
: APPLICANT: Zhang, Zemin  
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
: FILE REFERENCE: P2730P1C55  
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Query Match 100.0%; Score 71; DB 10; Length 99;  
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Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEBSTIENYASRPEAFNTPLNIDKLSAFKADEFNLNWHALFESIKRKLPLNLNWDAPFKL 60  
DB 29 EEBSTIENYASRPEAFNTPLNIDKLSAFKADEFNLNWHALFESIKRKLPLNLNWDAPFKL 88  
OY 61 KGLRSATPDAQ 71  
DB 89 KGLRSATPDAQ 99

RESULT 13

US-09-992-598-201  
; Sequence 201, Application US/09992598  
; Patent No. US20020160384A1  
; GENERAL INFORMATION:  
; APPLICANT: Aehkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
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; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C20  
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QY 61 KGLRSATPDAQ 71  
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; Sequence 142, Application US/09984245  
; Patent No. US20020165374A1

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; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/984,245
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
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; PRIOR FILING DATE: 1997-10-02
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US-09-984-245-142

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C66
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Db 29 EEESTIENYASRPEAFNTPLINIDKLSAFKADEFILNWHALFESIKRKLPLNWDAPPKL 88  
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Sat Nov 29 17:52:37 2003

us-10-059-395-142\_copy\_29\_99.011.rapb

Page 23

Db 89 KGLRSATPDAQ 99

Search completed: November 28, 2003, 13:45:14  
Job time : 24 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 11:46:00 ; Search time 2640 Seconds

(without alignments)  
1100.221 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	71	100.0	415	6	AX403313	AX403313 Sequence
7	71	100.0	415	6	AX454546	AX454546 Sequence
8	71	100.0	415	6	AX491024	AX491024 Sequence
9	71	100.0	415	6	AX574494	AX574494 Sequence
10	71	100.0	432	6	AX080815	AX080815 Sequence
11	71	100.0	432	6	AX080818	AX080818 Sequence
12	71	100.0	456	6	BD082389	BD082389 87 human
13	71	100.0	490	6	AX080817	AX080817 Sequence
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24	8	11.3	2590	6	AK025078	AK025078 Homo sapi
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35	8	11.3	43342	10	AL928978	AL928978 Mouse DNA
36	8	11.3	46401	2	AC011928	AC011928 Homo sapi
37	8	11.3	67870	2	AC083787	AC083787 Homo sapi
38	8	11.3	69520	10	AL669925	AL669925 Mouse DNA
39	8	11.3	74149	2	AC123879_3	Continuation (4 of
40	8	11.3	89012	9	AC011406	AC011406 Homo sapi
41	8	11.3	98530	2	AC113088	AC113088 Mus muscu
42	8	11.3	100296	9	AL590308	AL590308 Human DNA
43	8	11.3	101579	2	AC008227	AC008227 Drosophil
44	8	11.3	101622	2	AC123648_3	Continuation (4 of
45	8	11.3	108449	9	AC112650	AC112650 Homo sapi

RESULT 1

ALIGNMENTS



AX055438  
LOCUS AX055438 414 bp DNA linear PAT 13-JAN-2001  
DEFINITION Sequence 68 from Patent WO0073452.  
ACCESSION AX055438  
VERSION AX055438.1 GI:12228711  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS 1 Ashkenazi, A.J., Baker, K.P., Chan, B., Goddard, A., Godowski, P.J.,  
Gurney, A.L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D.L.,  
Tumas, D., Watanabe, C.K. and Wood, W.I.  
TITLE Compositions and methods for the treatment of immune related  
diseases  
JOURNAL Patent: WO 0073452-A 68 07-DEC-2000;  
Genentech, Inc. (US)  
FEATURES  
Source 1. 414  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 98 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 2.33e-69 Length: 414  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX055438 (1-414)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 97 GAGGAAGAAAGCACCATTGAGAAATATGCGTCACGACCGAGCCCTTAACACCCCGTTC 156  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACAAATTGCGATCTGCTTAAAGGCTGATGAGTTCCTGAACGCGACGCC 216  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 217 CTCTTGAGTCTATCAAAAGAAACTCTTCTCAACTGGATGCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGACTGAGGAGCGCACTCTGATGCCAG 309  
ORIGIN

RESULT 2  
AR252517  
LOCUS AR252517 415 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 200 from patent US 6478825.  
ACCESSION AR252517  
VERSION AR252517.1 GI:27300425  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS 1 (bases 1 to 415)  
TITLE Wintrobottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.  
JOURNAL Patent: US 6478825-A 200 12-NOV-2002;  
FEATURES  
Source 1. 415  
/organism="unknown"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 2.34e-69 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AR252517 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 97 GAGGAAGAAAGCACCATTGAGAAATATGCGTCACGACCGAGCCCTTAACACCCCGTTC 156  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACAAATTGCGATCTGCTTAAAGGCTGATGAGTTCCTGAACGCGACGCC 216  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 277 AAAGACTGAGGAGCGCACTCTGATGCCAG 309  
ORIGIN

RESULT 3  
AX077031  
LOCUS AX077031 415 bp DNA linear PAT 22-FEB-2001  
DEFINITION Sequence 19 from Patent WO0105972.  
ACCESSION AX077031  
VERSION AX077031.1 GI:13121661  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS 1 Ashkenazi, A.J., Baker, K.P., Fong, S., Goddard, A., Godowski, P.J.,  
Gurney, A.L., Hillan, K.J., Mark, M.R., Marsters, S.A., Pitti, R.M.,  
Tumas, D., Watanabe, C.K. and Wood, W.I.  
TITLE Compositions and methods for the treatment of immune related  
diseases  
JOURNAL Patent: WO 0105972-A 19 25-JAN-2001;  
Genentech, Inc. (US)  
FEATURES  
Source 1. 415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 2.34e-69 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX077031 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 97 GAGGAAGAAAGCACCATTGAGAAATATGCGTCACGACCGAGCCCTTAACACCCCGTTC 156  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACAAATTGCGATCTGCTTAAAGGCTGATGAGTTCCTGAACGCGACGCC 216  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 277 AAAGACTGAGGAGCGCACTCTGATGCCAG 309  
ORIGIN

Db 217 CTCTTGAGTCTATCAAAAGAACTCTCTTCCCTCACTGGATGCCCTTCTTAAGCTG 276

QY 61 LYSGLYLEUARGSERAlaThrProAspAlaGln 71  
|||||  
Db 277 AAAGACTGAGGAGCGCACTCTGATGCCAG 309

RESULT 4  
AX358892 415 bp DNA linear PAT 13-FEB-2002  
LOCUS AX358892  
DEFINITION Sequence 145 from Patent WO0193983.  
ACCESSION AX358892  
VERSION AX358892.1 GI:18675347  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS 1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,  
Watanabe, C.K. and Wood, W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0193983-A 145 13-DEC-2001;  
Genentech Inc. (US)  
FEATURES  
source 1. .415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t

ORIGIN

Alignment Scores:  
Pred. No.: 2.34e-69 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX358892 (1-415)

QY 1 GUGUGUGUSeThrIleGluAsnTYRAAserARgProGluAlaPheAsnThrProPhe 20  
|||||  
Db 97 GAGGAAGAAAGCAACCATTTGAAATTATGCGTCAAGACCCGAGCCCTTAAACCCCGTTTC 156

QY 21 LeuAsnIleAspLYsLeuArgSerAlaPheLYsAlaAspGluPheLeuAsnTrpHisAla 40  
|||||  
Db 157 CTGAACATCGACAATGCGATCTGCGTTTAAAGGCTGATGAGTTCTTGAAGTGGACGCC 216

QY 41 LeuPheGluSerIleLYsArgLYsLeuProPheLeuAsnTrpAspAlaPheProLYsLeu 60  
|||||  
Db 217 CTCTTGAGTCTATCAAAAGAACTCTTCTTCACTGGATGCCCTTCTTAAGCTG 276

QY 61 LYSGLYLEUARGSERAlaThrProAspAlaGln 71  
|||||  
Db 277 AAAGACTGAGGAGCGCACTCTGATGCCAG 309

RESULT 5  
AX362385 415 bp DNA linear PAT 15-FEB-2002  
LOCUS AX362385  
DEFINITION Sequence 145 from Patent WO0208288.  
ACCESSION AX362385  
VERSION AX362385.1 GI:18694650  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS 1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,

Watanabe, C.K. and Wood, W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0208288-A 145 31-JAN-2002;  
Genentech, Inc. (US)  
FEATURES  
source 1. .415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t

ORIGIN

Alignment Scores:  
Pred. No.: 2.34e-69 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX362385 (1-415)

QY 1 GUGUGUGUSeThrIleGluAsnTYRAAserARgProGluAlaPheAsnThrProPhe 20  
|||||  
Db 97 GAGGAAGAAAGCAACCATTTGAAATTATGCGTCAAGACCCGAGCCCTTAAACCCCGTTTC 156

QY 21 LeuAsnIleAspLYsLeuArgSerAlaPheLYsAlaAspGluPheLeuAsnTrpHisAla 40  
|||||  
Db 157 CTGAACATCGACAATGCGATCTGCGTTTAAAGGCTGATGAGTTCTTGAAGTGGACGCC 216

QY 41 LeuPheGluSerIleLYsArgLYsLeuProPheLeuAsnTrpAspAlaPheProLYsLeu 60  
|||||  
Db 217 CTCTTGAGTCTATCAAAAGAACTCTTCTTCACTGGATGCCCTTCTTAAGCTG 276

QY 61 LYSGLYLEUARGSERAlaThrProAspAlaGln 71  
|||||  
Db 277 AAAGACTGAGGAGCGCACTCTGATGCCAG 309

RESULT 6  
AX403313 415 bp DNA linear PAT 14-JUN-2002  
LOCUS AX403313  
DEFINITION Sequence 200 from Patent WO0073454.  
ACCESSION AX403313  
VERSION AX403313.1 GI:21436871  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS 1 Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Eaton, D.,  
Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P.,  
Grimaldi, C.J., Gurney, A.L., Kijavica, I., Napier, M.A., Pan, J.,  
Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,  
Williams, P., Wood, W.I. and Zhang, Z.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0073454-A 200 07-DEC-2000;  
Genentech Inc. (US)  
FEATURES  
source 1. .415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t

ORIGIN

Alignment Scores:  
Pred. No.: 2.34e-69 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX403313 (1-415)

QY	1	GIUGLUGLuserThrrlleglUAenTYrAlaSerArgProglUAlaPheAsnThrProPhe	20
DB	97	GAGGAAGAAAGCACCATTGAGAAATTATGCGTCACGACCCGAGGCCCTTAAACACCCCGTTC	156
QY	21	LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla	40
DB	157	CTGAACATCGACAATATGCGATCTGCGTTAAGCGTGATGAGTTCTCGAACTGGACGCCC	216
QY	41	LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu	60
DB	217	CTCTTGAGTCTATCAAAAGAACTTCCTTCTCTCAACTGGATGCGCTTCTTAAGCTG	276
QY	61	LysGlyLeuArgSerAlaThrProAspAlaGln	71
DB	277	AAAGGACTGAGAGCGCACTCCTGATGCCAG	309

RESULT 7

AX454546	415 bp	DNA	linear	PAT 06-JUL-2002
LOCUS				
DEFINITION	Sequence 131 from Patent WO0208284.			
ACCESSION	AX454546			
VERSION	AX454546.1	GI:21713897		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.B., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.			
TITLE	Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis			
JOURNAL	Patent: WO 0208284-A 131.31-JAN-2002; Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)			

FEATURES

Location/Qualifiers

1..415	/organism="Homo sapiens"
	/mol_type="genomic DNA"
	/db_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t

ORIGIN

Alignment Scores:

Score:	2.34e-69	Length:	415
Percent Similarity:	71.00	Matches:	71
Best local Similarity:	100.00%	Conservative:	0
Query Match:	100.00%	Mismatches:	0
DB:	6	Indels:	0
		Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX454546 (1-415)

QY	1	GIUGLUGLuserThrrlleglUAenTYrAlaSerArgProglUAlaPheAsnThrProPhe	20
DB	97	GAGGAAGAAAGCACCATTGAGAAATTATGCGTCACGACCCGAGGCCCTTAAACACCCCGTTC	156
QY	21	LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla	40
DB	157	CTGAACATCGACAATATGCGATCTGCGTTAAGCGTGATGAGTTCTCGAACTGGACGCCC	216

QY	Db	RESULT 8	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	BASE COUNT	ORIGIN	Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	US-10-059-395-142_COPY_29_99 (1-71) x AX491024 (1-415)
QY	41	Leuphegluserilelysa	grylsleu	Prophel	leuasntrpaspalaph	Prolysl	leu 60																	
Db	217	CTCTTGAGTCTATCAAAAGGAACTTCCTTCTCAACTGGATGCTTCTTAAGCTG	276																					
QY	61	lysglyleuargserala	thrproaspalagln	71																				
Db	277	AAAGACTGAGAGCGCAACTCCTGATGCCAG	309																					
QY	AX491024	AX491024	415 bp	DNA	linear	PAT 16-AUG-2002																		
DEFINITION	Sequence 131 from Patent WO0200690.																							
ACCESSION	AX491024																							
VERSION	AX491024.1	GI:22323849																						
KEYWORDS	Homo sapiens (human)																							
SOURCE	Homo sapiens																							
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.																							
REFERENCE	1	Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Masters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.																						
AUTHORS	Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis																							
	Patent: WO 0200690-A 131 03-JAN-2002;																							
	Genentech, Inc. (US)																							
	Location/Qualifiers																							
	1..415																							
	/organism="Homo sapiens"																							
	/mol_type="genomic DNA"																							
	/db_xref="taxon:9606"																							
	99 a 126 c 92 g 98 t																							
	Alignment Scores:																							
	Pred. No.:	2.34e-69																						
	Score:	71.00																						
	Percent Similarity:	100.00%																						
	Best Local Similarity:	100.00%																						
	Query Match:	100.00%																						
	DB:	6																						
	Gaps:	0																						
QY	1	GLUGLUGLuserthrilegluasntyrAlasera	rgProglua	lapha	anthrProphe	20																		
Db	97	GAGGAAGAAAGCACCATTTGAGAAATTATGCGTACGACCGAGGCCCTTTAACACCCCGTTC	156																					

REFERENCE 1  
AUTHORS Baker, K.P., Eaton, D.L., Filvaroff, E., Goddard, A., Grimaldi, J.C.,  
Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K., Wood, W.I.,  
Zhang, Z., and Fong, S.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0224888-A 21 28-MAR-2002;  
GENENTECH, INC. (US)  
FEATURES Location/Qualifiers  
source 1..415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 2.34e-69 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX574494 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
|||  
Db 97 GAGGAAGAAAGCACCATTGAGATTATGCGTCACGACCCGAGCCTTAACACCCCGCTC 156

QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
|||  
Db 157 CTGAACATCGACAATTGCGATCTGCGTTAAGGCTGATGAGTTCTGAACCTGGACGCC 216

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
|||  
Db 217 CTCTTGAGTCTATCAAAAGGAACTCTCTTCTCACTGGAGTCCCTTCTTAAGCTG 276

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
|||  
Db 277 AAAGGACTGAGGAGCGCACTCTGATGCCAG 309

RESULT 10  
AX080815  
LOCUS AX080815 432 bp DNA linear PAT 27-FEB-2001  
DEFINITION Sequence 61 from Patent WO0109327.  
ACCESSION AX080815  
VERSION AX080815.1 GI:13169784  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Klajavin, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Plicti, R.M.,  
Watanabe, C.K., and Wood, W.I.  
TITLE Method of preventing the injury or death of retinal cells and  
treating ocular diseases  
JOURNAL Patent: WO 0109327-A 61 08-FEB-2001;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..432  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Virtual DNA fragment used in the isolation of  
DNAS57694."

BASE COUNT 106 a 127 c 94 g 102 t 3 others  
ORIGIN

Alignment Scores:  
Pred. No.: 2.43e-69 Length: 432  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX080815 (1-432)

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX080815 (1-432)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
|||  
Db 96 GAGGAAGAAAGCACCATTGAGATTATGCGTCACGACCCGAGGCCCTTAACACCCCGCTC 155

QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
|||  
Db 156 CTGAACATCGACAATTGCGATCTGCGTTAAGGCTGATGAGTTCTGAACCTGGACGCC 215

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
|||  
Db 216 CTCTTGAGTCTATCAAAAGGAACTCTCTTCTCACTGGAGTCCCTTCTTAAGCTG 275

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
|||  
Db 276 AAAGGACTGAGGAGCGCACTCTGATGCCAA 308

RESULT 11  
AX080818  
LOCUS AX080818 432 bp DNA linear PAT 27-FEB-2001  
DEFINITION Sequence 64 from Patent WO0109327.  
ACCESSION AX080818  
VERSION AX080818.1 GI:13169787  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Klajavin, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Plicti, R.M.,  
Watanabe, C.K., and Wood, W.I.  
TITLE Method of preventing the injury or death of retinal cells and  
treating ocular diseases  
JOURNAL Patent: WO 0109327-A 64 08-FEB-2001;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..432  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 106 a 127 c 94 g 102 t 3 others  
ORIGIN

Alignment Scores:  
Pred. No.: 2.43e-69 Length: 432  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX080818 (1-432)

|||||  
Db 276 AAAGACTGAGAGCGCAACTCCTGATGCCCA 308  
RESULT 12  
BD082389  
LOCUS BD082389 456 bp DNA linear PAT 27-AUG-2002  
DEFINITION 87 human secreted proteins.  
ACCESSION BD082389  
VERSION BD082389.1 GI:22627999  
KEYWORDS JP 2001522239-A/31.  
SOURCE Mastadenovirus  
ORGANISM Mastadenovirus  
REFERENCE Viruses; dsDNA viruses, no RNA stage; Adenoviridae.  
AUTHORS 1 (bases 1 to 456)  
Young, P., Greene, J.M., Ferrie, A.M., Ruben, S.M., Rosen, C.A.,  
Duan, R.D., Hu, J.S., Florence, K.A., Olsen, H.S., Ebner, R.,  
Brewer, L.A., Moore, P.A., Shi, Y., Lafleur, D.W. and Ni, J.  
TITLE 87 human secreted proteins  
JOURNAL Patent: JP 2001522239-A 31 13-NOV-2001;  
HUMAN GENOME SCIENCES INC SECRETARY OF THE DEPARTMENT OF HEALTH  
COMMENT HUMAN SERVICES  
PN JP 2001522239-A/31  
PD 13-NOV-2001  
PF 19-MAR-1998 JP 1998542119  
PR 21-MAR-1997 US 60/041281, 21-MAR-1997 US 60/041276 PR  
21-MAR-1997 US 60/042344, 21-MAR-1997 US 60/041277 PR  
30-MAY-1997 US 60/048355, 30-MAY-1997 US 60/048096 PR  
30-MAY-1997 US 60/048351, 30-MAY-1997 US 60/048154 PR  
30-MAY-1997 US 60/048160, 30-MAY-1997 US 60/048069 PR  
30-MAY-1997 US 60/048131, 30-MAY-1997 US 60/048186 PR  
30-MAY-1997 US 60/048095, 30-MAY-1997 US 60/048187 PR  
30-MAY-1997 US 60/048099, 30-MAY-1997 US 60/050937 PR  
30-MAY-1997 US 60/048352, 30-MAY-1997 US 60/048135 PR  
30-MAY-1997 US 60/048188, 30-MAY-1997 US 60/048135 PR  
30-MAY-1997 US 60/048350, 05-AUG-1997 US 60/054804 PR  
19-AUG-1997 US 60/056370, 02-OCT-1997 US 60/060862 PI PAUL  
YOUNG, JOHN M GREENE, ANN M FERRIE, STEVEN M RUBEN, CRAIG A PI  
ROSEN,  
PI ROXANNE D DUAN, JING SHAN HU, KIMBERLY A FLORENCE, HENRIK S  
OLSEN,  
PI REINHARD EBNER, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W  
PI LAFLEUR,  
PI JIAN NI  
PC C07K14/00  
CC Strandedness: Double;  
CC Topology: Linear;  
FH key Location/Qualifiers.  
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source 1. 456  
/organism="Mastadenovirus"  
/mol\_type="genomic DNA"  
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BASE COUNT 117 a 136 c 104 g 98 t 1 others  
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Pred. No.: 71.00 Matches: 71  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
DB: 6  
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Db 105 GAGGAAGAAAGCACCATTGAGATTATGCGTCACGACCGAGCCCTTAACACCCCGTTTC 164  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 165 CTGAACATCGACAATGCGATCTGCGTTTAAGCGTGAATGATTCTTGAACGCGACGCC 224

QY 41 LeupheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 225 CTCTTTGAGTCTATCAAAAGAAACTTCTTCTCACTGGATGCCCTTCTTAAGCTG 284  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 285 AAAGACTGAGAGCGCAACTCCTGATGCCAG 317  
RESULT 13  
AX080817  
LOCUS AX080817 490 bp DNA linear PAT 27-FEB-2001  
DEFINITION Sequence 63 from Patent WO0109327.  
ACCESSION AX080817  
VERSION AX080817.1 GI:13169786  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Kljavin, I.J., Lafleur, M., Mark, M.R., Masters, S.A., Pitti, R.M.,  
Watanabe, C.K., and Wood, W.T.  
TITLE Method of preventing the injury or death of retinal cells and  
JOURNAL treating ocular diseases  
Genentech, Inc. (US)  
PATENT: WO 0109327-A 63 08-FEB-2001;  
FEATURES Location/Qualifiers  
source 1. 490  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
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/note="Virtual DNA fragment used in the isolation of  
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ORIGIN  
Alignment Scores: 2.72e-69 Length: 490  
Pred. No.: 71.00 Matches: 71  
Score: 100.00% Conservative: 0  
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Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
DB: 6  
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QY 1 GIUGLUGLuserThriIleGIuAsnTYrAlaSerArgProGIuAlaPheAsnThrProPhe 20  
Db 164 GAGGAAGAAAGCACCATTGAGATTATGCGTCACGACCGAGCCCTTAACACCCCGTTTC 223  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 224 CTGAACATCGACAATGCGATCTGCGTTTAAGCGTGAATGATTCTTGAACGCGACGCC 283  
QY 41 LeupheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 284 CTCTTTGAGTCTATCAAAAGAAACTTCTTCTCACTGGATGCCCTTCTTAAGCTG 343  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 344 AAAGACTGAGAGCGCAACTCCTGATGCCAG 376  
RESULT 14  
AX080816  
LOCUS AX080816 435 bp DNA linear PAT 27-FEB-2001  
DEFINITION Sequence 62 from Patent WO0109327.  
ACCESSION AX080816  
VERSION AX080816.1 GI:13169785  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Kljavin, I.J., Lafleur, M., Mark, M.R., Masters, S.A., Pitti, R.M.,  
Watanabe, C.K., and Wood, W.T.  
TITLE Method of preventing the injury or death of retinal cells and  
JOURNAL treating ocular diseases  
Genentech, Inc. (US)  
PATENT: WO 0109327-A 62 08-FEB-2001;  
FEATURES Location/Qualifiers  
source 1. 435  
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/mol\_type="genomic DNA"  
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Best Local Similarity: 100.00% Indels: 0  
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DB: 6  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AX080816 (1-435)  
QY 1 GIUGLUGLuserThriIleGIuAsnTYrAlaSerArgProGIuAlaPheAsnThrProPhe 20  
Db 164 GAGGAAGAAAGCACCATTGAGATTATGCGTCACGACCGAGCCCTTAACACCCCGTTTC 223  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 224 CTGAACATCGACAATGCGATCTGCGTTTAAGCGTGAATGATTCTTGAACGCGACGCC 283  
QY 41 LeupheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 284 CTCTTTGAGTCTATCAAAAGAAACTTCTTCTCACTGGATGCCCTTCTTAAGCTG 343  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 344 AAAGACTGAGAGCGCAACTCCTGATGCCAG 376



REFERENCE 1  
AUTHORS Ashkenazi,A.J., Baker,K.P., Goddard,A., Godowski,P.J., Gurney,A.L.,  
Klajavin,I.J., Lafleur,M., Mark,M.R., Masters,S.A., Pitti,R.M.,  
Watanabe,C.K. and Wood,W.I.  
TITLE Method of preventing the injury or death of retinal cells and  
treating ocular diseases  
JOURNAL Patent: WO 0109327-A 62 08-FEB-2001;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
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BASE COUNT 108 a 130 c 96 g 101 t  
ORIGIN

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Pred. No.: 4.92e-56 Length: 435  
Score: 59.00 Matches: 59  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 83.10% Indels: 0  
DB: Gaps: 6

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX080816 (1-435)

QY 13 ProGluAlaPheAsnThrProPheLeuAsnIleAspIleuArgSerAlaPheIysAla 32  
Db 136 CCCGAGGCCTTAAACACCCCGTCTCTGACATCGACAAATTGCGATCTGCCGTTTAAAGGCT 195  
QY 33 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleIysArgIysLeuProPheLeu 52  
Db 196 GATGAGTCTCTGAACGACGCGCTCTTGTAGTCTATCAAAAGGAACCTTCTTCTC 255  
QY 53 AsnTrpAspAlaPheProIysLeuIysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 256 AACTGGATGCCCTTCTTAACTGAAGAGACTGAGAGCGCAACTCCTGATGCCAG 312

RESULT 15  
AX041085/c 278 bp DNA linear PAT 23-NOV-2000  
LOCUS Sequence 3 from Patent WO0065053.  
DEFINITION AX041085  
ACCESSION AX041085  
VERSION AX041085.1 GI:11340655  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Wang,T. and Dillon,D.C.  
TITLE Compositions and methods for therapy and diagnosis of head/neck and  
lung squamous cell carcinoma  
JOURNAL Patent: WO 0065053-A 3 02-NOV-2000;  
CORIXA CORPORATION (US)  
FEATURES Location/Qualifiers  
source 1..278  
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BASE COUNT 70 a 57 c 80 g 71 t  
ORIGIN

Alignment Scores:  
Pred. No.: 6.9e-53 Length: 278  
Score: 56.00 Matches: 56  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
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DB: Gaps: 6

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX041085 (1-278)

QY 16 PheAsnThrProPheLeuAsnIleAspIleuArgSerAlaPheIysAlaAspGluPhe 35  
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QY 36 LeuAsnTrpHisAlaLeuPheGluSerIleIysArgIysLeuProPheLeuAsnTrpAsp 55  
Db 209 CTGAACGACGCGCTCTTGTAGTCTATCAAAAGGAACCTTCTTCTCAACTGGAT 150  
QY 56 AlaPheProIysLeuIysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 149 GCCTTCTTAACTGAAGAGACTGAGAGCGCAACTCCTGATGCCAG 102

Search completed: November 28, 2003, 13:05:56  
Job time : 2642 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 11:01:55 ; Search time 217 Seconds

(without alignments)  
883.226 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

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Searched: 2552756 seqs, 1349719017 residues

Word size: 1

Total number of hits satisfying chosen parameters: 5103067

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-LIST=45 -DOCALLIGN=200 -THR\_SCORE=quality -THR\_MIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	71	100.0	414	22	AAC91475	Human PRO826 cDNA.
2	71	100.0	414	24	ABK28600	Human DNA57694-134
3	71	100.0	415	21	AAZ65018	Membrane-bound pro
4	71	100.0	415	22	AAF30059	Human cDNA encodin
5	71	100.0	415	22	AAF44164	Human PRO826 (UNQ4
6	71	100.0	415	22	AAC97491	Human angiogenesis
7	71	100.0	415	24	ABL95626	Human angiogenesis
8	71	100.0	415	24	ABK69971	cDNA encoding huma
9	71	100.0	415	24	ABL88137	Human PRO826 cDNA
10	71	100.0	415	24	ABK33608	cDNA encoding huma
11	71	100.0	415	25	ABX80255	Novel human secret
12	71	100.0	415	25	ABX80759	Novel human secret
13	71	100.0	415	25	ABX81142	Novel human secret
14	71	100.0	415	25	ABX90232	Human secreted/tra
15	71	100.0	415	25	ABX77843	Human PRO polynuc
16	71	100.0	415	25	ABX79439	Human secreted/tra
17	71	100.0	415	25	ABX64078	Human encoding huma
18	71	100.0	415	25	ABX17042	Human PRO polynuc
19	71	100.0	428	24	ABZ11803	Human polynucleoti
20	71	100.0	456	20	AAK00632	Human secreted pro
21	71	100.0	518	22	ABA09519	Human secreted pro
22	56	78.9	278	21	ABK68806	Human head/neck tu
23	43	60.6	386	24	ABZ11804	Human polynucleoti
24	28	39.4	305	24	ABZ11886	Human polynucleoti
25	8	11.3	2001	24	ABN67971	Streptococcus poly
26	8	11.3	2298	21	AAC59576	Human secreted pro
27	8	11.3	12069	24	ABK39931	Human chemically p
28	8	11.3	12212	24	ABK12920	Human SLC26A2 (sol
29	8	11.3	12212	24	ABK12975	Human SLC26A2 (sol
30	8	11.3	33795	24	ABN95686	Gene #2184 used to
31	8	11.3	215561	24	ABN71527	Streptococcus poly
32	7	9.9	65	24	ABN31537	Rat spliced transc
33	7	9.9	198	21	AAC24586	Human secreted pro
34	7	9.9	231	20	AAH86401	Human single nucle
35	7	9.9	231	20	AAH86402	Human single nucle
36	7	9.9	238	21	AAA45447	Human secreted exp
37	7	9.9	251	21	AAC07741	Human secreted pro
38	7	9.9	256	25	ABX31899	Human GDP-mannose
39	7	9.9	283	21	AAC94607	Cat flea hindgut a
40	7	9.9	294	20	AAZ13185	Human gene express
41	7	9.9	300	20	AAZ98312	Human cancer cell
42	7	9.9	300	21	AAA00085	Human colon cancer
43	7	9.9	368	19	AAV66404	cDNA clone AA37708
44	7	9.9	419	21	AAC31437	Human secreted pro
45	7	9.9	438	24	ABK29813	Colon adenocarcino

# ALIGNMENTS

RESULT 1	
AAC91475	
ID AAC91475	standard; cDNA; 414 BP.
XX AAC91475;	
AC AAC91475;	
XX 21-MAR-2001	(first entry)
DT 21-MAR-2001	(first entry)
XX DE	Human PRO826 cDNA.
XX	Human; PRO; antiinflammatory; dermatological; antiarthritic;
KW	antiinflammatory; cardiatic; antianemic; immunosuppressive; antithyroid;
KW	antidiabetic; nocitropic; neuroprotective; hepatotropic; virucide;
KW	antiallergic; antiaslathmatic; immune related disorder;
KW	hepatobiliary disease; autoimmune disease; allergy; ss.
XX	
OS	Homo sapiens.

XX WO200073452-A2.  
XX  
PD 07-DEC-2000.  
XX  
PF 02-JUN-2000; 2000WO-US15264.  
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PR 02-JUN-1999; 99WO-US12252.  
PR 20-JUL-1999; 99US-0144732.  
PR 20-JUL-1999; 99US-0144758.  
PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 29-OCT-1999; 99US-0162506.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28634.  
PR 09-DEC-1999; 99US-0170262.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;  
PI Wood WI;  
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XX WPI; 2001-025253/03.  
DR P-PSDB; AAB50916.  
XX  
PT Thirty three nucleic acids encoding PRO polypeptides which are useful  
PT in the diagnosis and treatment of immune related disorders, e.g.  
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
PT thyroiditis and diabetes mellitus -  
XX  
XX Claim 48; Fig 29; 218pp; English.  
XX  
XX The present sequence is one of thirty three nucleic acids encoding PRO  
XX polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and  
XX antagonists are useful for treating and diagnosing immune related  
XX disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
XX osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
XX systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
XX syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
XX anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
XX immune-mediated renal disease, demyelinating diseases of the central  
XX and peripheral nervous systems (such as multiple sclerosis, idiopathic  
XX demyelinating polynuropathy or Guillain-Barre syndrome, and chronic  
XX inflammatory demyelinating polynuropathy), hepatobiliary diseases  
XX (such as infectious, autoimmune chronic active hepatitis, primary  
XX biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
XX inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
XX disease, autoimmune or immune-mediated skin diseases (such as bullous  
XX skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
XX allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
XX food hypersensitivity and urticaria), immunological diseases of the  
XX lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
XX and hypersensitivity pneumonitis), transplantation associated diseases  
XX including graft rejection and graft-versus-host diseases.  
XX  
SQ Sequence 414 BP; 98 A; 126 C; 92 G; 98 T; 0 other;

Alignment Scores:  
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Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0  
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QY 1 GIUGLUGLuserThrIleGLUAsnTYrAlaSerArgProGLuAlaPheAsnThrProphe 20  
DB 97 GAGGAAGAAAGCACCATTGAGAAATTATGCGTCACGACCCGAGGCTTTAAACACCCCGTTC 156  
QY 21 LeuAsnIleAspLYsLeuArgSerAlaPheLYsAlaAspGLuPheLeuAsnTrpHisAla 40  
DB 157 CTGAACATCGACCAAAATTGGCATCTGCCCTTTAAGGCTGATGAGTTCCTGAACCTGGCAGCC 216  
QY 41 LeupheGLuSerIleLYsArgLYsLeuProPheLeuAsnTrpAspAlaPheProLYsLeu 60  
DB 217 CTCTTTGAGCTATCAAAAGAACTCTTCTCACTCACTGGAGTGCCTTCTTAAGCTG 276  
QY 61 LysGLYLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGAGAGCGCAACTCCTGATGCCAG 309  
RESULT 2  
ABK28600  
ID ABK28600 standard; cDNA; 414 BP.  
XX  
AC ABK28600;  
XX  
DT 09-APR-2002 (first entry)  
XX  
XX Human DNA57694-1341 encoding PRO826.  
DE  
XX Human; ss; gene; PRO; antiinflammatory; ophthalmological; vasotropic;  
KW retinal cell injury; ocular disease; retinitis pigmentosa;  
KW macular degeneration; retinal detachment; retinal tear; retinopathy;  
KW retinal degenerative disease; macular hole; degenerative myopia;  
KW acute retinal necrosis syndrome; traumatic choroidretinopathy;  
KW Puttcher's retinopathy; oedema; ischaemic condition;  
KW retinal vision occlusion; collagen vascular disease;  
KW thrombocytopenic purpura; uveitis; retinal vasculitis; Bales disease;  
KW systemic lupus erythematosus; environmental trauma.  
XX  
OS Homo sapiens.  
XX  
XX WO200109327-A2.  
PN  
XX  
XX 08-FEB-2001.  
PD  
XX  
PF 28-JUL-2000; 2000WO-US20710.  
XX  
XX 28-JUL-1999; 99US-146222P.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
XX  
PA (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;  
PI Kljavin IJ, Lafleur M, Mark MR, Marsters SA, Pitti RM;  
PI Watanabe CK, Wood WI;  
XX  
DR WPI; 2002-130120/17.  
DR P-PSDB; AAU81964.  
XX  
PT Promoting survival of retinal cells, or delaying or preventing retinal  
PT cell injury or death, by contacting retinal cells with PRO175, 220,  
PT 216, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132  
PT polypeptide -  
XX  
PS Claim 33; Fig 24; 152pp; English.  
XX  
CC The invention relates to promoting the survival of retinal cells, or  
CC delaying or preventing retinal cell injury or death, by contacting the  
CC retinal cells with the polypeptide such as PRO175, PRO220, PRO216,  
CC PRO243, PRO306, PRO346, PRO322, PRO536, PRO943, PRO840, PRO828, PRO826,  
CC PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids  
CC encoding the PRO proteins, a vector comprising the nucleic acid, a host  
CC cell comprising the vector, and anti-PRO antibody. The PRO proteins are  
CC useful for promoting survival of retinal cells (retinal neurons such as  
CC retinal ganglion cells, displaced retinal ganglion cells, amacrine  
CC cells, displaced amacrine cells, horizontal neurons or bipolar neurons,  
CC rod photoreceptors, or supportive cells such as Muller cells or pigment  
CC epithelial cells), or delaying or preventing retinal cell injury or  
CC death caused by ocular disease (which is or is associated with  
CC retinitis pigmentosa, macular degeneration, retinal detachment, retinal  
CC tear, retinopathy, retinal degenerative disease, macular hole,  
CC degenerative myopia, acute retinal necrosis syndrome, traumatic  
CC chorioretinopathy or contusion, Purtscher's retinopathy, oedema, an  
CC ischaemic condition, central or branch retinal vision occlusion, an  
CC collagen vascular disease, thrombocytopaenic purpura, uveitis, retinal  
CC vasculitis, occlusion associated with Bales disease or systemic lupus  
CC erythematosus), retinal injury or environmental trauma. The retinal  
CC cell injury or death is delayed or prevented by substantially not  
CC causing angiogenesis or mitogenesis. The present sequence is a cDNA  
CC encoding a PRO protein.  
XX  
SQ Sequence 414 BP; 98 A; 126 C; 92 G; 98 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 3.23e-66 Length: 414  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0  
  
US-10-059-395-142\_COPY\_29\_99 (1-71) x ABK28600 (1-414)  
QY 1 GUGUGUGUSeThrITLeGluAsnTYrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAGAAAGCACCATTTGAGATTATGCTGACGACCCGAGGCCCTTTTAAACACCCCGTTC 156  
QY 21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnTrpHisAla 40  
DB 157 CTGAACATCGACAAATTGCGATCTGCGTTTAAAGCTGATGAGTCTCTGAACCTGGACGCGC 216  
QY 41 LeupheGluSerIleIysArgIysLeuProPheLeuAsnTrpAspAlaPheProIysLeu 60  
DB 217 CTCTTGAGTCTATCAAAAGAACTCTCTTCTCAACTGGATGCGCTTCTCTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGGACTGAGGAGCGCACTCTGATGCCGAG 309  
  
RESULT 3  
AAZ65018  
ID AAZ65018 standard; cDNA; 415 BP.  
XX  
AC AAZ65018;

XX 05-APR-2000 (first entry)  
DT 05-APR-2000 (first entry)  
XX  
XX Membrane-bound protein PRO826 encoding cDNA.  
DE Membrane-bound protein PRO826 encoding cDNA.  
XX  
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9963088-A2.  
PN  
XX  
PD 09-DEC-1999.  
XX  
PF 02-JUN-1999; 99WO-US12252.  
XX  
PR 02-JUN-1998; 98US-0087607.  
PR 02-JUN-1998; 98US-0087609.  
PR 02-JUN-1998; 98US-0087759.  
PR 03-JUN-1998; 98US-0087827.  
PR 04-JUN-1998; 98US-0088021.  
PR 04-JUN-1998; 98US-0088025.  
PR 04-JUN-1998; 98US-0088028.  
PR 04-JUN-1998; 98US-0088029.  
PR 04-JUN-1998; 98US-0088030.  
PR 04-JUN-1998; 98US-0088033.  
PR 04-JUN-1998; 98US-0088326.  
PR 05-JUN-1998; 98US-0088167.  
PR 05-JUN-1998; 98US-0088202.  
PR 05-JUN-1998; 98US-0088212.  
PR 05-JUN-1998; 98US-0088217.  
PR 05-JUN-1998; 98US-0088217.  
PR 09-JUN-1998; 98US-0088655.  
PR 10-JUN-1998; 98US-0088722.  
PR 10-JUN-1998; 98US-0088730.  
PR 10-JUN-1998; 98US-0088734.  
PR 10-JUN-1998; 98US-0088738.  
PR 10-JUN-1998; 98US-0088740.  
PR 10-JUN-1998; 98US-0088741.  
PR 10-JUN-1998; 98US-0088742.  
PR 10-JUN-1998; 98US-0088810.  
PR 10-JUN-1998; 98US-0088811.  
PR 10-JUN-1998; 98US-0088824.  
PR 10-JUN-1998; 98US-0088825.  
PR 10-JUN-1998; 98US-0088826.  
PR 11-JUN-1998; 98US-0088858.  
PR 11-JUN-1998; 98US-0088861.  
PR 11-JUN-1998; 98US-0088863.  
PR 11-JUN-1998; 98US-0088876.  
PR 12-JUN-1998; 98US-0089090.  
PR 12-JUN-1998; 98US-0089105.  
PR 16-JUN-1998; 98US-0089440.  
PR 16-JUN-1998; 98US-0089512.  
PR 16-JUN-1998; 98US-0089514.  
PR 17-JUN-1998; 98US-0089532.  
PR 17-JUN-1998; 98US-0089538.  
PR 17-JUN-1998; 98US-0089598.  
PR 17-JUN-1998; 98US-0089599.  
PR 17-JUN-1998; 98US-0089600.  
PR 17-JUN-1998; 98US-0089653.  
PR 18-JUN-1998; 98US-0089801.  
PR 18-JUN-1998; 98US-0089907.  
PR 18-JUN-1998; 98US-0089908.  
PR 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089948.  
PR 19-JUN-1998; 98US-0089952.  
PR 22-JUN-1998; 98US-0090246.  
PR 22-JUN-1998; 98US-0090252.  
PR 22-JUN-1998; 98US-0090254.  
PR 23-JUN-1998; 98US-0090349.  
PR 23-JUN-1998; 98US-0090355.  
PR 24-JUN-1998; 98US-0090429.  
PR 24-JUN-1998; 98US-0090431.  
PR 24-JUN-1998; 98US-0090435.

PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090445.  
PR 24-JUN-1998; 98US-0090461.  
PR 24-JUN-1998; 98US-0090472.  
PR 24-JUN-1998; 98US-0090535.  
PR 24-JUN-1998; 98US-0090538.  
PR 24-JUN-1998; 98US-0090540.  
PR 24-JUN-1998; 98US-0090557.  
PR 25-JUN-1998; 98US-0090676.  
PR 25-JUN-1998; 98US-0090678.  
PR 25-JUN-1998; 98US-0090688.  
PR 25-JUN-1998; 98US-0090690.  
PR 25-JUN-1998; 98US-0090691.  
PR 25-JUN-1998; 98US-0090694.  
PR 25-JUN-1998; 98US-0090695.  
PR 25-JUN-1998; 98US-0090696.  
PR 26-JUN-1998; 98US-0090862.  
PR 26-JUN-1998; 98US-0090863.  
PR 01-JUL-1998; 98US-0091358.  
PR 01-JUL-1998; 98US-0091360.  
PR 01-JUL-1998; 98US-0091544.  
PR 02-JUL-1998; 98US-0091478.  
PR 02-JUL-1998; 98US-0091486.  
PR 02-JUL-1998; 98US-0091519.  
PR 02-JUL-1998; 98US-0091626.  
PR 02-JUL-1998; 98US-0091628.  
PR 02-JUL-1998; 98US-0091646.  
PR 02-JUL-1998; 98US-0091633.  
PR 02-JUL-1998; 98US-0091673.  
PR 07-JUL-1998; 98US-0091978.  
PR 07-JUL-1998; 98US-0091982.  
PR 09-JUL-1998; 98US-0092182.  
PR 10-JUL-1998; 98US-0092472.  
PR 30-JUL-1998; 98US-0094651.  
PR 04-AUG-1998; 98US-0095282.  
PR 04-AUG-1998; 98US-0095285.  
PR 04-AUG-1998; 98US-0095301.  
PR 04-AUG-1998; 98US-0095302.  
PR 04-AUG-1998; 98US-0095318.  
PR 04-AUG-1998; 98US-0095321.  
PR 04-AUG-1998; 98US-0095325.  
PR 10-AUG-1998; 98US-0095916.  
PR 10-AUG-1998; 98US-0095929.  
PR 10-AUG-1998; 98US-0096012.  
PR 11-AUG-1998; 98US-0096143.  
PR 11-AUG-1998; 98US-0096146.  
PR 12-AUG-1998; 98US-0096329.  
PR 17-AUG-1998; 98US-0096757.  
PR 17-AUG-1998; 98US-0096766.  
PR 17-AUG-1998; 98US-0096768.  
PR 17-AUG-1998; 98US-0096773.  
PR 17-AUG-1998; 98US-0096791.  
PR 17-AUG-1998; 98US-0096867.  
PR 17-AUG-1998; 98US-0096891.  
PR 17-AUG-1998; 98US-0096894.  
PR 17-AUG-1998; 98US-0096895.  
PR 17-AUG-1998; 98US-0096897.  
PR 18-AUG-1998; 98US-0096949.  
PR 18-AUG-1998; 98US-0096950.  
PR 18-AUG-1998; 98US-0096959.  
PR 18-AUG-1998; 98US-0096960.  
PR 18-AUG-1998; 98US-0097022.  
PR 19-AUG-1998; 98US-0097141.  
PR 20-AUG-1998; 98US-0097218.  
PR 24-AUG-1998; 98US-0097661.  
PR 26-AUG-1998; 98US-0097951.  
PR 26-AUG-1998; 98US-0097952.  
PR 26-AUG-1998; 98US-0097954.  
PR 26-AUG-1998; 98US-0097955.  
PR 26-AUG-1998; 98US-0097971.  
PR 26-AUG-1998; 98US-0097974.  
PR 26-AUG-1998; 98US-0097978.

PR 26-AUG-1998; 98US-0097979.  
PR 26-AUG-1998; 98US-0097986.  
PR 26-AUG-1998; 98US-0098014.  
PR 31-AUG-1998; 98US-0098525.  
PR 16-SEP-1998; 98US-0100634.  
PR 12-JAN-1999; 99US-0115565.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood WI, Yuan J;  
XX  
XX WPI; 2000-072883/06.  
DR P-PSDB; AAY66681.  
XX  
PT Membrane-bound proteins and related nucleotide sequences -  
XX  
PS Claim 2; Fig 128; 822pp; English.  
XX  
CC The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIE  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
CC will also be useful for the preparation of PRO polypeptides, especially  
CC by recombinant techniques.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
SQ  
Alignment Scores:  
Pred. No.: 3.24e-66 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 21 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AAZ65018 (1-415)  
QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAAGAAAGCACCATTGAGAAATTATGCGTCACGACCAGGCGCTTAAACACCCCGTTTC 156  
QY 21 IeuAsnIleAspIlyLeuArgSerAlaPheIlyAlaAspGluPheIeuAsnTrpHisAla 40  
DB 157 CTGAACATGACCAAAATTGCGATCTGCGTTTAAAGGCTGATGAGTTCCTGAACGACGCC 216  
QY 41 IeuPheGluSerIleIlyAspGlyLeuProPheIeuAsnTrpAspAlaPheProIlyLeu 60  
DB 217 CTCTTTGAGTCTATCAAAAGAACTCTTCTCACTGAGTGGATGCTTCTTAAGCTG 276  
QY 61 IySGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGGACTGAGGAGCGCACTCCTGATGCCAG 309  
RESULT 4  
AAF30059  
ID AAF30059 standard, cDNA, 415 BP.  
XX  
AC AAF30059;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Human cDNA encoding PRO826.  
XX  
KW PRO826; UNQ467; human; immune disease; autoimmune disease;



KW antirheumatic; antiarthritic; antiinflammatory; antianaemic;  
KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
KW hepatotropic; virucide; dermatological; antipsoriatic;  
KW antiasthmatic; antiallergic; immunostimulant; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 13..312  
FT sig\_peptide /\*tag= a  
FT /\*tag= 13..78  
FT mat\_peptide /\*tag= b  
FT /\*tag= 79..309  
XX  
XX WO200105972-A1.  
XX  
PD 25-JAN-2001.  
XX  
PF 15-MAR-2000; 2000WO-US06884.  
XX  
PR 20-JUL-1999; 99US-0144758.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL,  
PI Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK,  
PI Wood WI;  
XX  
DR WPI; 2001-103149/11.  
DR P-PSDB; AAB20117.  
XX  
PT New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
PT diagnosing and treating immune-related disorders, such as multiple  
PT sclerosis, rheumatoid arthritis and diabetes -  
XX  
XX Claim 21; Fig 19; 127pp; English.  
XX  
XX The present sequence is that of cDNA clone DNA57694-1341 (ATCC 203017)  
CC encoding novel human immunomodulator protein PRO826 (UNQ467) (see  
CC AAB20117). The clone was isolated following a database search by  
CC applying a signal sequence algorithm. The predicted protein has a  
CC mol.wt. of 11 kDa and a pI of 7.47. The invention provides  
CC polynucleotides (see AAF30050-62) encoding novel human PRO proteins  
CC (see AAB20108-20) including PRO826. Claimed compositions  
CC comprising these proteins or their agonists are useful for increasing  
CC infiltration of inflammatory cells into a tissue of a mammal,  
CC stimulating or enhancing an immune response in a mammal, or  
CC increasing the proliferation of T-lymphocytes in a mammal in response  
CC to an antigen. Claimed compositions comprising the PRO polypeptide  
CC or its antagonist have the opposite effect. A claimed method for  
CC treating an immune related disorder, such as a T cell disorder,  
CC involves administering the PRO polypeptide, an agonist antibody or  
CC an antagonist antibody. The disorder is selected from systemic  
CC lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
CC juvenile chronic arthritis, spondyloarthritis, systemic  
CC sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome,  
CC systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia,  
CC autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinated diseases (such as  
CC multiple sclerosis), autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
CC inflammatory bowel disease (ulcerative colitis and Crohn's disease),  
CC gluten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated  
CC skin diseases (such as bullous skin disease, erythema multiforme and  
CC psoriasis), allergic diseases (such as asthma, allergic rhinitis,  
CC atopic dermatitis, food hypersensitivity and urticaria), immunologic  
CC diseases of the lung and transplantation associated diseases (such  
CC as graft rejection and graft-versus-host disease) (all claimed).  
CC Claimed methods of diagnosing these disorders comprise detecting  
CC the level of expression of the PRO gene. Also claimed are a method  
CC of identifying a compound capable of inhibiting the expression or  
CC activity of the PRO polypeptide, vectors, host cells, antibodies

CC and a method of stimulating the proliferation of T-lymphocytes  
CC using PRO826.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
Alignment Scores:  
Pred. No.: 3.24e-66 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AAF30059 (1-415)  
QY 1 GluGluGluSerThrIleGluAsnTYRAIAserArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAAGAAACACCAATTCGATCTGCCCTTAAGCGTATGATGACTCTGAACACCCGCTTC 156  
QY 21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnTrpHisAla 40  
DB 157 CTGAACATCGACAATTCGATCTGCCCTTAAGCGTATGATGACTCTGAACACCCGCTTC 216  
QY 41 LeuPheGluSerIleIysArgIysLeuProPheLeuAsnTrpAspAlaPheProIysLeu 60  
DB 217 CTCCTTGAGTCTATCAAAAGGAACCTCTTCTCACTGGAGTGCCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGAGCGCAACTCCTGATGCCAG 309  
RESULT 5  
AAF44164  
ID AAF44164 standard; cDNA; 415 BP.  
XX  
XX AC AAF44164;  
XX  
DT 02-APR-2001 (first entry)  
XX  
XX Human PRO826 (UNQ467) nucleotide sequence SEQ ID NO:200.  
DE  
XX Human; secreted and transmembrane protein; PRO; cytosratic;  
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
KW diagnostic assay; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200073454-A1.  
XX  
PD 07-DEC-2000.  
XX  
PF 30-MAR-2000; 2000WO-US08439.  
XX  
XX 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 07-JUL-1999; 99US-0143048.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146222.  
PR 17-AUG-1999; 99US-0149396.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 08-OCT-1999; 99US-0158663.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.

PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gertlisen ME, Goddard A, Godowski PJ;  
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
DR WPI; 2001-032160/04.  
DR P-PSDB; AAB65204.  
XX  
PT PRO polynucleotides used to produce polypeptides used to target  
PT bioactive molecules such as toxins, radiolabels or antibodies, to  
PT specific cells, to cause targeted cell death -  
PS  
PS Claim 2; Fig 128; 935pp; English.  
XX  
CC The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins  
CC can be used for targeted delivery of bioactive molecules, such as  
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridisation probes, in  
CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
CC and DNA. They may also be used to produce transgenic animals which are  
CC used to develop and screen therapeutically useful reagents. The PRO  
CC nucleotide and protein sequence can be used for tissue typing and in  
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
XX  
Alignment Scores:  
Pred. No.: 3.24e-66 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AAF44164 (1-415)  
QY 1 GIUGLUGLuserThriIegluAsnTYrAlaSerArgProGIuAlaPheAsnThrProPhe 20  
Db 97 GAGGAAGAAAGCACCATTGAGAAATTATGCGTCACGAGCCGAGGCTTTAACACCCCGTTTC 156  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACAAATTGCGATTCGTTAAGGCTGATGAGTTCTTGAACCTGGCAGCC 216  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 217 CTCTTTGAGTCTATCAAAAGAACTTCCTTCTCAACTGGGATGCTTCTCTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGACTGAGAGCGCAACTCTGATGCCAG 309  
RESULT 6  
AAC97491  
ID AAC97491 standard; cDNA; 415 BP.  
XX  
AC AAC97491;  
XX  
DT 28-FEB-2001 (first entry)  
XX

DE Human angiogenesis-associated protein PRO826 cDNA, SEQ ID NO:157.  
XX  
KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
KW gene therapy; transgenic animal; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200053753-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 05-JAN-2000; 2000WO-US00219.  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
XX  
DR WPI; 2001-090793/10.  
DR P-PSDB; AAB53094.  
XX  
PT New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
XX  
PS Claim 58; Fig 61; 293pp; English.  
XX  
CC The invention relates to novel human angiogenesis-associated proteins  
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
CC PRO proteins. The invention also relates to vectors and host cells  
CC comprising a PRO nucleic acid, the recombinant production of a PRO  
CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
CC compounds which inhibit the expression of a PRO gene. The invention  
CC additionally encompasses methods of identifying modulators of PRO  
CC expression or activity; diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
CC mutations in a PRO gene, or the expression level of a PRO gene within a  
CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
CC administration of a PRO protein, or an agonist or antagonist thereof.  
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
CC agonists and PRO antagonists may be used as therapeutic agents to treat  
CC cardiovascular, endothelial or angiogenic disorders, such as  
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's

CC disease, or stroke. PRO nucleic acids are additionally useful in the  
CC recombinant production of PRO proteins, as hybridisation probes to  
CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
CC animals useful for the development and screening of potential  
CC therapeutic agents. The present sequence represents a cDNA encoding a PRO  
CC protein of the invention.

XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

## Alignment Scores:

Pred. No.:	3.24e-66	Length:	415
Score:	71.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AAC97491 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20

DB 97 GAGGAGAAAGCACCATTTGAGATATATGCGTCACGACCCGAGCCCTTAAACCCCGCTC 156

QY 21 LeuAsnIleApyLysLeuArgSerAlaPheLysAlaApyGluPheLeuAsnThrPheAla 40

DB 157 CTGAACATCGACAAATTGCGATCTGCGTTAAGCGCTGATGAGTCTCTGAACGCGACGCC 216

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnThrPaspAlaPheProLysLeu 60

DB 217 CTCTTGAGTCTATCAAAAGAACTCTTCTCTCAACTGGAGTCCCTTCTTAAGCTG 276

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71

DB 277 AAAGACTGAGGAGCGCAACTCTGATGCCAG 309

## RESULT 7

ABL95626  
ID ABL95626 standard; cDNA; 415 BP.

XX ABL95626;

DT 19-JUL-2002 (first entry)

DE Human angiogenesis related cDNA PRO826 SEQ ID NO: 131.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;

KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;

KM cardiant; cytosolic; antiangiogenic; hypotensive; vulnary;

XX antiarteriosclerotic; gene; ss.

OS Homo sapiens.

XX WO200208284-A2.

PD 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US21735.

PR 20-JUL-2000; 2000US-219556P.

PR 25-JUL-2000; 2000US-220624P.

PR 28-JUL-2000; 2000US-220664P.

PR 02-AUG-2000; 2000US-222695P.

PR 17-AUG-2000; 2000US-0643657.

PR 23-AUG-2000; 2000WO-US23522.

PR 24-AUG-2000; 2000WO-US23328.

PR 07-SEP-2000; 2000US-230978P.

PR 15-SEP-2000; 2000US-000000P.

PR 18-SEP-2000; 2000US-0664610.

PR 18-SEP-2000; 2000US-0665350.

PR 24-OCT-2000; 2000US-242922P.

PR 08-NOV-2000; 2000US-0709238.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 28-JUN-2001; 2001WO-US00000.

PA (GETH ) GENENTECH INC.

PA (BAKE/) BAKER K P.

PA (FERR/) FERRARA N.

PA (GERB/) GERBER H.

PA (GERR/) GERRITSEN M E.

PA (GODD/) GODDARD A.

PA (GODO/) GODOWSKI P J.

PA (GURN/) GURNEY A L.

PA (HILL/) HILLAN K J.

PA (MARS/) MARSTERS S A.

PA (PANJ/) PAN J.

PA (PAON/) PAONTI N F.

PA (STEP/) STEPHAN J F.

PA (WATA/) WATANABE C K.

PA (WILL/) WILLIAMS P M.

PA (WOOD/) WOOD W I.

XX Baker KP, Ferrera N, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX MPI; 2002-171999/22.

DR P-PSDB; ABB95488.

XX Claim 1; Fig 131; 567bp; English.

XX The present invention provides the protein and coding sequences of human

CC PRO proteins. These are useful for treating or diagnosing a

CC cardiovascular, endothelial or angiogenic disorder, including cardiac

CC hypertrophy, trauma, cancer, age-related macular degeneration,

CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,

CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour

CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound

CC healing. The present sequence is a coding sequence of the invention.

## Alignment Scores:

Pred. No.:	3.24e-66	Length:	415
Score:	71.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

```
US-10-059-395-142_COPY_29_99 (1-71) x ABL95626 (1-415)
OY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20
DB 97 GAGGAAGAAAGCACCATTTGAGAATTATGCGTCACGACCCGAGCCTTTAAACACCCCGTTTC 156
OY 21 LeuAsnIleAspIlyLeuArgSerAlaPheIlyAlaAspGluPheLeuAsnTrpHisAla 40
DB 157 CTGAACATCGACCAATTGCGATCTGCGTTTAAGGCTGATGAGTCTCTGAAGTGGCAGCC 216
OY 41 LeuPheGluSerIleIlyAsArgIlyLeuProPheLeuAsnTrpAspAlaPheProIlyLeu 60
DB 217 CTCTTGAGTCTATCAAAAGAACTCTCTTCTCAACTGGATGCTTCTTAAGCTG 276
OY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71
DB 277 AAAGACTGAGGAGCGCACTCTGATGCCAG 309
RESULT 8
ABK69971
ID ABK69971 standard; DNA; 415 BP.
XX
AC ABK69971;
XX
DT 15-JUL-2002 (first entry)
XX
DE cDNA encoding human Pro peptide #11.
XX
KW Human; ss; gene; PRO; secreted protein; transmembrane protein;
KW genetic disorder; tumour; cancer.
XX
OS Homo sapiens.
XX
PN WO200224888-A2.
XX
PD 28-MAR-2002.
XX
PF 29-AUG-2001; 2001WO-US27099.
XX
PR 01-SEP-2000; 2000US-229896P.
PR 05-SEP-2000; 2000US-230621P.
PR 22-SEP-2000; 2000US-235147P.
PR 10-NOV-2000; 2000WO-US30873.
PR 12-JAN-2001; 2001US-261878P.
PR 16-JAN-2001; 2001US-261910P.
PR 16-JAN-2001; 2001US-261939P.
PR 16-JAN-2001; 2001US-262150P.
PR 25-JAN-2001; 2001US-264395P.
PR 02-FEB-2001; 2001US-266421P.
PR 09-FEB-2001; 2001US-267623P.
PR 28-FEB-2001; 2001WO-US06520.
PR 09-MAR-2001; 2001US-274399P.
PR 03-APR-2001; 2001US-280982P.
PR 04-APR-2001; 2001US-282129P.
PR 04-APR-2001; 2001US-282199P.
PR 09-MAY-2001; 2001US-290589P.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z,
PI Fong S;
XX
DR WPI; 2002-362426/39.
DR P-PSDB; ABG34040.
XX
PT New PRO polypeptides and polynucleotides encoding the polypeptides,
```

```
PT useful in gene therapy, chromosome identification, tissue typing, or
PT for genetic analysis of individuals with genetic disorders
XX
XX Claim 2; Figure 21; 218bp; English.
XX
XX This invention relates to the cDNA and protein sequences of novel
XX secreted and transmembrane polypeptides PRO polypeptides. The
XX invention also comprises a method for producing the proteins of the
XX invention by recombinant means and antibodies specific for the protein
XX of the invention. The antibody may be used for detecting the PRO
XX proteins of the invention and may be used to modify their activity.
XX polynucleotides may be used as hybridisation probes for a cDNA library
XX to isolate the full-length PRO cDNA or to isolate other cDNAs, to
XX construct hybridisation probes for mapping the gene which encodes that
XX PRO and for genetic analysis of individuals with genetic disorders, in
XX assays to identify other proteins or molecules involved in binding
XX reaction, to generate transgenic animals or knock-out animals which in
XX turn are useful in the development and screening of therapeutically
XX useful reagents, for chromosome identification, and tissue typing. The
XX PRO polypeptides are useful in gene therapy, and as molecular weight
XX markers for protein electrophoresis purposes. The sequences may
XX also be used to detect overexpression on PRO polypeptides in cancerous
XX tumours and for screening for differentially expressed genes using
XX microarray technology. The present sequence represents a cDNA encoding
XX a human PRO protein of the invention.
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 3.24e-66 Length: 415
XX Score: 71.00 Matches: 71
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 24 Gaps: 0
XX
US-10-059-395-142_COPY_29_99 (1-71) x ABK69971 (1-415)
OY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20
DB 97 GAGGAAGAAAGCACCATTTGAGAATTATGCGTCACGACCCGAGCCTTTAAACACCCCGTTTC 156
OY 21 LeuAsnIleAspIlyLeuArgSerAlaPheIlyAlaAspGluPheLeuAsnTrpHisAla 40
DB 157 CTGAACATCGACCAATTGCGATCTGCGTTTAAGGCTGATGAGTCTCTGAAGTGGCAGCC 216
OY 41 LeuPheGluSerIleIlyAsArgIlyLeuProPheLeuAsnTrpAspAlaPheProIlyLeu 60
DB 217 CTCTTGAGTCTATCAAAAGAACTCTCTTCTCAACTGGATGCTTCTTAAGCTG 276
OY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71
DB 277 AAAGACTGAGGAGCGCACTCTGATGCCAG 309
RESULT 9
ABL88137
ID ABL88137 standard; cDNA; 415 BP.
XX
AC ABL88137;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO826 cDNA sequence SEQ ID NO:131.
XX
XX Human; angiogenesis; cardiant; cyostatic; antiangiogenic; hypotensive;
XX vulnerable; arteriosclerotic; PRO agonist; PRO antagonist; trauma;
XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
XX age-related macular degeneration; arterial restenosis; angina;
XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;
XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
XX wound healing; chromosome mapping; gene mapping; gene; ss.
```

OS Homo sapiens.  
XX  
PN WO200200690-A2.  
XX  
PD 03-JAN-2002.  
XX  
PF 20-JUN-2001; 2001WO-US19692.  
XX  
PR 23-JUN-2000; 2000US-213637P.  
PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 02-AUG-2000; 2000US-222695P.  
PR 17-AUG-2000; 2000US-0643657.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 07-SEP-2000; 2000US-230978P.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-0709238.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06665.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX  
DR MPI; 2002-090516/12.  
DR P-PSDB; ABB84882.  
XX  
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal -  
XX  
PS Claim 2; Fig 131; 565pp; English.  
XX  
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
CC activities, and can be used in gene therapy. The PRO polynucleotides,  
CC proteins, agonists and antagonists are useful for treating or diagnosing  
CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
CC carcinoma) and wound healing. The PRO polynucleotides have applications  
CC in molecular biology, including use as hybridisation probes, and in  
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
CC probes used in the exemplification of the present invention.

XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
Alignment Scores:  
Pred. No.: 3.24e-66 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x ABL88137 (1-415)  
QY 1 GluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 97 GAGGAAGAAAGCACCATTTGAGATTATGCGTCACGACCCGAGCCCTTAACACCCCGTTC 156  
QY 21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACAATTGCCATCTGCGTTTAAGGCTGATGATGATCCCTGAACGGCAGCC 216  
QY 41 LeuPheGluSerIleIysArgIysLeuProPheLeuAsnTrpAspAlaPheProIysLeu 60  
Db 217 CTCTTGAGTCTATCAAAAGAACTTCCTTCTCAACTGGATGCCCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGACTGAGGAGCGCAACTCCTGATGCCAG 309  
RESULT 10  
ABK33608  
ID ABK33608 standard; cDNA; 415 BP.  
XX  
AC ABK33608;  
XX  
DT 08-MAY-2002 (first entry)  
XX  
DE cDNA encoding human PRO protein, Seq ID No 145.  
XX  
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
KW pericyte cell proliferation; chondrocyte cell proliferation;  
KW tumour necrosis factor-alpha; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200208288-A2.  
XX  
PD 31-JAN-2002.  
XX  
PF 29-JUN-2001; 2001WO-US21066.  
XX  
PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220585P.  
PR 25-JUL-2000; 2000US-220605P.  
PR 25-JUL-2000; 2000US-220607P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220638P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 25-JUL-2000; 2000US-220666P.  
PR 26-JUL-2000; 2000US-220893P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 15-SEP-2000; 2000US-000000P.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 28-NOV-2000; 2000US-253646P.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001WO-US17092.



XX (GETH ) GENENTECH INC.  
PA  
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,  
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI,  
XX WPI; 2002-172001/22.  
DR P-PSDB; AAU83664.  
XX  
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,  
PT useful for treating a PRO related disorder and for diagnosing tumours  
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal  
PT tumour or liver tumour -  
XX  
PS Claim 2; Figure 145; 359pp; English.  
XX  
CC The invention relates to one hundred and twenty two nucleic acids  
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
CC agonists and antagonists are useful for treating a PRO related disorder.  
CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
CC liver tumour. The PRO polypeptides are useful for stimulating the  
CC proliferation of, or gene expression, in pericyte cells, for stimulating  
CC the proliferation or differentiation of chondrocyte cells, for  
CC stimulating the release of tumour necrosis factor-alpha from human blood,  
CC for stimulating or inhibiting the proliferation of normal human dermal  
CC fibroblast cells. The PRO polypeptide may also be used as molecular  
CC weight markers and for tissue typing. The PRO nucleic acids have  
CC applications in molecular biology, including use as hybridisation probes,  
CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human  
CC PRO protein coding sequences of the invention.  
XX  
SQ Sequence 415 BP, 99 A, 126 C, 92 G, 98 T, 0 other;  
  
Alignment Scores:  
Pred. No.: 3,24e-66 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0  
  
US-10-059-395-142\_COPY\_29\_99 (1-71) x ABK33608 (1-415)  
  
QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 97 GAGGAGAAAGCACCATTTGAGATTATGCGTCACGACCGAGGCGCTTTAAACACCCCGTTC 156  
  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACAAATTGCGATCTGCGTTTAAGGCTGATGAGTTCCTGAACCTGGACAGCC 216  
  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 217 CTCTTGAGTCTATCAAAAGGAAACTTCCTTCTCAACTGGATGCTTCTTAAGCTG 276  
  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGGACTGAGAGCGCAACTCCTGATGCCAG 309  
  
RESULT 11  
ABX80255  
ID ABX80255 standard; DNA; 415 BP.  
XX  
AC ABX80255;  
XX  
DT 28-APR-2003 (first entry)  
XX  
DE Novel human secreted or transmembrane protein PRO819 DNA.  
XX  
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;

KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN US2002132252-A1.  
XX  
PD 19-SEP-2002.  
XX  
PF 14-NOV-2001; 2001US-0990442.  
XX  
XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 06-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.

PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
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PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089599P.  
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PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 28-AUG-2001; 2001US-0941992.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
XX WPI; 2003-247083/24.  
DR P-PSDB; ABUS9098.  
XX  
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
PT are therapeutically useful for enhancing immune response and in cancer  
PT treatments -  
XX  
XX Claim 2; Fig 130; 648pp; English.  
PS  
XX  
XX The invention describes an isolated human PRO polypeptide. The PRO  
CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
CC in modulating at least one biological activity of a cell expressing a PRO  
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
CC useful for treating conditions or disorders where angiogenesis would be  
CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
CC useful for treating cancerous tumours. PRO812 inhibits vascular  
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
CC cells and is thus useful for inhibiting endothelial cell growth in  
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
CC stimulated T-lymphocytes and are therapeutically useful for enhancing

CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
CC rod photoreceptor cells) and therefore are useful for treating retinal  
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813  
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
CC and therefore are useful for treating kidney disorders associated with  
CC decreased mesangial cell function such as Berger disease or other  
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
CC proliferation and/or redifferentiation of chondrocytes in culture and  
CC are thus useful for treating sports injuries, and arthritis. This  
CC sequence represents a novel human PRO protein polynucleotide.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
Alignment Scores:  
Pred. No.: 3.24e-66 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 25 Gaps: 0  
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QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAAGAAAGACACCAATTGAGAATTATGCGTCACGACCCGAGCCTTAAACACCCGTTTC 156  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
DB 157 CTGAACATCGAACAAATGCGATCTGCGTTAAGGCTGATGAGTCTCGAACTGCGACGCC 216  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
DB 217 CTCTTGAGTCTATCAAAAGAACTCTCTTCTCACTGGATGCGCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGGAGCGCACTCTGATGCCAG 309  
RESULT 12  
ABX80759  
ID ABX80759 standard; cDNA; 415 BP.  
XX  
XX AC ABX80759;  
XX  
XX 22-APR-2003 (first entry)  
XX  
XX Human secreted/transmembrane protein cDNA, #78.  
DE  
XX  
XX Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;  
KW diagnostic; biosensor; bioreactor; tumour; therapeutic;  
KW gene therapy; tumour-associated antigenic target; TAT; ADEPT;  
KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2003027162-A1.  
PN  
XX  
XX 06-FEB-2003.  
PD  
XX  
XX 15-NOV-2001; 2001US-0997428.  
PF  
XX  
XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.

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PR 05-JAN-2000; 2000WO-US02119.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
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PR 24-AUG-2000; 2000WO-US23328.  
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PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
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PR 29-JUN-2001; 2001WO-US21066.  
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PR 28-MAY-1998; 98US-087106P.  
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PR 04-JUN-1998; 98US-088021P.  
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PR 22-JUN-1998; 98US-090246P.  
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PR 23-JUN-1998; 98US-090349P.  
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PR 24-JUN-1998; 98US-090429P.  
PR 24-JUN-1998; 98US-090431P.  
PR 24-JUN-1998; 98US-090435P.  
PR 24-JUN-1998; 98US-090444P.  
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PR 24-JUN-1998; 98US-090472P.  
PR 24-JUN-1998; 98US-090535P.  
PR 24-JUN-1998; 98US-090540P.  
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PR 24-JUN-1998; 98US-090557P.  
PR 25-JUN-1998; 98US-090676P.  
PR 25-JUN-1998; 98US-090678P.  
PR 25-JUN-1998; 98US-090690P.  
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PR 01-JUL-1998; 98US-091360P.  
PR 01-JUL-1998; 98US-091544P.  
PR 02-JUL-1998; 98US-091478P.  
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PR 02-JUL-1998; 98US-091626P.  
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PR 02-JUL-1998; 98US-091646P.  
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PR 07-JUL-1998; 98US-091978P.  
PR 07-JUL-1998; 98US-091982P.  
PR 09-JUL-1998; 98US-092182P.  
PR 10-JUL-1998; 98US-092472P.  
PR 20-JUL-1998; 98US-093339P.  
PR 30-JUL-1998; 98US-094651P.  
PR 04-AUG-1998; 98US-095282P.  
PR 04-AUG-1998; 98US-095285P.  
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PR 04-AUG-1998; 98US-095321P.  
PR 04-AUG-1998; 98US-095325P.  
PR 10-AUG-1998; 98US-095916P.  
PR 10-AUG-1998; 98US-095929P.  
PR 10-AUG-1998; 98US-096012P.  
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PR 12-AUG-1998; 98US-096757P.  
PR 17-AUG-1998; 98US-096766P.  
PR 17-AUG-1998; 98US-096768P.  
PR 17-AUG-1998; 98US-096773P.  
PR 17-AUG-1998; 98US-096791P.  
PR 17-AUG-1998; 98US-096867P.  
PR 17-AUG-1998; 98US-096891P.  
PR 17-AUG-1998; 98US-096894P.  
PR 17-AUG-1998; 98US-096895P.

PR 17-AUG-1998; 98US-096897P.  
PR 18-AUG-1998; 98US-096949P.  
PR 18-AUG-1998; 98US-096950P.  
PR 18-AUG-1998; 98US-096959P.  
PR 18-AUG-1998; 98US-096960P.  
PR 18-AUG-1998; 98US-097022P.  
PR 19-AUG-1998; 98US-097141P.  
PR 20-AUG-1998; 98US-097218P.  
PR 24-AUG-1998; 98US-097661P.  
PR 26-AUG-1998; 98US-097952P.  
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PR 26-AUG-1998; 98US-097955P.  
PR 26-AUG-1998; 98US-097971P.  
PR 26-AUG-1998; 98US-097974P.  
PR 26-AUG-1998; 98US-097978P.  
PR 26-AUG-1998; 98US-097979P.  
PR 26-AUG-1998; 98US-097986P.  
PR 31-AUG-1998; 98US-098014P.  
PR 16-SEP-1998; 98US-100634P.  
PR 17-SEP-1998; 98US-100858P.  
PR 22-DEC-1998; 98US-113296P.  
PR 12-MAR-1999; 99US-123957P.  
PR 23-JUN-1999; 99US-141037P.

## Alignment Scores:

Pred. No.:	3.24e-66	Length:	415.
Score:	71.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	25	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x ABX80759 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
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DB 97 GAGGAGAAAGCACCATTTGAGATTATGCGTCACGACCGAGCGCTTTAACACCCCGTTC 156  
  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTyrHisAla 40  
|||  
DB 157 CTGAACATCGAACAAATTCGATCTGCGTTTAAGCTGATGAGTTCCTGAACGTGCACGCC 216  
  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTyrAspAlaPheProLysLeu 60  
|||  
DB 217 CTCCTTGAGTCTATCAAAAGGAACTTCCTTCTCAACTGGGATGCCCTTCTTAAGCTG 276  
  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
|||  
DB 277 AAAGGACTGAGGAGCGCAACTCCTGATGCCAG 309

## RESULT 13

ABX81142  
ID ABX81142 standard; DNA; 415 BP.

AC ABX81142;

DT 22-APR-2003 (first entry)

DE Novel human secreted or transmembrane protein PRO819 DNA.

KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosum; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
XX Homo sapiens.  
OS

XX PN US2003027985-A1.  
XX PD 06-FEB-2003.  
XX PF 14-NOV-2001; 2001US-0990562.  
PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
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PR 09-JUL-1998; 98US-092182P.  
PR 10-JUL-1998; 98US-092472P.  
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PR 10-AUG-1998; 98US-096012P.  
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PR 26-AUG-1998; 98US-097978P.  
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PR 26-AUG-1998; 98US-097986P.  
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## Alignment Scores:

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QY 1 GluGluGluSerThrIleGluGluGluTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAGGAAGCACCATTGAGATTATGCGTCACGACCCGAGCCTTAAACACCCCGTTC 156  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
DB 157 CTGAACATCGACAATTGCGATTCGCTTTAAGGCTGATGAGTTCTGAACGGCACGCC 216  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
DB 217 CTCTTGAGTCTATCAAAAGGAAGAACTTCCTTCTCAACTGGATGCGCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGGAGCGCAACTCCTGATGCCACG 309

## RESULT 14

ABX90232  
ID ABX90232 standard; cDNA; 415 BP.

XX AC ABX90232;

XX DT 01-MAY-2003 (first entry)

DE Human secreted/transmembrane protein cDNA, #78.

XX Human; gene; ss; PRO; secreted; transmembrane; signal peptide;

KW pharmaceutical; diagnostic; therapeutic; gene therapy.



XX Homo sapiens.  
OS  
XX  
PN US2002160384-A1.  
XX  
PD 31-OCT-2002.  
PF 14-NOV-2001; 2001US-0992598.  
XX  
PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
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PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
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PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
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PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
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PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
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PR 04-JUN-1998; 98US-088033P.

PR 04-JUN-1998; 98US-088326P.  
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PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
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PR 09-JUN-1998; 98US-088655P.  
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PR 10-JUN-1998; 98US-088738P.  
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PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
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PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
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PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 28-AUG-2001; 2001US-0941992.  
XX  
PA (GETH ) GENENTECH, INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrera N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gunney AL, Kljavin IC, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
DR WPI; 2003-288106/28.  
DR P-PSDB; ABU60528.  
XX  
PT New transmembrane polypeptides and nucleic acids encoding the  
PT polypeptides, useful in gene therapy, in chromosome identification, as  
PT chromosome markers, or in generating probes -  
XX  
PS Claim 2; Fig 128; 650pp; English.  
XX  
CC The invention discloses isolated PRO secreted/transmembrane polypeptides  
CC comprising a sequence without signal peptide and the nucleic acid  
CC encoding them. The polypeptides can be used to raise antibodies that  
CC specifically bind to the PRO polypeptide, for linking a bioactive  
CC molecule to a cell expressing a PRO protein and for modulating at least  
CC one biological activity of a cell. The PRO polypeptides or  
CC polynucleotides are also useful in gene therapy, in chromosome  
CC identification, as chromosome markers, or in generating probes. The PRO  
CC polypeptides are useful as molecular markers for protein  
CC electrophoresis, and the isolated nucleic acids may be used for  
CC recombinantly expressing those markers. The PRO polypeptides and nucleic  
CC acids may also be used in tissue typing. Anti-PRO antibodies are useful  
CC in diagnostic assays for PRO, and in affinity purification of PRO from  
CC recombinant cell culture or natural sources. The sequences presented in  
CC ABX90083-ABX90468 are the genes encoding, the primers amplifying, and the  
CC probes detecting the PRO polynucleotides of the invention.  
CC Note: The sequence data for this patent is also available in electronic  
CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

Alignment Scores:  
Pred. No.: 3.24e-66 length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0  
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QY 1 GluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 97 GAGGAGAAAGCACCATTTGAGATTATGCGTCAAGACCCGAGGCGCTTTAACACCCCGTTC 156

QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATGACCAAAATTGCGATCTGCGTTTAAGGCTGATGAGTCTGAACTGGCAGCC 216

QY 41 LeupheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 217 CTCTTGAGTCTATCAAAAGAAACTTCTTCTCAACTGGAGTGCCTTCTTAAGCTG 276

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGGACTGAGAGCGCAACTCCTGATGCCAG 309

## RESULT 15

ABX77843  
ID ABX77843 standard; cDNA; 415 BP.

XX AC ABX77843;

DT 14-APR-2003 (first entry)

XX DE Human PRO polynucleotide #51.

KW Human; PRO; gene; ss; cytosstatic; tumour; cancer; breast; lung; stomach;  
KW liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;  
KW antibody-dependent enzyme mediated prodrug therapy.

XX OS Homo sapiens.

XX PN US2003027163-A1.

XX PD 06-FEB-2003.

XX PF 15-NOV-2001; 2001US-0997666.

XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
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PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
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PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
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PR 24-JUN-1998; 98US-090435P.

PR 24-JUN-1998; 98US-090444P.  
PR 24-JUN-1998; 98US-090445P.  
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PR 24-JUN-1998; 98US-090557P.  
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PR 02-JUL-1998; 98US-091633P.  
PR 02-JUL-1998; 98US-091646P.  
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GenCore version 5.1.6  
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#### SUMMARIES

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#### ALIGNMENTS

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Sequence 200, Application US/09989722  
Patent No. US20020072067A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary B.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
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## RESULT 2

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; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
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;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C62
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; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C56  
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; PRIOR FILING DATE: 1998-07-09

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; GENERAL INFORMATION:
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; APPLICANT: Baker, Kevin P.
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; APPLICANT: Zhang, Zemin
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;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.:	7.74e-66	Length:	415
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DB:	9	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-989-727-200 (1-415)

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QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
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; Patent No. US20020103125A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnuyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey J.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C70  
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;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

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## RESULT 6

US-09-989-732-200

Sequence 200, Application US/09989732

Patent No. US20020123463A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
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;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
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;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730F1C57  
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;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

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Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

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## RESULT 7

US-09-991-073-200

;; Sequence 200, Application US/09991073  
;; Patent No. US20020127576A1

## GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
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;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730P1C15  
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; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
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; APPLICANT: Desnoyers, Luc  
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; APPLICANT: Baker, Kevin P.  
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; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zhenh  
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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
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QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGAGCGCAACTCCTGATGCCACG 309

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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
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;; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

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; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

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DB: 10 Gaps: 0  
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; Patent No. US20020160384A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerltsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C20  
; CURRENT APPLICATION NUMBER: US/09/992,598  
; PRIOR FILING DATE: 2001-11-14  
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; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
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; PRIOR APPLICATION NUMBER: 60/084600

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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

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; APPLICANT: Baker, Kevin P.  
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; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

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## RESULT 15

US-09-989-735-200

; Sequence 200, Application US/09989735

; Publication No. US20020193299A1

; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Baton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerltsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
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;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kljavin, Ivar J.  
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;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; TITLE OF INVENTION: Acids Encoding the Same

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Alignment Scores:

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Query Match:	100.00%	Indels:	0
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US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-989-735-200 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
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QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrPHisAla 40  
Db 157 CTGAACATCGACAAATGCGATCTGCGTTTAAGGCTGATGAGTTCTCTGAACGACGCC 216  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnThrAspAlaPheProLysLeu 60  
Db 217 CTCTTTGAGTCTATCAAAAGAACTCTTCTCTCAACTGGGATGCCCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGGACTGAGGAGCGCACTCCTGATGCCAG 309

Search completed: November 28, 2003, 13:38:07  
Job time : 251 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 10:23:55 ; Search time 2638 Seconds  
(without alignments)  
1101.055 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99  
Perfect score: 71

Sequence: 1 EESTIENYASRPEAFNTPF.....LNWDAFPKLGKLSATPDAQ 71

Scoring table:

OLIGO	
Xgapop 60.0 , Xgapext 60.0	
Ygapop 60.0 , Ygapext 60.0	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 2888711 seqs, 20454813386 residues

Word size: 1

Total number of hits satisfying chosen parameters: 5772890

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

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37: em\_htg\_vrt:\*  
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40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	100.0	414	6 AX055438	AX055438 Sequence
2	71	100.0	415	6 AR252517	AR252517 Sequence
3	71	100.0	415	6 AX077031	AX077031 Sequence
4	71	100.0	415	6 AX358892	AX358892 Sequence
5	71	100.0	415	6 AX362385	AX362385 Sequence
6	71	100.0	415	6 AX403313	AX403313 Sequence
7	71	100.0	415	6 AX454546	AX454546 Sequence
8	71	100.0	415	6 AX491024	AX491024 Sequence
9	71	100.0	415	6 AX574494	AX574494 Sequence
10	71	100.0	432	6 AX080815	AX080815 Sequence
11	71	100.0	432	6 AX080818	AX080818 Sequence
12	71	100.0	456	6 BD082389	BD082389 87 human
13	71	100.0	490	6 AX080817	AX080817 Sequence
14	59	83.1	435	6 AX041085	AX041085 Sequence
15	56	78.9	278	6 HSA293408	AJ293408 Homo sapi
16	46	64.8	529	6 AX014081	AX014081 Sequence
17	16	22.5	44679	9 CH19F21246	AD001502 Homo sapi
18	9	12.7	205812	2 AC141146	AC141146 Rattus no
19	9	12.7	218382	2 AC142461	AC142461 Rattus no
20	9	12.7	236199	2 AC110643	AC110643 Rattus no
21	8	11.3	710	1 YPUS0903	U50903 Yersinia pe
22	8	11.3	943	3 AF259957	AF259957 Glossina
23	8	11.3	2004	6 AX606817	AX606817 Sequence
24	8	11.3	2590	6 AK025078	AK025078 Homo sapi
25	8	11.3	7675	1 AF157015	AF157015 Streptoco
26	8	11.3	10193	1 AF093787	AF093787 Streptoco
27	8	11.3	10786	1 AB013792	AB013792 Yersinia
28	8	11.3	12035	14 AF201902	AF201902 Equine fo
29	8	11.3	12069	6 AX348317	AX348317 Sequence
30	8	11.3	14530	1 AE007605	AE007605 Clostridi
31	8	11.3	20609	1 AE014221	AE014221 Streptoco
32	8	11.3	22162	2 AC017198	AC017198 Drosophila
33	8	11.3	33795	6 AX409537	AX409537 Sequence
34	8	11.3	33795	9 AF253417	AF253417 Homo sapi
35	8	11.3	43342	10 AL928978	AL928978 Mouse DNA
36	8	11.3	46401	2 AC011928	AC011928 Homo sapi
37	8	11.3	67870	2 AC083787	AC083787 Homo sapi
38	8	11.3	69520	10 AL669925	AL669925 Mouse DNA
39	8	11.3	74149	2 AC123879_3	Continuation (4 of
40	8	11.3	89012	9 AC011406	AC011406 Homo sapi
41	8	11.3	98530	2 AC113088	AC113088 Mus muscu
42	8	11.3	100296	2 AL590308	AL590308 Human DNA
43	8	11.3	101579	2 AC008227	AC008227 Drosophila
44	8	11.3	101622	2 AC123648_3	Continuation (4 of
45	8	11.3	108449	9 AC112650	AC112650 Homo sapi

RESULT 1

#### ALIGNMENTS

AX055438  
LOCUS AX055438 414 bp DNA linear PAT 13-JAN-2001  
DEFINITION Sequence 68 from Patent WO0073452.  
ACCESSION AX055438  
VERSION AX055438.1 GI:12228711  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1  
Ashkenazi, A.J., Baker, K.P., Chan, B., Goddard, A., Godowski, P.J., Gurney, A.L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D.L., Tumas, D., Watanabe, C.K. and Wood, W.I.  
Compositions and methods for the treatment of immune related diseases  
Patent: WO 0073452-A 68 07-DEC-2000;  
Genentech, Inc. (US)

TITLE  
JOURNAL  
FEATURES  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 98 a 126 c 92 g 98 t  
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Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

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QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACAAATTGCGATCTGCGTTTAAAGGCTGATGAGTCTCTGAACCTGCGACGCC 216  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 217 CTCTTGAGTCTATCAAAAGAAACTTCTTCTCTCAACTGGATGCCCTTCTTAAGCTG 276  
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Db 277 AAAGGACTGAGAGCGCAACTCCTGATGCCAG 309

RESULT 2  
AR252517  
LOCUS AR252517 415 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 200 from patent US 6478825.  
ACCESSION AR252517  
VERSION AR252517.1 GI:27300425  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 415)  
AUTHORS Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.  
TITLE Implant, method of making same and use of the implant for the treatment of bone defects  
JOURNAL Patent: US 6478825-A 200 12-NOV-2002;  
FEATURES Location/Qualifiers  
1..415  
/organism="unknown"  
BASE COUNT 99 a 126 c 92 g 98 t  
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Alignment Scores:  
Pred. No.: 2.34e-69 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
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DB: 6 Gaps: 0

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QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
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QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACAAATTGCGATCTGCGTTTAAAGGCTGATGAGTCTCTGAACCTGCGACGCC 216  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 277 AAAGGACTGAGAGCGCAACTCCTGATGCCAG 309

RESULT 3  
AX077031  
LOCUS AX077031 415 bp DNA linear PAT 22-FEB-2001  
DEFINITION Sequence 19 from Patent WO0105972.  
ACCESSION AX077031  
VERSION AX077031.1 GI:13121661  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1  
Ashkenazi, A.J., Baker, K.P., Fong, S., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Mark, M.R., Marsters, S.A., Plicci, R.M., Tumas, D., Watanabe, C.K. and Wood, W.I.  
Compositions and methods for the treatment of immune related diseases  
Patent: WO 0105972-A 19 25-JAN-2001;  
Genentech, Inc. (US)

TITLE  
JOURNAL  
FEATURES  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
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BASE COUNT 99 a 126 c 92 g 98 t  
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Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
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QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACAAATTGCGATCTGCGTTTAAAGGCTGATGAGTCTCTGAACCTGCGACGCC 216  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 277 AAAGGACTGAGAGCGCAACTCCTGATGCCAG 309



Db 217 CTCTTTGAGTCTATCAAAAGAACTCTCTTCTCTCACTGGAGTGCCTTCTTAAGCTG 276

Qy 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
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277 AAAGGACTGAGAGCGCAACTCTGTATGCCAG 309

RESULT 4  
AX358892 415 bp DNA linear PAT 13-FEB-2002  
DEFINITION Sequence 145 from Patent WO0193983.  
ACCESSION AX358892  
VERSION AX358892.1 GI:18675347

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE  
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,  
Watanabe, C.K. and Wood, W.I.  
1 Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0193983-A 145 13-DEC-2001;  
Genentech Inc. (US)  
FEATURES Location/Qualifiers  
source 1..415  
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BASE COUNT 99 a 126 c 92 g 98 t

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Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX358892 (1-415)

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Db 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
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157 CTGAACATCGACAAATTGCGATCTGCGTTTAAGCTGATGAGTTCCTGAAGTGGACGCC 216

Qy 41 LeupheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
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217 CTCTTTGAGTCTATCAAAAGAACTCTCTTCTCAACTGGATGCTTTCTTAAGCTG 276

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RESULT 5  
AX362385 415 bp DNA linear PAT 15-FEB-2002  
DEFINITION Sequence 145 from Patent WO0208288.  
ACCESSION AX362385  
VERSION AX362385.1 GI:18694650

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE  
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,

Watanabe, C.K. and Wood, W.I.  
1 Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0208288-A 145 31-JAN-2002;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
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BASE COUNT 99 a 126 c 92 g 98 t

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Best Local Similarity: 100.00% Mismatches: 0  
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DB: Gaps: 0

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Qy 41 LeupheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
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Db 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
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277 AAAGGACTGAGAGCGCAACTCTGTATGCCAG 309

RESULT 6  
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DEFINITION Sequence 200 from Patent WO0073454.  
ACCESSION AX403313  
VERSION AX403313.1 GI:21436871

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE  
AUTHORS Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Eaton, D.,  
Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P.,  
Grimaldi, C.J., Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J.,  
Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,  
Williams, P., Wood, W.I. and Zhang, Z.  
1 Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0073454-A 200 07-DEC-2000;  
Genentech Inc. (US)  
FEATURES Location/Qualifiers  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t

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Score: 71.00 Matches: 71  
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Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
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QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
DB 157 CTGAACATCGACAAATTGCGATCTGCGTTTAAAGCTGATGAGTTCCTGAACCTGGCAGCC 216

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
DB 217 CTCTTGAGTCTATCAAAAGAAAGAACTCTTCTCTCAACTGGATGCTTCTTAAGCTG 276

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGAGCGCAACTCTGATGCCAG 309

RESULT 7  
AX454546 415 bp DNA linear PAT 06-JUL-2002  
LOCUS Sequence 131 from Patent WO0208284.  
ACCESSION AX454546  
VERSION AX454546.1 GI:21713897  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,  
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,  
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.  
and Ye,W.  
Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
Patent: WO 0208284-A 131 31-JAN-2002;  
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone  
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,  
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;  
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)  
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;  
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William  
I. (US)

TITLE  
Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis

JOURNAL  
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone  
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,  
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;  
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)  
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;  
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William  
I. (US)

FEATURES  
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BASE COUNT 99 a 126 c 92 g 98 t

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Alignment Scores: 2.34e-69 Length: 415  
Pred. No.: 71.00 Matches: 71  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
DB: 6

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX454546 (1-415)

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DB 157 CTGAACATCGACAAATTGCGATCTGCGTTTAAAGCTGATGAGTTCCTGAACCTGGCAGCC 216

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
DB 217 CTCTTGAGTCTATCAAAAGAAAGAACTCTTCTCTCAACTGGATGCCCTTCTTAAGCTG 276

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGAGCGCAACTCTGATGCCAG 309

RESULT 8  
AX491024 415 bp DNA linear PAT 16-AUG-2002  
LOCUS Sequence 131 from Patent WO0200690.  
DEFINITION AX491024  
ACCESSION AX491024  
VERSION AX491024.1 GI:22323849  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,  
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,  
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.  
and Ye,W.  
Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
Patent: WO 0200690-A 131 03-JAN-2002;  
Genentech, Inc. (US)

TITLE  
Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis

JOURNAL  
Genentech, Inc. (US)

FEATURES  
source 1. .415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t

ORIGIN  
Alignment Scores: 2.34e-69 Length: 415  
Pred. No.: 71.00 Matches: 71  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
DB: 6

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX491024 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAGAAAGCACCATTGAGATTATGCGTCACGACCCGAGGCTTTTAACACCCCGCTTC 156

QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
DB 157 CTGAACATCGACAAATTGCGATCTGCGTTTAAAGCTGATGAGTTCCTGAACCTGGCAGCC 216

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
DB 217 CTCTTGAGTCTATCAAAAGAAAGAACTCTTCTCTCAACTGGATGCCCTTCTTAAGCTG 276

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGAGCGCAACTCTGATGCCAG 309

RESULT 9  
AX574494 415 bp DNA linear PAT 07-JAN-2003  
LOCUS Sequence 21 from Patent WO0224888.  
DEFINITION AX574494  
ACCESSION AX574494  
VERSION AX574494.1 GI:27551800  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 Baker, K.P., Eaton, D.L., Filvaroff, E., Goddard, A., Grimaldi, J.C.,  
AUTHORS Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K., Wood, W.I.,  
Zhang, Z., and Fong, S.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0224888-A 21 28-MAR-2002;  
GENENTECH, INC. (US)  
FEATURES location/Qualifiers  
source 1..415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 2.34e-69 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX574494 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAAGAAAGCACCATTTGAGAAATTATGCGTCACGACCCGAGGCGCTTAAACACCCCGTTTC 156

QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
DB 157 CTGAACATCGACAAATTCGATCTGCGTTAAGCTGATGATGATTCCTGAACCTGACGCGC 216

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
DB 217 CTCTTGAGTCTATCAAAAGAAACTTCCTTCTCAACTGGATGCTTCTCTAAAGCTG 276

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGGAGCGCACTCTGATGCCAG 309

RESULT 10  
AX080815 432 bp DNA linear PAT 27-FEB-2001  
LOCUS Sequence 61 from Patent WO0109327.  
DEFINITION AX080815  
ACCESSION AX080815  
VERSION AX080815.1 GI:13169784  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Kljavin, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Pitti, R.M.,  
Watanabe, C.K., and Wood, W.I.  
TITLE Method of preventing the injury or death of retinal cells and  
treating ocular diseases  
JOURNAL Patent: WO 0109327-A 61 08-FEB-2001;  
Genentech, Inc. (US)  
FEATURES location/Qualifiers  
source 1..432  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Virtual DNA fragment used in the isolation of  
DNA57694."  
BASE COUNT 106 a 127 c 94 g 102 t 3 others  
ORIGIN

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Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX080815 (1-432)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 96 GAGGAAGAAAGCACCATTTGAGAAATTATGCGTCACGACCCGAGGCGCTTAAACACCCCGTTTC 155

QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
DB 156 CTGAACATCGACAAATTCGATCTGCGTTAAGCTGATGATGATTCCTGAACCTGACGCGC 215

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
DB 216 CTCTTGAGTCTATCAAAAGAAACTTCCTTCTCAACTGGATGCTTCTCTAAAGCTG 275

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 276 AAAGACTGAGGAGCGCACTCTGATGCCAA 308

RESULT 11  
AX080818 432 bp DNA linear PAT 27-FEB-2001  
LOCUS Sequence 64 from Patent WO0109327.  
DEFINITION AX080818  
ACCESSION AX080818  
VERSION AX080818.1 GI:13169787  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Kljavin, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Pitti, R.M.,  
Watanabe, C.K., and Wood, W.I.  
TITLE Method of preventing the injury or death of retinal cells and  
treating ocular diseases  
JOURNAL Patent: WO 0109327-A 64 08-FEB-2001;  
Genentech, Inc. (US)  
FEATURES location/Qualifiers  
source 1..432  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 106 a 127 c 94 g 102 t 3 others  
ORIGIN

Alignment Scores:  
Pred. No.: 2.43e-69 Length: 432  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX080818 (1-432)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 96 GAGGAAGAAAGCACCATTTGAGAAATTATGCGTCACGACCCGAGGCGCTTAAACACCCCGTTTC 155

QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
DB 156 CTGAACATCGACAAATTCGATCTGCGTTAAGCTGATGATGATTCCTGAACCTGACGCGC 215

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
DB 216 CTCTTGAGTCTATCAAAAGAAACTTCCTTCTCAACTGGATGCTTCTCTAAAGCTG 275

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71

Db 276 AAAGACTGAGAGCGCACTCTGATGCCCA 308  
RESULT 12  
LOCUS BD082389 456 bp DNA linear PAT 27-AUG-2002  
DEFINITION 87 human secreted proteins.  
ACCESSION BD082389  
VERSION BD082389.1 GI:22627999  
KEYWORDS JP 2001522239-A/31.  
SOURCE Mastadenovirus  
ORGANISM Mastadenovirus  
REFERENCE 1 (bases 1 to 456)  
AUTHORS Young,P., Greene,J.M., Ferrie,A.M., Ruben,S.M., Rosen,C.A., Duan,R.D., Hu,J.S., Florence,K.A., Olsen,H.S., Ebner,R., Brewer,L.A., Moore,P.A., Shi,Y., Lafleur,D.W. and Ni,J.  
87 human secreted proteins  
Patent: JP 2001522239-A 31 13-NOV-2001;  
TITLE HUMAN GENOME SCIENCES INC SECRETARY OF THE DEPARTMENT OF HEALTH  
JOURNAL HUMAN SERVICES  
COMMENT PN JP 2001522239-A/31  
PD 13-NOV-2001  
PF 19-MAR-1998 JP 1998542119  
PR 21-MAR-1997 US 60/041281,21-MAR-1997 US 60/041276 PR  
21-MAR-1997 US 60/042344,21-MAR-1997 US 60/041277 PR  
30-MAY-1997 US 60/048355,30-MAY-1997 US 60/048096 PR  
30-MAY-1997 US 60/048351,30-MAY-1997 US 60/048154 PR  
30-MAY-1997 US 60/048160,30-MAY-1997 US 60/048069 PR  
30-MAY-1997 US 60/048131,30-MAY-1997 US 60/048186 PR  
30-MAY-1997 US 60/048095,30-MAY-1997 US 60/048187 PR  
30-MAY-1997 US 60/048099,30-MAY-1997 US 60/050937 PR  
30-MAY-1997 US 60/048352,30-MAY-1997 US 60/048135 PR  
30-MAY-1997 US 60/048188,30-MAY-1997 US 60/048094 PR  
30-MAY-1997 US 60/048350,05-AUG-1997 US 60/054804 PR  
19-AUG-1997 US 60/056370,02-OCT-1997 US 60/060862 PI PAUL  
YOUNG,JOHN M GREENE,ANN M FERRIE,STEVEN M RUBEN,CRAIG A PI  
ROSEN,  
PI ROXANNE D DUAN,JING SHAN HU,KIMBERLY A FLORENCE,HENRIK S  
OLSEN,  
PI REINHARD EBNER,LAURIE A BREWER,PAUL A MOORE,YANGU SHI,DAVID W  
PI LAFLEUR,  
PI JIAN NI  
PC C07K14/00  
CC Strandedness: Double;  
CC Topology: Linear;  
FH Key Location/Qualifiers.  
FEATURES  
source 1. .456  
/organism="Mastadenovirus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10509"  
BASE COUNT 117 a 136 c 104 g 98 t 1 others  
ORIGIN  
Alignment Scores:  
Pred. No.: 2.55e-69 Length: 456  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x BD082389 (1-456)  
QY 1 GIUGIUGIuserThriIleGIuAsnTYrAlaSerArgProGIuAlaPheAsnThrProPhe 20  
Db 105 GAGAGAGAAAGCACCATTTGAGATTATGCGTCACGACCGAGCCCTTTAAACACCCCGTTC 164  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGIuPheLeuAsnTrpHisAla 40  
Db 165 CTGAACATCGACAATGTGCGATCTGCGTTTAAGCGTGAATGCTTCTGAAGTGGACGCC 224

QY 41 LeuPheGIuSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 225 CTCCTTGAGTCTATCAAAAGAACTTCCTTCTCACTGGATGCCCTTCTTAAGCTG 284  
QY 61 LysGIuLeuArgSerAlaThrProAspAlaGln 71  
Db 285 AAAGACTGAGAGCGCACTCTGATGCCCAG 317  
RESULT 13  
LOCUS AX080817 490 bp DNA linear PAT 27-FEB-2001  
DEFINITION Sequence 63 from Patent WO0109327.  
ACCESSION AX080817  
VERSION AX080817.1 GI:13169786  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Ashkenazi,A.J., Baker,K.P., Goddard,A., Godowski,P.J., Gurney,A.L., Kljavin,I.J., Lafleur,M., Mark,M.R., Marsters,S.A., Pitti,R.M., Watanabe,C.K. and Wood,W.I.  
Method of preventing the injury or death of retinal cells and treating ocular diseases  
Patent: WO 0109327-A 63 08-FEB-2001;  
Genentech, Inc. (US)  
TITLE Location/Qualifiers  
JOURNAL 1. .490  
FEATURES  
source /organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Virtual DNA fragment used in the isolation of DNA57694."  
BASE COUNT 118 a 149 c 116 g 107 t  
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Alignment Scores:  
Pred. No.: 2.72e-69 Length: 490  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AX080817 (1-490)  
QY 1 GIUGIUGIuserThriIleGIuAsnTYrAlaSerArgProGIuAlaPheAsnThrProPhe 20  
Db 164 GAGAGAGAAAGCACCATTTGAGATTATGCGTCACGACCGAGCCCTTTAAACACCCCGTTC 223  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGIuPheLeuAsnTrpHisAla 40  
Db 224 CTGAACATCGACAATGTGCGATCTGCGTTTAAGCGTGAATGCTTCTGAAGTGGACGCC 283  
QY 41 LeuPheGIuSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 284 CTCCTTGAGTCTATCAAAAGAACTTCCTTCTCACTGGATGCCCTTCTTAAGCTG 343  
QY 61 LysGIuLeuArgSerAlaThrProAspAlaGln 71  
Db 344 AAAGACTGAGAGCGCACTCTGATGCCCAG 376  
RESULT 14  
LOCUS AX080816 435 bp DNA linear PAT 27-FEB-2001  
DEFINITION Sequence 62 from Patent WO0109327.  
ACCESSION AX080816  
VERSION AX080816.1 GI:13169785  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Ashkenazi,A.J., Baker,K.P., Goddard,A., Godowski,P.J., Gurney,A.L., Kljavin,I.J., Lafleur,M., Mark,M.R., Marsters,S.A., Pitti,R.M., Watanabe,C.K. and Wood,W.I.  
Method of preventing the injury or death of retinal cells and treating ocular diseases  
Patent: WO 0109327-A 62 08-FEB-2001;  
Genentech, Inc. (US)  
TITLE Location/Qualifiers  
JOURNAL 1. .435  
FEATURES  
source /organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Virtual DNA fragment used in the isolation of DNA57694."  
BASE COUNT 118 a 149 c 116 g 107 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 2.72e-69 Length: 435  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AX080816 (1-435)  
QY 1 GIUGIUGIuserThriIleGIuAsnTYrAlaSerArgProGIuAlaPheAsnThrProPhe 20  
Db 164 GAGAGAGAAAGCACCATTTGAGATTATGCGTCACGACCGAGCCCTTTAAACACCCCGTTC 223  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGIuPheLeuAsnTrpHisAla 40  
Db 224 CTGAACATCGACAATGTGCGATCTGCGTTTAAGCGTGAATGCTTCTGAAGTGGACGCC 283  
QY 41 LeuPheGIuSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 284 CTCCTTGAGTCTATCAAAAGAACTTCCTTCTCACTGGATGCCCTTCTTAAGCTG 343  
QY 61 LysGIuLeuArgSerAlaThrProAspAlaGln 71  
Db 344 AAAGACTGAGAGCGCACTCTGATGCCCAG 376

REFERENCE 1  
AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Klajavin, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Pitti, R.M.,  
Watanabe, C.K. and Wood, W.I.  
TITLE Method of preventing the injury or death of retinal cells and  
treating ocular diseases  
JOURNAL Patent: WO 0109327-A 62 08-FEB-2001;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..435  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Virtual DNA fragment used in the isolation fo  
DNA57694."

BASE COUNT 108 a 130 c 96 g 101 t  
ORIGIN

Alignment Scores:  
Pred. No.: 4.92e-56 length: 435  
Score: 59.00 Matches: 59  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 83.10% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX041085 (1-435)

QY 13 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 32  
Db 136 CCCGAGGCGCTTAACACCCCGCTTCTGACATCGACAATTGCGATCGCTTAAGGCT 195

QY 33 AspGluPheLeuAsnThrPheAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 52  
Db 196 GATGAGTTCCTGAACTGGCAAGCCCTCTTGTGATCTATCAAAAGAACTTCTTCTC 255

QY 53 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 256 AACTGGATGCTTCTTAAGCTGAAGAGACTGAGAGCGCAACTCTGATGCCAG 312

RESULT 15  
AX041085/c 278 bp DNA linear PAT 23-NOV-2000  
LOCUS Sequence 3 from Patent WO0065053.  
DEFINITION AX041085  
ACCESSION AX041085  
VERSION AX041085.1 GI:11340655  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1  
AUTHORS Wang, T. and Dillon, D.C.  
TITLE Compositions and methods for therapy and diagnosis of head/neck and  
lung squamous cell carcinoma  
JOURNAL Patent: WO 0065053-A 3 02-NOV-2000;  
CORIXA CORPORATION (US)  
FEATURES Location/Qualifiers  
source 1..278  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 70 a 57 c 80 g 71 t  
ORIGIN

Alignment Scores:  
Pred. No.: 6.9e-53 length: 278  
Score: 56.00 Matches: 56  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 78.87% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX041085 (1-278)

QY 16 PheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPhe 35  
Db 269 TTTAACACCCCGCTTCTGAACTGACATCGACAATTGCGATCGCTTAAAGCTGATGATTC 210

QY 36 LeuAsnTrpHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAsp 55  
Db 209 CTGAAGTGGACGCGCTCTTGTGATCTATCAAAAGAACTTCTTCTCAACTGGGAT 150

QY 56 AlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 149 GCCTTCTTAAGCTGAAGAGACTGAGAGCGCAACTCTGATGCCAG 102

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Job time : 2644 secs



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 09:42:35 ; Search time 217 Seconds

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Title: US-10-059-395-142\_COPY\_29\_99

Perfect score: 71

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Searched: 2552756 seqs, 1349719017 residues

Word size: 1

Total number of hits satisfying chosen parameters: 5103067

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21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*  
22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*  
25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	100.0	414	22 AAC91475	Human PRO826 cDNA.
2	71	100.0	414	24 ABK28600	Human DNA57694-134
3	71	100.0	415	21 AAZ65018	Membrane-bound pro
4	71	100.0	415	22 AAF30059	Human cDNA encodin
5	71	100.0	415	22 AAF44164	Human PRO826 (UNQ4
6	71	100.0	415	22 AAC97491	Human angiogenesis
7	71	100.0	415	24 ABL95626	Human angiogenesis
8	71	100.0	415	24 ABK69971	CDNA encoding huma
9	71	100.0	415	24 ABL88137	Human PRO826 cDNA
10	71	100.0	415	24 ABK33608	CDNA encoding huma
11	71	100.0	415	25 ABX80255	Novel human secret
12	71	100.0	415	25 ABX80759	Human secreted/tr
13	71	100.0	415	25 ABX81142	Novel human secret
14	71	100.0	415	25 ABX90232	Human secreted/tr
15	71	100.0	415	25 ABX77843	Human PRO polynucl
16	71	100.0	415	25 ABX79439	Human secreted/tr
17	71	100.0	415	25 ABX64078	Human secreted/tr
18	71	100.0	415	25 ABX17042	CDNA encoding huma
19	71	100.0	428	24 ABZ11803	Human PRO polynucl
20	71	100.0	456	20 AA00632	Human secreted pro
21	71	100.0	518	22 ABA09519	Human secreted pro
22	56	78.9	278	21 AAC68806	Human head/neck tu
23	43	60.6	386	24 ABZ11804	Human polynucleoti
24	28	39.4	305	24 ABZ11886	Human polynucleoti
25	8	11.3	2001	24 ABN67971	Streptococcus poly
26	8	11.3	2298	21 AAC59576	Human secreted pro
27	8	11.3	12069	24 ABK39931	Human chemically p
28	8	11.3	12212	24 ABK12920	Human SLC26A2 (sol
29	8	11.3	12212	24 ABK12975	Human SLC26A2 (sol
30	8	11.3	33795	24 ABN95686	Gene #2184 used to
31	8	11.3	215561	24 ABN71527	Streptococcus poly
32	7	9.9	65	24 ABN31537	Rat spliced trans
33	7	9.9	198	21 AAC24586	Human secreted pro
34	7	9.9	231	20 AAH86401	Human single nucle
35	7	9.9	231	20 AAH86402	Human single nucle
36	7	9.9	238	21 AAA45447	Human secreted exp
37	7	9.9	251	21 AAC07741	Human secreted pro
38	7	9.9	256	25 ABX31899	Human GDP-mannose
39	7	9.9	283	21 AAC94607	Cat flea hindgut a
40	7	9.9	294	20 AAZ13185	Human gene express
41	7	9.9	300	20 AA093312	Human cancer cell
42	7	9.9	300	21 AAA00085	Human colon cancer
43	7	9.9	368	19 AA066404	CDNA clone AA37708
44	7	9.9	419	21 AAC31437	Human secreted pro
45	7	9.9	438	24 ABK29813	Colon adenocarcino

#### ALIGNMENTS

RESULT 1  
AAC91475 standard; cDNA; 414 BP.  
XX  
AC AAC91475;  
XX  
DT 21-MAR-2001 (first entry)  
XX  
DE Human PRO826 cDNA.  
XX  
KW Human; PRO; antiinflammatory; dermatological; antiarthritic;  
KW antirheumatic; cardiac; antianaemic; immunosuppressive; antithyroid;  
KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;  
KW antiallergic; antiastatic; immune related disorder;  
KW hepatobiliary disease; autoimmune disease; allergy; ss.  
XX  
OS Homo sapiens.

XX WO200073452-A2.  
PN  
XX  
PD 07-DEC-2000.  
XX  
PF 02-JUN-2000; 2000WO-US15264.  
XX  
PR 02-JUN-1999; 99WO-US12252.  
PR 20-JUL-1999; 99US-0144732.  
PR 20-JUL-1999; 99US-0144758.  
PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 29-OCT-1999; 99US-0162506.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28634.  
PR 09-DEC-1999; 99US-0170262.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
XX  
PA (GETH ) GENENTECH INC.  
PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;  
PI Wood WI;  
XX  
XX WPI; 2001-025253/03.  
DR P-PSDB; AAB50916.  
XX  
PT Thirty three nucleic acids encoding PRO polypeptides which are useful  
PT in the diagnosis and treatment of immune related disorders, e.g.  
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
PT thyroiditis and diabetes mellitus -  
XX  
PS Claim 48, Fig 29; 218bp; English.  
XX  
XX The present sequence is one of thirty three nucleic acids encoding PRO  
CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and  
CC antagonists are useful for treating and diagnosing immune related  
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
CC demyelinating polynuropathy or Guillain-Barre syndrome, and chronic  
CC inflammatory demyelinating polynuropathy), hepatobiliary diseases  
CC (such as infectious, autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
CC food hypersensitivity and urticaria), immunological diseases of the  
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
CC and hypersensitivity pneumonitis), transplantation associated diseases  
CC including graft rejection and graft-versus-host diseases.  
XX  
SQ Sequence 414 BP; 98 A; 126 C; 92 G; 98 T; 0 other;

Alignment Scores:  
Pred. No.: 3.23e-66 Length: 414  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0  
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QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAAGAACCAACATTGAGAAATTGCGATCGCTTTAAGCGTGAAGCTGATGAGTTCCTGAACCTGGCAGCC 156  
QY 21 LeuAsnIleAspIlySleuArgSerAlaPheIlySAlaaspGluPheIleuAsnTrpHisAla 40  
DB 157 CTGAACATCGACAATTGCGATCGCTTTAAGCGTGAAGCTGATGAGTTCCTGAACCTGGCAGCC 216  
QY 41 LeuPheGluSerIleIlySArgIlySleuProPheIleuAsnTrpAspAlaPheProIlySleu 60  
DB 217 CTCTTGAGTCTATCAAAAGAACTCTCTTCTCACTGGGATGCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGAGCGCAACTCTGATGCCAG 309  
RESULT 2  
ABK28600  
ID ABK28600 standard; cDNA; 414 BP.  
XX  
AC ABK28600;  
XX  
DT 09-APR-2002 (first entry)  
XX  
DE Human DNA57694-1341 encoding PRO826.  
XX  
XX Human; ss; gene; PRO; antiinflammatory; ophthalmological; vasotropic;  
KW retinal cell injury; ocular disease; retinitis pigmentosa;  
KW macular degenerative disease; retinal detachment; retinal tear; retinopathy;  
KW retinal degenerative disease; macular hole; degenerative myopia;  
KW acute retinal necrosis syndrome; traumatic choriorretinopathy;  
KW Purtscher's retinopathy; oedema; ischaemic condition;  
KW retinal vision occlusion; collagen vascular disease;  
KW thrombocytopenic purpura; uveitis; retinal vasculitis; Bales disease;  
KW systemic lupus erythematosus; environmental trauma.  
XX  
OS Homo sapiens.  
XX  
PN WO200109327-A2.  
XX  
PD 08-FEB-2001.  
XX  
PF 28-JUL-2000; 2000WO-US20710.  
XX  
PR 28-JUL-1999; 99US-146222P.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
XX  
PA (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;  
PI Kljavin IJ, Lafleur M, Mark MR, Marsters SA, Pitti RM;  
PI Watanabe CK, Wood WI;  
XX  
DR WPI; 2002-130120/17.  
DR P-PSDB; AAU81964.  
XX  
PT Promoting survival of retinal cells, or delaying or preventing retinal  
PT cell injury or death, by contacting retinal cells with PRO175, 220,  
PT 216, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132  
PT polypeptide -  
XX  
PS Claim 33; Fig 24; 152pp; English.  
XX  
CC The invention relates to promoting the survival of retinal cells, or  
CC delaying or preventing retinal cell injury or death, by contacting the  
CC retinal cells with the polypeptide such as PRO175, PRO220, PRO216,  
CC PRO243, PRO306, PRO346, PRO322, PRO536, PRO943, PRO840, PRO828, PRO826,  
CC PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids  
CC encoding the PRO proteins, a vector comprising the nucleic acid, a host  
CC cell comprising the vector, and anti-PRO antibody. The PRO proteins are  
CC useful for promoting survival of retinal cells (retinal neurons such as  
CC retinal ganglion cells, displaced retinal ganglion cells, amacrine  
CC cells, displaced amacrine cells, horizontal neurons or bipolar neurons,  
CC rod photoreceptors, or supportive cells such as Muller cells or pigment  
CC epithelial cells), or delaying or preventing retinal cell injury or  
CC death caused by ocular disease (which is or is associated with  
CC retinitis pigmentosa, macular degeneration, retinal detachment, retinal  
CC tear, retinopathy, retinal degenerative disease, macular hole,  
CC degenerative myopia, acute retinal necrosis syndrome, traumatic  
CC chorioretinopathy or contusion, Purtscher's retinopathy, edema, an  
CC ischaemic condition, central or branch retinal vision occlusion, an  
CC collagen vascular disease, thrombocytopenic purpura, uveitis, retinal  
CC vasculitis, occlusion associated with Eales disease or systemic lupus  
CC erythematosus), retinal injury or environmental trauma. The retinal  
CC cell injury or death is delayed or prevented by substantially not  
CC causing angiogenesis or mitogenesis. The present sequence is a cDNA  
CC encoding a PRO protein.  
XX  
SQ Sequence 414 BP; 98 A; 126 C; 92 G; 98 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 3 23e-66 Length: 414  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0  
  
US-10-059-395-142\_COPY\_29\_99 (1-71) x ABK28600 (1-414)  
  
QY 1 GUGUGUGUSeThrILlegLUASnTYrAlaSeArqProGluAlaPheAnThrProphe 20  
Db 97 GAGGAGAAAGCACCATTGAGATATGCGTCACGACCCGAGGCCCTTAAACACCCCGTTC 156  
  
QY 21 LeuAsnIleAspIleuArGSeRAlaPheIyAlaSpGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACAAATTGCGATCTGCGTTAAGGCTGATGAGTTCTTGAAGTGCACGCC 216  
  
QY 41 LeuPheGluSerIleIySARGLySleuProPheLeuAsnTrpAspAlaPheProLySleu 60  
Db 217 CTCTTGAGTCTATCAAAAGAAACTTCCTTCTCAACTGGATGCTTTCCTAAAGCTG 276  
  
QY 61 LysGlyLeuArGSeRAlaThrProAspAlaGln 71  
Db 277 AAAGACTGAGAGCGCAACTCCTGATGCCAG 309  
  
RESULT 3  
AAZ65018  
ID AAZ65018 standard; cDNA; 415 BP.  
XX  
AC AAZ65018;

XX 05-APR-2000 (first entry)  
DT  
XX Membrane-bound protein PRO826 encoding cDNA.  
DE  
XX  
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9963088-A2.  
PD  
XX 09-DEC-1999.  
PF  
XX 02-JUN-1999; 99WO-US12252.  
XX  
PR 02-JUN-1998; 98US-0087607.  
PR 02-JUN-1998; 98US-0087609.  
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PR 04-JUN-1998; 98US-0088326.  
PR 05-JUN-1998; 98US-0088167.  
PR 05-JUN-1998; 98US-0088202.  
PR 05-JUN-1998; 98US-0088212.  
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PR 10-JUN-1998; 98US-0088741.  
PR 10-JUN-1998; 98US-0088742.  
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PR 10-JUN-1998; 98US-0088811.  
PR 10-JUN-1998; 98US-0088824.  
PR 10-JUN-1998; 98US-0088825.  
PR 10-JUN-1998; 98US-0088826.  
PR 11-JUN-1998; 98US-0088858.  
PR 11-JUN-1998; 98US-0088861.  
PR 11-JUN-1998; 98US-0088863.  
PR 11-JUN-1998; 98US-0088876.  
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PR 12-JUN-1998; 98US-0089105.  
PR 16-JUN-1998; 98US-0089440.  
PR 16-JUN-1998; 98US-0089512.  
PR 16-JUN-1998; 98US-0089514.  
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PR 17-JUN-1998; 98US-0089599.  
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PR 18-JUN-1998; 98US-0089907.  
PR 18-JUN-1998; 98US-0089908.  
PR 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089948.  
PR 19-JUN-1998; 98US-0089952.  
PR 22-JUN-1998; 98US-0090246.  
PR 22-JUN-1998; 98US-0090252.  
PR 22-JUN-1998; 98US-0090254.  
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PR 24-JUN-1998; 98US-0090431.  
PR 24-JUN-1998; 98US-0090435.

PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090445.  
PR 24-JUN-1998; 98US-0090461.  
PR 24-JUN-1998; 98US-0090472.  
PR 24-JUN-1998; 98US-0090535.  
PR 24-JUN-1998; 98US-0090538.  
PR 24-JUN-1998; 98US-0090540.  
PR 24-JUN-1998; 98US-0090557.  
PR 25-JUN-1998; 98US-0090676.  
PR 25-JUN-1998; 98US-0090678.  
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PR 25-JUN-1998; 98US-0090691.  
PR 25-JUN-1998; 98US-0090694.  
PR 25-JUN-1998; 98US-0090695.  
PR 25-JUN-1998; 98US-0090696.  
PR 26-JUN-1998; 98US-0090862.  
PR 26-JUN-1998; 98US-0090863.  
PR 01-JUL-1998; 98US-0091358.  
PR 01-JUL-1998; 98US-0091360.  
PR 01-JUL-1998; 98US-0091544.  
PR 02-JUL-1998; 98US-0091478.  
PR 02-JUL-1998; 98US-0091486.  
PR 02-JUL-1998; 98US-0091519.  
PR 02-JUL-1998; 98US-0091626.  
PR 02-JUL-1998; 98US-0091628.  
PR 02-JUL-1998; 98US-0091633.  
PR 02-JUL-1998; 98US-0091633.  
PR 02-JUL-1998; 98US-0091646.  
PR 07-JUL-1998; 98US-0091673.  
PR 07-JUL-1998; 98US-0091978.  
PR 07-JUL-1998; 98US-0091982.  
PR 09-JUL-1998; 98US-0092182.  
PR 10-JUL-1998; 98US-0092472.  
PR 20-JUL-1998; 98US-0093339.  
PR 30-JUL-1998; 98US-0094651.  
PR 04-AUG-1998; 98US-0095282.  
PR 04-AUG-1998; 98US-0095285.  
PR 04-AUG-1998; 98US-0095301.  
PR 04-AUG-1998; 98US-0095302.  
PR 04-AUG-1998; 98US-0095318.  
PR 04-AUG-1998; 98US-0095321.  
PR 04-AUG-1998; 98US-0095325.  
PR 10-AUG-1998; 98US-0095916.  
PR 10-AUG-1998; 98US-0095929.  
PR 10-AUG-1998; 98US-0096012.  
PR 11-AUG-1998; 98US-0096143.  
PR 11-AUG-1998; 98US-0096146.  
PR 12-AUG-1998; 98US-0096329.  
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PR 17-AUG-1998; 98US-0096766.  
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PR 17-AUG-1998; 98US-0096894.  
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PR 17-AUG-1998; 98US-0096897.  
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PR 18-AUG-1998; 98US-0096950.  
PR 18-AUG-1998; 98US-0096959.  
PR 18-AUG-1998; 98US-0096960.  
PR 18-AUG-1998; 98US-0097022.  
PR 19-AUG-1998; 98US-0097141.  
PR 20-AUG-1998; 98US-0097218.  
PR 24-AUG-1998; 98US-0097661.  
PR 26-AUG-1998; 98US-0097951.  
PR 26-AUG-1998; 98US-0097952.  
PR 26-AUG-1998; 98US-0097954.  
PR 26-AUG-1998; 98US-0097955.  
PR 26-AUG-1998; 98US-0097971.  
PR 26-AUG-1998; 98US-0097974.  
PR 26-AUG-1998; 98US-0097978.

PR 26-AUG-1998; 98US-0097979.  
PR 26-AUG-1998; 98US-0097986.  
PR 26-AUG-1998; 98US-0098014.  
PR 31-AUG-1998; 98US-0098525.  
PR 16-SEP-1998; 98US-0100634.  
PR 12-JAN-1999; 99US-0115565.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood WI, Yuan J;  
XX  
DR WPI; 2000-072883/06.  
XX P-PSDB; AAY66681.  
PT Membrane-bound proteins and related nucleotide sequences -  
XX  
PS Claim 2; Fig 128; 822pp; English.  
XX  
CC The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIE  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
CC will also be useful for the preparation of PRO polypeptides, especially  
CC by recombinant techniques.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
SQ  
Alignment Scores:  
Pred. No.: 3.24e-66 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 21 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AAZ65018 (1-415)  
QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAAGAAAGCACCATTTGAGATTATGCGTCACGACCCGAGGCTTTAACACCCCGCTTC 156  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
DB 157 CTGAACATCGACAATTTGCGATCTGCGTTAAGCGTGATGAGTTCTGAACCTGGCACGCC 216  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
DB 217 CTCTTTGAGTCTATCAAAAGGAACCTTCTTCTCAACTGGGATGCCCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGGACTGAGGAGCGCACTCCTGATGCCAG 309  
RESULT 4  
AAF30059  
ID AAF30059 standard; cDNA; 415 BP.  
XX  
AC AAF30059;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Human cDNA encoding PRO826.  
XX  
KW PRO826; UNQ467; human; immune disease; autoimmune disease;

KM antirheumatic; antiarthritic; antiinflammatory; antianaemic;  
KM immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
KM hepatotropic; virucide; dermatological; antipsoriatic;  
KM antiasthmatic; antiallergic; immunostimulant; ss.  
XX Homo sapiens.  
OS  
FH Key Location/Qualifiers  
FT CDS 13..312  
FT sig\_peptide /\*tag= a  
FT /tag= 13..78  
FT mat\_peptide /tag= b  
FT /tag= 79..309  
FT /tag= c  
XX  
XX WO200105972-A1.  
XX  
XX 25-JAN-2001.  
XX  
XX 15-MAR-2000; 2000WO-US06884.  
XX  
XX 20-JUL-1999; 99US-0144758.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL,  
PI Hillan KJ, Mark MR, Masters SA, Pitti RM, Tumas D, Watanabe CK,  
PI Wood WI;  
XX  
XX WPI; 2001-103149/11.  
DR P-PSDB; AAB20117.  
XX  
XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
PT diagnosing and treating immune-related disorders, such as multiple  
PT sclerosis, rheumatoid arthritis and diabetes -  
XX  
XX Claim 21; Fig 19; 127pp; English.  
XX  
XX The present sequence is that of cDNA clone DNA57694-1341 (ATCC 203017)  
CC encoding novel human immunomodulator protein PRO826 (UNQ467) (see  
CC AAB20117). The clone was isolated following a database search by  
CC applying a signal sequence algorithm. The predicted protein has a  
CC mol. wt. of 11 kDa and a pI of 7.47. The invention provides  
CC polynucleotides (see AAF30050-62) encoding novel human PRO proteins  
CC (see AAB20108-20) including PRO826. Claimed compositions  
CC comprising these proteins or their agonists are useful for increasing  
CC infiltration of inflammatory cells into a tissue of a mammal,  
CC stimulating or enhancing an immune response in a mammal, or  
CC increasing the proliferation of T-lymphocytes in a mammal in response  
CC to an antigen. Claimed compositions comprising the PRO polypeptide  
CC or its antagonist have the opposite effect. A claimed method for  
CC treating an immune related disorder, such as a T cell disorder,  
CC involves administering the PRO polypeptide, an agonist antibody or  
CC an antagonist antibody. The disorder is selected from systemic  
CC lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
CC juvenile chronic arthritis, spondyloarthritis, systemic  
CC sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome,  
CC systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia,  
CC autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinated diseases (such as  
CC multiple sclerosis), autoimmune chronic active hepatitis (such as  
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis),  
CC inflammatory bowel disease (ulcerative colitis and Crohn's disease),  
CC gluten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated  
CC skin diseases (such as bullous skin disease, erythema multiforme and  
CC psoriasis), allergic diseases (such as asthma, allergic rhinitis,  
CC atopic dermatitis, food hypersensitivity and urticaria), immunologic  
CC diseases of the lung and transplantation associated diseases (such  
CC as graft rejection and graft-versus-host disease) (all claimed).  
CC Claimed methods of diagnosing these disorders comprise detecting  
CC the level of expression of the PRO gene. Also claimed are a method  
CC of identifying a compound capable of inhibiting the expression or  
CC activity of the PRO polypeptide, vectors, host cells, antibodies

CC and a method of stimulating the proliferation of T-lymphocytes  
CC using PRO826.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
Alignment Scores:  
Pred. No.: 3,24e-66 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AAF30059 (1-415)  
QY 1 GluGluGluSerThrIleGluAsnTYRAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAAGAAGCACCATTGAGATTATGCGTCAAGACCCGAGGCTTTAACAACCCGCTTC 156  
QY 21 LeuAsnIleAspIleuArgSerAlaPheIleuAlaAspGluPheLeuAsnTrpHisAla 40  
DB 157 CTGAACATGCACAAATTGCGATCTGCTTTAAGGCTGATGATGCTTCAACTGCGACGCC 216  
QY 41 LeuPheGluSerIleIleuArgIleuProPheLeuAsnTrpAspAlaPheProIleu 60  
DB 217 CTCTTGAGTCTATCAAAAGAACTTCTTCTCAACTGGGATGCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGAGCGCAACTCTGATGCCAG 309  
RESULT 5  
AAF44164  
ID AAF44164 standard; cDNA; 415 BP.  
XX  
XX AAF44164;  
AC  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Human PRO826 (UNQ467) nucleotide sequence SEQ ID NO:200.  
XX  
KM Human; secreted and transmembrane protein; PRO; cytostatic;  
KM cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
KM diagnostic assay; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200073454-A1.  
PN  
XX  
PD 07-DEC-2000.  
XX  
PF 30-MAR-2000; 2000WO-US08439.  
XX  
XX 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 07-JUL-1999; 99US-0143048.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146222.  
PR 17-AUG-1999; 99US-0149396.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 08-OCT-1999; 99US-0158663.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00376.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.



PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,  
PI Grimaldi CJ, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
DR WPI; 2001-032160/04.  
DR P-PSDB; AAB65204.  
XX  
XX  
PT PRO polynucleotides used to produce polypeptides used to target  
PT bioactive molecules such as toxins, radiolabels or antibodies, to  
PT specific cells, to cause targeted cell death -  
XX  
XX  
PS Claim 2; Fig 128, 935pp; English.  
XX  
CC The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins  
CC can be used for targeted delivery of bioactive molecules, such as  
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridisation probes, in  
CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
CC and DNA. They may also be used to produce transgenic animals which are  
CC used to develop and screen therapeutically useful reagents. The PRO  
CC nucleotide and protein sequence can be used for tissue typing and in  
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
XX  
Alignment Scores:  
Pred. No.: 3.24e-66 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AAF44164 (1-415)  
QY 1 GluGluGluSerThrIleGluAsnTYRAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 97 GAGGAAGAAAGCACCATGTGAGAAATTATGCGTCACGACCCGAGGCTTTAAACCCCGTTTC 156  
QY 21 LeuAsnIleAspIlyLeuArgSerAlaPheIlyAlaAspGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACAATTGCGATCTGCTTAAAGCTGATGAGTTCTTGAACGACGCGC 216  
QY 41 LeuPheGluSerIleIysArgIlyLeuProPheLeuAsnTrpAspAlaPheProIlyLeu 60  
Db 217 CTCTTGAGTCTATCAAAAGAAACTCTTCTTCTCAACTGGATGCTTCTTAAGCTG 276  
QY 61 IySGIlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGGACTGAGGAGCGCACTCCTGATGCCAG 309  
RESULT 6  
AAC97491  
ID AAC97491 standard; cDNA; 415 BP.  
XX  
AC AAC97491;  
XX  
DT 28-FEB-2001 (first entry)  
XX

DE Human angiogenesis-associated protein PRO826 cDNA, SEQ ID NO:157.  
XX  
XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
KW gene therapy; transgenic animal; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200053753-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 05-JAN-2000; 2000WO-US00219.  
XX  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX  
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
XX  
XX WPI; 2001-090793/10.  
DR P-PSDB; AAB53094.  
XX  
PT New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
XX  
XX  
PS Claim 58; Fig 61; 293pp; English.  
XX  
XX The invention relates to novel human angiogenesis-associated proteins  
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
CC PRO proteins. The invention also relates to vectors and host cells  
CC comprising a PRO nucleic acid, the recombinant production of a PRO  
CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
CC compounds which inhibit the expression of a PRO gene. The invention  
CC additionally encompasses methods of identifying modulators of PRO  
CC expression or activity; diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
CC mutations in a PRO gene, or the expression level of a PRO gene within a  
CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
CC administration of a PRO protein, or an agonist or antagonist thereof.  
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
CC agonists and PRO antagonists may be used as therapeutic agents to treat  
CC cardiovascular, endothelial or angiogenic disorders, such as  
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
CC endometriosis, ulcers, cancer, Alzheimer's disease, Huntington's

CC disease, or stroke. PRO nucleic acids are additionally useful in the  
CC recombinant production of PRO proteins, as hybridisation probes to  
CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
CC animals useful for the development and screening of potential  
CC therapeutic agents. The present sequence represents a cDNA encoding a PRO  
CC protein of the invention.

XX Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

#### Alignment Scores:

Pred. No.:	3.24e-66	Length:	415
Score:	71.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AAC97491 (1-415)

OY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20

Db 97 GAGGAGAGAAAGCACCAATTGAGATTATGCGTCACGACCCGAGCCCTTAACGCCCGCTTC 156

OY 21 leuAsnIleAspIleuArgSerAlaPheIleuAspGluPheIleuAsnThrPheIleu 40

Db 157 CTGAACATCGACCAATTGGCATCTGCGTTTAAGCTGATGATCTCTGAACTGGCACGCC 216

OY 41 leuPheGluSerIleIleGluLeuArgIleuProPheIleuAsnThrPaspalaPheProLysleu 60

Db 217 CTCTTGAGTCTATCAAAAGGAACTTCCTTCTCACTGGATGCCCTTCTTAAGCTG 276

OY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71

Db 277 AAAGACTGAGGAGCGCACTCTGATGCCAG 309

#### RESULT 7

ABL95626  
ID ABL95626 standard; cDNA; 415 BP.

XX ABL95626;

DT 19-JUL-2002 (first entry)

DE Human angiogenesis related cDNA PRO826 SEQ ID NO: 131.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;

KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;

KM cardiant; cytosolic; antiangiogenic; hypotensive; vulnery;

XX antiarteriosclerotic; gene; ss.

OS Homo sapiens.

XX WO200208284-A2.

PD 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US21735.

PR 20-JUL-2000; 2000US-219556P.

PR 25-JUL-2000; 2000US-220624P.

PR 25-JUL-2000; 2000US-220664P.

PR 28-JUL-2000; 2000WO-US20710.

PR 02-AUG-2000; 2000US-222695P.

PR 17-AUG-2000; 2000US-0643657.

PR 23-AUG-2000; 2000WO-US23522.

PR 24-AUG-2000; 2000WO-US23328.

PR 07-SEP-2000; 2000US-230978P.

PR 15-SEP-2000; 2000US-000000P.

PR 18-SEP-2000; 2000US-0664610.

PR 18-SEP-2000; 2000US-0665350.

PR 24-OCT-2000; 2000US-242922P.

PR 08-NOV-2000; 2000US-0709238.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 28-JUN-2001; 2001WO-US00000.

XX (GETH ) GENENTECH INC.

PA (BAKE/) BAKER K P.

PA (FERR/) FERRARA N.

PA (GERB/) GERBER H.

PA (GERR/) GERRITSEN M E.

PA (GODD/) GODDARD A.

PA (GODO/) GODOWSKI P J.

PA (GURN/) GURNEY A L.

PA (HILL/) HILLAN K J.

PA (MARS/) MARSTERS S A.

PA (PANJ/) PAN J.

PA (PAON/) PAONI N F.

PA (STEP/) STEPHAN J F.

PA (WATA/) WATANABE C K.

PA (WILL/) WILLIAMS P M.

PA (WOOD/) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,

PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,

PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,

XX WPI; 2002-171999/22.

DR P-PSDB; ABB95488.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial

PT infarction), endothelial or angiogenic disorders in a mammal -

XX Claim 1; Fig 131; 567pp; English.

PS The present invention provides the protein and coding sequences of human

XX PRO proteins. These are useful for treating or diagnosing a

CC cardiovascular, endothelial or angiogenic disorder, including cardiac

CC hypertrophy, trauma, cancer, age-related macular degeneration,

CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,

CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour

CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound

CC healing. The present sequence is a coding sequence of the invention.

SO Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

#### Alignment Scores:

Pred. No.:	3.24e-66	Length:	415
Score:	71.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

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US-10-059-395-142_COPY_29_99 (1-71) x ABL95626 (1-415)

QY      1  GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20
        |||
        97  GAGGAGAGAAAGCACCATGTGAGATTATGCGTACGACCGAGCCCTTTAACACCCCGCTTC 156

QY      21  LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40
        |||
        157  CTGAACATCGACAAATTGCGATCTGCGTTAAAGCTGATGAGTTCTGAACCTGGACAGCC 216

QY      41  LeupheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60
        |||
        217  CTCTTGAGTCTATCAAAAGAAACTTCTTCTCAACTGGATGCTTTCTTAAGCTG 276

QY      61  LysGlyLeuArgSerAlaThrProAspAlaGln 71
        |||
        277  AAAGACTGAGAGCGCAACTCTGATGCCAG 309

Db      277  AAAGACTGAGAGCGCAACTCTGATGCCAG 309

RESULT 8
ABK69971
ID      ABK69971 standard; DNA; 415 BP.
XX
AC      ABK69971;
XX
DT      15-JUL-2002 (first entry)
XX
DE      cDNA encoding human Pro peptide #11.
XX
KW      Human; ss; gene; PRO; secreted protein; transmembrane protein;
KM      genetic disorder; tumour; cancer.
XX
OS      Homo sapiens.
XX
PN      WO200224888-A2.
XX
PD      28-MAR-2002.
XX
PF      29-AUG-2001; 2001WO-US27099.
XX
PR      01-SEP-2000; 2000US-229896P.
PR      05-SEP-2000; 2000US-230621P.
PR      22-SEP-2000; 2000US-235147P.
PR      10-NOV-2000; 2000WO-US30873.
PR      12-JAN-2001; 2001US-261878P.
PR      16-JAN-2001; 2001US-261910P.
PR      16-JAN-2001; 2001US-261939P.
PR      16-JAN-2001; 2001US-262150P.
PR      25-JAN-2001; 2001US-264395P.
PR      02-FEB-2001; 2001US-266421P.
PR      09-FEB-2001; 2001US-267623P.
PR      28-FEB-2001; 2001WO-US06520.
PR      09-MAR-2001; 2001US-274399P.
PR      03-APR-2001; 2001US-280982P.
PR      04-APR-2001; 2001US-282129P.
PR      04-APR-2001; 2001US-282199P.
PR      09-MAY-2001; 2001US-290589P.
PR      25-MAY-2001; 2001WO-US17092.
PR      01-JUN-2001; 2001WO-US17800.
PR      20-JUN-2001; 2001WO-US19692.
PR      29-JUN-2001; 2001WO-US21066.
PR      09-JUL-2001; 2001WO-US21735.
XX
PA      (GETH ) GENENTECH INC.
XX
PI      Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI      Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z,
PI      Fong S;
XX
DR      WPI; 2002-362426/39.
DR      P-PSDB; ABG34040.
XX
PT      New PRO polypeptides and polynucleotides encoding the polypeptides,
```

```
PT      useful in gene therapy, chromosome identification, tissue typing, or
PT      for genetic analysis of individuals with genetic disorders
XX
PS      Claim 2; Figure 21; 218pp; English.
XX
CC      This invention relates to the cDNA and protein sequences of novel
CC      secreted and transmembrane polypeptides PRO polypeptides. The
CC      invention also comprises a method for producing the proteins of the
CC      invention by recombinant means and antibodies specific for the protein
CC      of the invention. The antibody may be used for detecting the PRO
CC      proteins of the invention and may be used to modify their activity.
CC      polynucleotides may be used as hybridisation probes for a cDNA library
CC      to isolate the full-length PRO cDNA or to isolate other cDNAs, to
CC      construct hybridisation probes for mapping the gene which encodes that
CC      PRO and for genetic analysis of individuals with genetic disorders, in
CC      assays to identify other proteins or molecules involved in binding
CC      reaction, to generate transgenic animals or knock-out animals which in
CC      turn are useful in the development and screening of therapeutically
CC      useful reagents, for chromosome identification, and tissue typing. The
CC      PRO polypeptides are useful in gene therapy, and as molecular weight
CC      markers for protein electrophoresis purposes. The sequences may
CC      also be used to detect overexpression on PRO polypeptides in cancerous
CC      tumours and for screening for differentially expressed genes using
CC      microarray technology. The present sequence represents a cDNA encoding
CC      a human PRO protein of the invention.
XX
SQ      Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

Alignment Scores:
Pred. No.:      3.24e-66      Length:      415
Score:          71.00      Matches:      71
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:             24      Gaps:      0

US-10-059-395-142_COPY_29_99 (1-71) x ABK69971 (1-415)

QY      1  GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20
        |||
        97  GAGGAGAGAAAGCACCATGTGAGATTATGCGTACGACCGAGCCCTTTAACACCCCGCTTC 156

QY      21  LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40
        |||
        157  CTGAACATCGACAAATTGCGATCTGCGTTAAAGCTGATGAGTTCTGAACCTGGACAGCC 216

QY      41  LeupheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60
        |||
        217  CTCTTGAGTCTATCAAAAGAAACTTCTTCTCAACTGGATGCTTTCTTAAGCTG 276

QY      61  LysGlyLeuArgSerAlaThrProAspAlaGln 71
        |||
        277  AAAGACTGAGAGCGCAACTCTGATGCCAG 309

Db      277  AAAGACTGAGAGCGCAACTCTGATGCCAG 309

RESULT 9
ABL88137
ID      ABL88137 standard; cDNA; 415 BP.
XX
AC      ABL88137;
XX
DT      16-MAY-2002 (first entry)
XX
DE      Human PRO826 cDNA sequence SEQ ID NO:131.
XX
KW      Human; angiogenesis; cardiant; cytostratic; antiangiogenic; hypotensive;
KW      vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW      gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW      angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW      age-related macular degeneration; arterial restenosis; angina;
KW      rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW      lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW      wound healing; chromosome mapping; gene mapping; gene; ss.
```

OS Homo sapiens.  
XX  
PN WO200200690-A2.  
XX  
PD 03-JAN-2002.  
XX  
PF 20-JUN-2001; 2001WO-US19692.  
XX  
PR 23-JUN-2000; 2000US-213637P.  
PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 02-AUG-2000; 2000US-222695P.  
PR 17-AUG-2000; 2000US-0643657.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 07-SEP-2000; 2000US-230978P.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-0709238.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX  
DR WPI; 2002-090516/12.  
DR P-PSDB; ABB84882.  
XX  
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal -  
XX  
PS Claim 2; Fig 131; 565pp; English.  
XX  
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
CC ABB85003. The PRO proteins and polynucleotides have cardiac, cytostatic,  
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
CC activities, and can be used in gene therapy. The PRO polynucleotides,  
CC proteins, agonists and antagonists are useful for treating or diagnosing  
CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
CC carcinoma) and wound healing. The PRO polynucleotides have applications  
CC in molecular biology, including use as hybridisation probes, and in  
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
CC probes used in the exemplification of the present invention.

XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
Alignment Scores:  
Pred. No.: 3.24e-66 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x ABL88137 (1-415)  
QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluValAlaPheAsnThrProPhe 20  
Db 97 GAGAGAAAGCAACCATTTGAGAAATTATGCGTCAACGAGCGCTTAAACACCCCGCTTC 156  
QY 21 LeuAsnIleAspIleuArgSerAlaPheIleuAlaAspGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGAACAATTGCGATCTGCGTTAAGCTGATGAGTTCCTGAACCTGCACGCC 216  
QY 41 LeuPheGluSerIleuArgIleuArgIleuProPheLeuAsnTrpAspAlaPheProIleu 60  
Db 217 CTCTTGAGTCTATCAAAAGAACTTCTTCTCAACTGGAGTCCCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGACTGAGAGCGCAACTCTGATGCCAG 309  
RESULT 10  
ABK33608  
ID ABK33608 standard; cDNA; 415 BP.  
XX  
AC ABK33608;  
XX  
DT 08-MAY-2002 (first entry)  
XX  
DE cDNA encoding human PRO protein, Seq ID No 145.  
XX  
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
KW pericyte cell proliferation; chondrocyte cell proliferation;  
KW tumour necrosis factor-alpha; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200208288-A2.  
XX  
PD 31-JAN-2002.  
XX  
PF 29-JUN-2001; 2001WO-US21066.  
XX  
PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220585P.  
PR 25-JUL-2000; 2000US-220605P.  
PR 25-JUL-2000; 2000US-220607P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220638P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 25-JUL-2000; 2000US-220666P.  
PR 26-JUL-2000; 2000US-220893P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 15-SEP-2000; 2000US-000000P.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 28-NOV-2000; 2000US-253646P.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001WO-US17092.

XX (GERTH ) GENENTECH INC.  
PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
PI WPI, 2002-172001/22.  
XX P-PSDB; AAU83664.  
DR  
XX  
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,  
PT useful for treating a PRO related disorder and for diagnosing tumours  
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal  
PT tumour or liver tumour -  
XX  
XX  
PS Claim 2; Figure 145; 359pp; English.  
XX  
CC The invention relates to one hundred and twenty two nucleic acids  
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
CC agonists and antagonists are useful for treating a PRO related disorder.  
CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
CC liver tumour. The PRO polypeptides are useful for stimulating the  
CC proliferation of, or gene expression, in pericyte cells, for stimulating  
CC the proliferation or differentiation of chondrocyte cells, for  
CC stimulating the release of tumour necrosis factor-alpha from human blood,  
CC for stimulating or inhibiting the proliferation of normal human dermal  
CC fibroblast cells. The PRO polypeptide may also be used as molecular  
CC weight markers and for tissue typing. The PRO nucleic acids have  
CC applications in molecular biology, including use as hybridisation probes,  
CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human  
CC PRO protein coding sequences of the invention.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 3.24e-66 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0  
  
US-10-059-395-142\_COPY\_29\_99 (1-71) x ABK33608 (1-415)  
  
QY 1 GUGUGUGUSeRThrIleGluAsnTYrAlaSeRArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAGAGAAAGCACCATTGAGAAATTATGCGTCACGACCCGAGCCCTTAAACACCCCGCTTC 156  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrPheAla 40  
DB 157 CTGAACATCGACAAATTGCGATTCGCTTAAAGGCTGATGAGTTCCTGAACCTGGACAGCC 216  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnThrAspAlaPheProLysLeu 60  
DB 217 CTCTTGAGTCTATCAAAAGAAAGAACTTCCTTCTCAACTGGATGCTTTCCTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGAGACTGAGAGCGCAACTCCTGATGCCAG 309  
  
RESULT 11  
ABX80255  
ID ABX80255 standard; DNA; 415 BP.  
XX  
AC ABX80255;  
XX  
DT 28-APR-2003 (first entry)  
XX  
DE Novel human secreted or transmembrane protein PRO819 DNA.  
XX  
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;

KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN US2002132252-A1.  
XX  
PD 19-SEP-2002.  
XX  
PF 14-NOV-2001; 2001US-0990442.  
XX  
XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 06-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.



PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089599P.  
PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 28-AUG-2001; 2001US-0941992.  
XX  
XX (GETH ) GENENTECH INC.  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferreira N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
XX WPI: 2003-247083/24.  
DR P-PSDB; ABUS9098.  
XX  
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
PT are therapeutically useful for enhancing immune response and in cancer  
PT treatments -  
XX  
XX Claim 2; Fig 130; 64Bpp; English.  
XX  
CC The invention describes an isolated human PRO polypeptide. The PRO  
CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
CC in modulating at least one biological activity of a cell expressing a PRO  
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
CC useful for treating conditions or disorders where angiogenesis would be  
CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
CC useful for treating cancerous tumours. PRO812 inhibits vascular  
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
CC cells and is thus useful for inhibiting endothelial cell growth in  
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
CC stimulated T-lymphocytes and are therapeutically useful for enhancing

CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
CC rod photoreceptor cells) and therefore are useful for treating retinal  
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813  
CC and PRO1106 induce proliferation of mammalian kidney mesangial cells,  
CC and therefore are useful for treating kidney disorders associated with  
CC decreased mesangial cell function such as Berger disease or other  
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
CC proliferation and/or redifferentiation of chondrocytes in culture and  
CC are thus useful for treating sports injuries, and arthritis. This  
CC sequence represents a novel human PRO protein polynucleotide.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
Alignment Scores:  
Pred. No.: 3.24e-66 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 25 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x ABX80255 (1-415)  
QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAAGAACCAACCAATTCGATGAGATTCGTCACGACCCGAGGCTTTAAACACCCGTTG 156  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheAsnTrpHisAla 40  
DB 157 CTGAACATGCACAATTCGATCTGCGTTTAAAGCTGATGATTCCTCGAACTGGCAGCC 216  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
DB 217 CTCTTGAGTCTATCAAAAGAAACTTCCTTCTCACTGGAGTGCCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGGAGCGCACTCCTGATGCCAG 309  
RESULT 12  
ABX80759  
ID ABX80759 standard; cDNA; 415 BP.  
XX  
AC ABX80759;  
XX  
DT 22-APR-2003 (first entry)  
XX  
DE Human secreted/transmembrane protein cDNA, #78.  
XX  
KW Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;  
KW diagnostic; biosensor; bioreactor; tumour; therapeutic;  
KW gene therapy; tumour-associated antigenic target; TAT; ADEPT;  
KW antibody-dependent enzyme mediated prodruq therapy; cyostatic.  
XX  
OS Homo sapiens.  
XX  
XX US2003027162-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 15-NOV-2001; 2001US-0997428.  
XX  
PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.

PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089599P.  
PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 19-JUN-1998; 98US-089947P.  
PR 19-JUN-1998; 98US-089948P.  
PR 19-JUN-1998; 98US-089952P.  
PR 22-JUN-1998; 98US-090246P.  
PR 22-JUN-1998; 98US-090252P.  
PR 22-JUN-1998; 98US-090254P.  
PR 23-JUN-1998; 98US-090349P.  
PR 23-JUN-1998; 98US-090355P.  
PR 24-JUN-1998; 98US-090429P.  
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PR 10-JUL-1998; 98US-092472P.  
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PR 30-JUL-1998; 98US-094651P.  
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PR 10-AUG-1998; 98US-095929P.  
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PR 18-AUG-1998; 98US-097022P.  
PR 19-AUG-1998; 98US-097141P.  
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PR 26-AUG-1998; 98US-097974P.  
PR 26-AUG-1998; 98US-097978P.  
PR 26-AUG-1998; 98US-097979P.  
PR 26-AUG-1998; 98US-097986P.  
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PR 31-AUG-1998; 98US-098525P.  
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Alignment Scores:

Pred. No.:	3, 24e-66	Length:	415
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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	25	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x ABX80759 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluValAlaPheAsnThrProPhe 20  
DB 97 GAGGAAGAAAGCACCATTGAGATTATGCGTCACGACCCGAGGCCCTTAAACACCCCGTTG 156  
QY 21 LeuAsnIleAspIleuArgSerAlaPheIleuAspGluPheLeuAsnTrpAlaPheProIleu 40  
DB 157 CTGACATCGACCAATTGCGATCTGCCGTTAAGCGTGATGATGATCTCTGAACCTGGCAGCC 216  
QY 41 LeuPheGluSerIleIleuArgIleuPheLeuAsnTrpAlaPheProIleu 60  
DB 217 CTCTTGAGTCTATCAAAAGAACTCTTCTCTCAACTGGAGTCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGGACTGAGGAGCGCAACTCCTGATGCCAG 309

RESULT 13  
ABX81142  
ID ABX81142 standard; DNA; 415 BP.

XX AC ABX81142;

XX DT 22-APR-2003 (first entry)

DE Novel human secreted or transmembrane protein PRO819 DNA.

KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
XX OS Homo sapiens.

XX US2003027985-A1.  
PN 06-FEB-2003.  
XX 14-NOV-2001; 2001US-0990562.  
PF 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
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PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
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PR 10-MAR-2000; 2000WO-US06319.  
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PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
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PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
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PR 05-JUN-1998; 98US-088217P.  
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PR 09-JUL-1998; 98US-092182P.  
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PR 10-AUG-1998; 98US-096012P.  
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PR 12-AUG-1998; 98US-096329P.  
PR 17-AUG-1998; 98US-096757P.  
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PR 17-AUG-1998; 98US-096773P.  
PR 17-AUG-1998; 98US-096791P.  
PR 17-AUG-1998; 98US-096867P.  
PR 17-AUG-1998; 98US-096891P.  
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PR 17-AUG-1998; 98US-096895P.  
PR 17-AUG-1998; 98US-096897P.  
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PR 18-AUG-1998; 98US-096960P.  
PR 18-AUG-1998; 98US-097022P.  
PR 19-AUG-1998; 98US-097141P.  
PR 20-AUG-1998; 98US-097218P.  
PR 24-AUG-1998; 98US-097661P.  
PR 26-AUG-1998; 98US-097952P.  
PR 26-AUG-1998; 98US-097954P.  
PR 26-AUG-1998; 98US-097955P.  
PR 26-AUG-1998; 98US-097971P.  
PR 26-AUG-1998; 98US-097974P.  
PR 26-AUG-1998; 98US-097978P.  
PR 26-AUG-1998; 98US-097979P.  
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Query Match: 100.00% Indels: 0  
DB: 25 Gaps: 0

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Db 157 CTGAACATCGACCAATTGCGATCTGCGTTTAAGGCTGATGAGTTCTGAACCTGGACGCC 216  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTyrAspAlaPheProLysLeu 60  
Db 217 CTCTTGAGTCTATCAAAAGGAACTTCTTCTCAACTGGATGCTTTCCTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGGACTGAGGAGCGCAACTCCTGATGCCAG 309  
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XX AC ABX90232;  
XX DT 01-MAY-2003 (first entry)  
XX DB Human secreted/transmembrane protein cDNA, #78.  
XX KW Human; gene; ss; PRO; secreted; transmembrane; signal peptide;  
KW pharmaceutical; diagnostic; therapeutic; gene therapy.

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XX Homo sapiens.
XX US2002160384-A1.
XX 31-OCT-2002.
XX 14-NOV-2001; 2001US-0992598.
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PR 05-NOV-1997; 97WO-US20069.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
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PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
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PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 16-JUN-1997; 97US-049787P.
PR 17-OCT-1997; 97US-062250P.
PR 12-NOV-1997; 97US-065186P.
PR 13-NOV-1997; 97US-065311P.
PR 24-NOV-1997; 97US-066770P.
PR 25-FEB-1998; 98US-075945P.
PR 20-MAR-1998; 98US-078910P.
PR 28-APR-1998; 98US-083322P.
PR 07-MAY-1998; 98US-084600P.
PR 28-MAY-1998; 98US-087106P.
PR 02-JUN-1998; 98US-087607P.
PR 02-JUN-1998; 98US-087609P.
PR 02-JUN-1998; 98US-087759P.
PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088021P.
PR 04-JUN-1998; 98US-088025P.
PR 04-JUN-1998; 98US-088026P.
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PR 10-JUN-1998; 98US-088734P.
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PR 11-JUN-1998; 98US-088861P.
PR 11-JUN-1998; 98US-088876P.
PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089440P.
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PR 18-JUN-1998; 98US-089908P.
PR 28-AUG-2001; 2001US-0941992.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrera N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-288106/28.
DR P-PSDB; ABU60528.
XX
PT New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes -
XX
PS Claim 2; Fig 128; 650pp; English.
XX
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful in gene therapy, in chromosome
CC identification, as chromosome markers, or in generating probes. The PRO
CC polypeptides are useful as molecular markers for protein
CC electrophoresis, and the isolated nucleic acids may be used for
CC recombinantly expressing those markers. The PRO polypeptides and nucleic
CC acids may also be used in tissue typing. Anti-PRO antibodies are useful
CC in diagnostic assays for PRO, and in affinity purification of PRO from
CC recombinant cell culture or natural sources. The sequences amplifying and the
CC ABX90083-ABX90468 are the genes encoding, the primers amplifying and the
CC probes detecting the PRO polynucleotides of the invention.
CC Note: The sequence data for this patent is also available in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;
XX
Alignment Scores:
Pred. No.: 3.24e-66 length: 415
Score: 71.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Query Match: 100.00% Indels: 0  
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QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
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KW antibody-dependent enzyme mediated prodnrg therapy.  
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#### SUMMARIES

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#### ALIGNMENTS

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; Patent No. US20020072067A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerltzen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC63  
CURRENT APPLICATION NUMBER: US/09/989,722  
CURRENT FILING DATE: 2001-11-19  
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PRIOR FILING DATE: 1997-06-16  
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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

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## RESULT 2

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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
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; APPLICANT: Goddard, Audrey

;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kljavin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
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;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
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; PRIOR FILING DATE: 1998-07-09

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; Sequence 200, Application US/09989279  
; Patent No. US20020072496A1  
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
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APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
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OY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
DB 157 CTGAACATCGACAAATGCGATCTGCGTTAAGGCTGATGAGTTCCTGAACCTGGCAGCC 216  
OY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
DB 217 CTCTTGAGTCTATCAAAAGAAACTCTTCTCAACTGGATGCGCTTCTCAAGCTG 276

OY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGAGCGCACTCTGATGCCAG 309

## RESULT 4

US-09-989-727-200

; Sequence 200, Application US/09989727  
; Patent No. US20020072497A1

## ; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
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; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C65

CURRENT APPLICATION NUMBER: US/09/989,727  
CURRENT FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
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; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

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Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

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Db 277 AAAGACTGAGGAGCGCACTCTGATGCCAG 309  
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; Patent No. US20020103125A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
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; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C70  
; CURRENT APPLICATION NUMBER: US/09/989,731  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
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;; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

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## RESULT 7

US-09-991-073-200

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;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
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;; APPLICANT: Williams, P. Mickey  
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;; FILE REFERENCE: P2730P1C15  
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## RESULT 8

US-09-990-442-200

; Sequence 200, Application US/09990442

; Patent No. US20020132252A1

## GENERAL INFORMATION:

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; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

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DB:	10	Gaps:	0

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US-09-991-163-200  
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; Patent No. US20020132253A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
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; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
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; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C17  
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; PRIOR FILING DATE: 1998-07-09

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RESULT 10  
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; Sequence 200, Application US/09993604  
; Patent No. US20020137075A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David

APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C25  
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;; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

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; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
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; APPLICANT: Ferrara, Napoleone  
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; PRIOR FILING DATE: 1998-07-09

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;; PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
Pred. No.: 7.74e-66  
Score: 71.00  
Percent Similarity: 100.00%

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; Patent No. US20020160384A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Geritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
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; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC20  
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; PRIOR FILING DATE: 1998-07-09

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; Patent No. US20020177164A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
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; APPLICANT: Roy, Margaret Ann  
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; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C66

; CURRENT APPLICATION NUMBER: US/09/989,293A

; PRIOR FILING DATE: 2001-11-20

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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
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US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-989-293A-200 (1-415)

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## RESULT 15

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US-09-989-735-200
; Sequence 200, Application US/09989735
; Publication No. US20020193299A1
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## GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Auecin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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[illegible]

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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-989-735-200 (1-415)

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QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
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Db 157 CTGAACATCGACAAATTGCGATCTGCGTTTAAGGCTGATGAGTTCTGAACTGGCACGCC 216  
  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
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Db 217 CTCTTTGAGTCTATCAAAAGAAACTTCTCTCAACTGGAGTGCTTCTTAAGCTG 276  
  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
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Db 277 AAAGACTGAGGAGCGCACTCTGATGCCAG 309

Search completed: November 28, 2003, 12:18:04  
Job time : 252 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2003, 12:21:56 ; Search time 47 Seconds  
(without alignments)  
239.778 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Perfect score: 375

Sequence: 1 EESTIENYASRPEAFNTPF.....LNWDAPFKLKGRSATPDQ 71

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	375	100.0	99	20	AAW67828	Human secreted pro
2	375	100.0	99	21	AAV66681	Membrane-bound pro
3	375	100.0	99	22	AAAB20117	Human immunostimul
4	375	100.0	99	22	AAAB65204	Human PRO826 (UNQ4
5	375	100.0	99	22	AAAB50916	Human PRO826 prote
6	375	100.0	99	22	AAAB53094	Human angiogenesis
7	375	100.0	99	23	ABP69586	Human polypeptide
8	375	100.0	99	23	ABB95488	Human angiogenesis
9	375	100.0	99	23	ABG34040	Human pro peptide

10	375	100.0	99	23	ABB84882	Human PRO826 prote
11	375	100.0	99	23	AAU83664	Human PRO protein,
12	375	100.0	99	23	AAU81964	Human PRO826. Hom
13	375	100.0	99	24	ABU59097	Novel human secret
14	375	100.0	99	24	ABU59244	Human secreted/tr
15	375	100.0	99	24	ABU59393	Novel human secret
16	375	100.0	99	24	ABU59393	Human secreted/tr
17	375	100.0	99	24	ABU58019	Human PRO polypept
18	375	100.0	99	24	ABU58950	Human secreted/tr
19	375	100.0	99	24	ABU13910	Human PRO826 polyp
20	375	100.0	99	24	ABU10865	Human PRO polypept
21	286	76.3	85	23	ABP69587	Human polypeptide
22	166	44.3	88	23	ABB72393	Murine protein iso
23	143	38.1	96	23	ABP69669	Human reproductive
24	65.5	17.5	116	22	AAW94219	Human endometrium
25	65.5	17.5	230	20	AAV60056	Human adult skin c
26	65.5	17.5	479	21	AAV50941	Human transferrase
27	65	17.3	123	22	AAW73503	Human secreted pro
28	64	17.1	72	21	AAW01482	Human secreted pro
29	64	17.1	72	21	AAW01483	Human secreted pro
30	64	17.1	387	21	AAW38324	Human secreted pro
31	64	17.1	808	23	ABG69063	Amino acid sequenc
32	62.5	16.7	526	21	AAV75474	Neisseria meningit
33	62.5	16.7	526	21	AAV75475	Neisseria meningit
34	62.5	16.7	526	21	AAV75476	Neisseria meningit
35	60.5	16.1	1544	22	ABB69002	Drosophila melanog
36	60	16.0	844	22	ABB59956	Drosophila melanog
37	58	15.5	369	21	AAV50940	Human adult skin c
38	58	15.5	440	21	AAV99354	Human PRO1411 (UNQ
39	58	15.5	440	22	AAU29124	Human PRO polypept
40	58	15.5	440	22	AAW7551	Human PRO1411. Ho
41	58	15.5	440	22	AAW31205	Amino acid sequenc
42	58	15.5	440	22	AAW31205	Protein of the inv
43	58	15.5	440	23	ABG95876	Human secreted/tr
44	58	15.5	440	23	ABB95497	Human angiogenesis
45	58	15.5	440	23	ABB84891	Human PRO1411 prot

ALIGNMENTS

RESULT 1	AAW67828	AAW67828 standard; Protein; 99 AA.
ID	AAW67828	
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DT	25-MAR-1999	(first entry)
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DE	Human secreted protein encoded by gene 22 clone HFEAF41.	
XX		
KW	Human; secreted protein; fusion protein; gene therapy; protein therapy;	
KW	diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;	
KW	developmental abnormality; foetal deficiency; blood; allergy; renal;	
KW	immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;	
KW	inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;	
KW	cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;	
KW	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;	
KW	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.	
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OS	Homo sapiens.	
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PN	WO9842738-A1.	
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PD	01-OCT-1998.	
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PF	19-MAR-1998;	98WO-US05311.
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PR	30-MAY-1997;	97US-0050937.
PR	21-MAR-1997;	97US-0041276.
PR	21-MAR-1997;	97US-0041277.
PR	21-MAR-1997;	97US-0041281.
PR	21-MAR-1997;	97US-0042344.

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PR 30-MAY-1997; 97US-0048135.  
PR 30-MAY-1997; 97US-0048154.  
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PR 30-MAY-1997; 97US-0048352.  
PR 30-MAY-1997; 97US-0048355.  
PR 05-AUG-1997; 97US-0054804.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA;  
PI Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS;  
PI Rosen CA, Ruben SM, Shi Y, Young P;  
XX  
DR WPI; 1999-070066/06.  
DR N-PSDB; AAX00632.  
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XX  
PT New isolated human genes and the secreted polypeptides they encode -  
PT useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders  
XX  
XX  
PS Claim 11; Page 285; 385pp; English.  
XX  
CC This sequence represents a secreted human protein encoded by the gene  
CC clone detailed in the descriptor line. The gene can be used to generate  
CC fusion proteins by linking to the gene to a human immunoglobulin Fc  
CC portion (e.g. AAX00602) for increasing the stability of the fused  
CC protein as compared to the human protein only.  
CC The invention relates to 87 novel genes and their fragments (nucleic  
CC acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004)  
CC which are useful for preventing, treating or ameliorating medical  
CC conditions e.g. by protein or gene therapy. Also, pathological  
CC conditions can be diagnosed by determining the amount of the new  
CC polypeptides in a sample or by determining the presence of mutations in  
CC the new polynucleotides. Specific uses are described for each of the 87  
CC polynucleotides, based on which tissues they are most highly expressed in  
CC (see AAX00611 for described uses).  
XX  
XX  
SQ Sequence 99 AA;  
Query Match 100.0%; Score 375; DB 20; Length 99;  
Best Local Similarity 100.0%; Pred. No. 5.1e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EEESTIENYASRPEAFNTPLFLNIDKLSAFKADEFNLWHALESIKRKLPLFLNWDAPFKL 60  
Db 29 EEESTIENYASRPEAFNTPLFLNIDKLSAFKADEFNLWHALESIKRKLPLFLNWDAPFKL 88  
QY 61 KGLRSATPDQAQ 71  
Db 89 KGLRSATPDQAQ 99

KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping.  
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OS Homo sapiens.  
XX WO9963088-A2.  
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PD 09-DEC-1999.  
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PF 02-JUN-1999; 99WO-US12252.  
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PR 11-JUN-1998; 98US-0088858.  
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PR 11-JUN-1998; 98US-0088863.  
PR 11-JUN-1998; 98US-0088876.  
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PR 12-JUN-1998; 98US-0089105.  
PR 16-JUN-1998; 98US-0089440.  
PR 16-JUN-1998; 98US-0089512.  
PR 16-JUN-1998; 98US-0089514.  
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PR 17-JUN-1998; 98US-0089538.  
PR 17-JUN-1998; 98US-0089598.  
PR 17-JUN-1998; 98US-0089599.  
PR 17-JUN-1998; 98US-0089600.  
PR 17-JUN-1998; 98US-0089653.  
PR 18-JUN-1998; 98US-0089801.  
PR 18-JUN-1998; 98US-0089907.  
PR 18-JUN-1998; 98US-0089908.  
PR 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089948.  
PR 19-JUN-1998; 98US-0089952.  
PR 22-JUN-1998; 98US-0090246.  
PR 22-JUN-1998; 98US-0090252.  
PR 22-JUN-1998; 98US-0090254.  
PR 23-JUN-1998; 98US-0090349.  
PR 23-JUN-1998; 98US-0090355.  
PR 24-JUN-1998; 98US-0090429.  
PR 24-JUN-1998; 98US-0090431.  
PR 24-JUN-1998; 98US-0090435.  
PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090445.  
PR 24-JUN-1998; 98US-0090461.  
PR 24-JUN-1998; 98US-0090472.  
PR 24-JUN-1998; 98US-0090535.

PR 24-JUN-1998; 98US-0090538.  
PR 24-JUN-1998; 98US-0090540.  
PR 24-JUN-1998; 98US-0090557.  
PR 25-JUN-1998; 98US-0090676.  
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PR 25-JUN-1998; 98US-0090688.  
PR 25-JUN-1998; 98US-0090690.  
PR 25-JUN-1998; 98US-0090691.  
PR 25-JUN-1998; 98US-0090694.  
PR 25-JUN-1998; 98US-0090695.  
PR 25-JUN-1998; 98US-0090696.  
PR 26-JUN-1998; 98US-0090862.  
PR 26-JUN-1998; 98US-0090863.  
PR 01-JUL-1998; 98US-0091358.  
PR 01-JUL-1998; 98US-0091360.  
PR 01-JUL-1998; 98US-0091544.  
PR 02-JUL-1998; 98US-0091478.  
PR 02-JUL-1998; 98US-0091486.  
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PR 02-JUL-1998; 98US-0091633.  
PR 02-JUL-1998; 98US-0091646.  
PR 02-JUL-1998; 98US-0091673.  
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PR 10-JUL-1998; 98US-0092472.  
PR 20-JUL-1998; 98US-0093339.  
PR 30-JUL-1998; 98US-0094651.  
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PR 04-AUG-1998; 98US-0095302.  
PR 04-AUG-1998; 98US-0095318.  
PR 04-AUG-1998; 98US-0095321.  
PR 04-AUG-1998; 98US-0095325.  
PR 10-AUG-1998; 98US-0095916.  
PR 10-AUG-1998; 98US-0095929.  
PR 10-AUG-1998; 98US-0096012.  
PR 11-AUG-1998; 98US-0096143.  
PR 11-AUG-1998; 98US-0096146.  
PR 12-AUG-1998; 98US-0096329.  
PR 17-AUG-1998; 98US-0096757.  
PR 17-AUG-1998; 98US-0096766.  
PR 17-AUG-1998; 98US-0096768.  
PR 17-AUG-1998; 98US-0096773.  
PR 17-AUG-1998; 98US-0096791.  
PR 17-AUG-1998; 98US-0096867.  
PR 17-AUG-1998; 98US-0096891.  
PR 17-AUG-1998; 98US-0096894.  
PR 17-AUG-1998; 98US-0096895.  
PR 17-AUG-1998; 98US-0096897.  
PR 18-AUG-1998; 98US-0096949.  
PR 18-AUG-1998; 98US-0096950.  
PR 18-AUG-1998; 98US-0096959.  
PR 18-AUG-1998; 98US-0096960.  
PR 18-AUG-1998; 98US-0097022.  
PR 19-AUG-1998; 98US-0097141.  
PR 20-AUG-1998; 98US-0097218.  
PR 24-AUG-1998; 98US-0097661.  
PR 26-AUG-1998; 98US-0097951.  
PR 26-AUG-1998; 98US-0097952.  
PR 26-AUG-1998; 98US-0097954.  
PR 26-AUG-1998; 98US-0097955.  
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PR 26-AUG-1998; 98US-0097978.  
PR 26-AUG-1998; 98US-0097979.  
PR 26-AUG-1998; 98US-0097986.  
PR 26-AUG-1998; 98US-0098014.  
PR 31-AUG-1998; 98US-0098525.  
PR 16-SEP-1998; 98US-0100634.

PR 12-JAN-1999; 99US-0115565.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood WI, Yuan J;  
XX  
DR WPI; 2000-072883/06.  
DR N-PSDB; AAZ65018.  
XX  
PT Membrane-bound proteins and related nucleotide sequences -  
XX  
PS claim 12; Fig 129; 822pp; English.  
XX  
CC The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIE  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
CC will also be useful for the preparation of PRO polypeptides, especially  
CC by recombinant techniques.  
XX  
SQ Sequence 99 AA;

Query Match 100.0%; Score 375; DB 21; Length 99;  
Best Local Similarity 100.0%; Pred. No. 5.1e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEESTIENYASRPEAFNTPLNIDKLSAFKADEFNLWHALESIKRKLPLNWDAPPL 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||  
29 EEESTIENYASRPEAFNTPLNIDKLSAFKADEFNLWHALESIKRKLPLNWDAPPL 88  
QY 61 KGLRSATPDAQ 71  
Db ||||||||||||  
89 KGLRSATPDAQ 99

RESULT 3  
AAB20117  
ID AAB20117 standard; Protein; 99 AA.  
XX

AC AAB20117;

DT 30-APR-2001 (first entry)

DE Human immunostimulant PRO826.

XX  
KW PRO826; UNQ467; human; immune disease; autoimmune disease;  
KW antirheumatic; antiarthritic; antiinflammatory; antianaemic;  
KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
KW hepatotropic; virucide; dermatological; antipsoriatic;  
KW antiasthmatic; antiallergic; immunostimulant.  
XX

OS Homo sapiens.

XX  
FH Key Location/Qualifiers  
FT Peptide 1..22

FT Protein /label= Signal\_peptide  
FT 23..99

FT Modified-site /label= Mature\_protein  
FT 22..28

FT Modified-site /note= "N-myristoylation site"  
FT 90..96

FT Modified-site /note= "N-myristoylation site"  
FT 16..48

FT Region /note= "homology to peroxidase"



XX WO200105972-A1.  
PN  
XX  
PD 25-JAN-2001.  
XX  
XX 15-MAR-2000; 2000WO-US06884.  
PF  
XX 20-JUL-1999; 99US-0144758.  
PR  
XX (GETH ) GENENTECH INC.  
PA  
XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL,  
PI Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK;  
PI Wood WI;  
XX  
XX WPI; 2001-103149/11.  
DR N-PSDB; AAF30059.  
DR  
XX  
XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
PT diagnosing and treating immune-related disorders, such as multiple  
PT sclerosis, rheumatoid arthritis and diabetes -  
XX  
XX  
PS Claim 20; Fig 20; 127pp; English.  
XX  
XX The present sequence is that of novel human immunomodulator PRO826  
CC (UNQ467), as deduced from cDNA (see AAF30059) isolated from a  
CC database screening. PRO826 has a mol.wt. of 11 kDa and a pI of  
CC 7.47. The invention provides polynucleotides (see AAF30050-62)  
CC encoding novel human PRO proteins (see AAB20108-20) including PRO826.  
CC Claimed compositions comprising these proteins or their agonists  
CC are useful for increasing infiltration of inflammatory cells into  
CC a tissue of a mammal, stimulating or enhancing an immune  
CC response, or increasing the proliferation of T-lymphocytes in a  
CC mammal in response to an antigen. Claimed compositions comprising  
CC a PRO polypeptide or its antagonist have the opposite effect. A  
CC claimed method for treating an immune related disorder, such as a T  
CC cell disorder, involves administering a PRO polypeptide, an agonist  
CC antibody or an antagonist antibody. The disorder is selected from  
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
CC juvenile chronic arthritis, spondyloarthritis, systemic sclerosis,  
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated  
CC renal disease, demyelinated diseases (such as multiple sclerosis),  
CC autoimmune chronic active hepatitis, primary biliary cirrhosis,  
CC granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel  
CC disease (ulcerative colitis and Crohn's disease), gluten-sensitive  
CC enteropathy, Whipple's disease, (auto)immune-mediated skin diseases  
CC (such as bullous skin disease, erythema multiforme and psoriasis),  
CC allergic diseases (such as asthma, allergic rhinitis, atopic  
CC dermatitis, food hypersensitivity and urticaria), immunologic  
CC diseases of the lung and transplantation associated diseases (such  
CC as graft rejection and graft-versus-host disease) (all claimed).  
CC Claimed methods of diagnosing these disorders comprise detecting  
CC the level of expression of the PRO gene. Also claimed are a method  
CC of identifying a compound capable of inhibiting the expression or  
CC activity of the PRO polypeptide, vectors, host cells, antibodies,  
CC and a method of stimulating the proliferation of T lymphocytes  
CC using PRO826.  
XX  
SQ Sequence 99 AA;  
Query Match 100.0%; Score 375; DB 22; Length 99;  
Best Local Similarity 100.0%; Pred. No. 5.1e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4  
AAB65204  
ID AAB65204 standard; Protein; 99 AA.  
XX  
AC AAB65204;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Human PRO826 (UNQ467) protein sequence SEQ ID NO:201.  
XX  
XX Human; secreted and transmembrane protein; PRO; cytostatic;  
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
KW diagnostic assay.  
XX  
OS Homo sapiens.  
XX  
XX WO200073454-A1.  
XX  
PD 07-DEC-2000.  
XX  
XX 30-MAR-2000; 2000WO-US08439.  
PF  
XX  
XX 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 07-JUL-1999; 99US-0143048.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146222.  
PR 17-AUG-1999; 99US-0149396.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 08-OCT-1999; 99US-0158663.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
XX WPI; 2001-032160/04.  
DR N-PSDB; AAF44164.  
DR  
XX  
XX PRO polynucleotides used to produce polypeptides used to target  
PT bioactive molecules such as toxins, radiolabels or antibodies, to  
PT specific cells, to cause targeted cell death -  
XX  
XX Claim 12; Fig 129; 935pp; English.

The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are

CC used to develop and screen therapeutically useful reagents. The PRO  
 CC nucleotide and protein sequence can be used for tissue typing and in  
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.

XX  
 SQ Sequence 99 AA;

Query Match 100.0%; Score 375; DB 22; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-41;  
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTIENYASRPEAFNTPTFLNIDKLSAFKADDFLWNLHAFESIKRKLPLNWDAPFKL 60  
 |||||  
 Db 29 EESTIENYASRPEAFNTPTFLNIDKLSAFKADDFLWNLHAFESIKRKLPLNWDAPFKL 88  
 QY 61 KGLRSATPDAQ 71  
 |||||  
 Db 89 KGLRSATPDAQ 99

RESULT 5  
 AAB50916  
 ID AAB50916 standard; Protein; 99 AA.

XX  
 AC AAB50916;

XX  
 DT 21-MAR-2001 (first entry)

XX  
 DE Human PRO826 protein.

XX  
 KW Human; PRO; antiinflammatory; dermatological; antiarthritic;  
 KW antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;  
 KW antidiabetic; nootropic; neuroprotective; hepatotropic; vitruclide;  
 KW antiallergic; antiasthmatic; immune related disorder;  
 KW hepatobiliary disease; autoimmune disease; allergy.

XX  
 OS Homo sapiens.

XX  
 PN WO200073452-A2.

XX  
 PD 07-DEC-2000.

XX  
 PF 02-JUN-2000; 2000WO-US15264.

XX  
 PR 02-JUN-1999; 99WO-US12252.

XX  
 PR 20-JUL-1999; 99US-0144732.

XX  
 PR 20-JUL-1999; 99US-0144758.

XX  
 PR 28-JUL-1999; 99US-0146222.

XX  
 PR 01-SEP-1999; 99WO-US20111.

XX  
 PR 15-SEP-1999; 99WO-US21090.

XX  
 PR 15-SEP-1999; 99WO-US21547.

XX  
 PR 29-OCT-1999; 99US-0162506.

XX  
 PR 30-NOV-1999; 99WO-US28313.

XX  
 PR 01-DEC-1999; 99WO-US28634.

XX  
 PR 09-DEC-1999; 99US-0170262.

XX  
 PR 20-DEC-1999; 99WO-US30911.

XX  
 PR 05-JAN-2000; 2000WO-US00219.

XX  
 PR 06-JAN-2000; 2000WO-US00376.

XX  
 PR 11-FEB-2000; 2000WO-US03565.

XX  
 PR 18-FEB-2000; 2000WO-US04341.

XX  
 PR 18-FEB-2000; 2000WO-US04342.

XX  
 PR 22-FEB-2000; 2000WO-US04414.

XX  
 PR 24-FEB-2000; 2000WO-US04914.

XX  
 PR 15-MAR-2000; 2000WO-US06884.

XX  
 PR 20-MAR-2000; 2000WO-US07377.

XX  
 PR 21-MAR-2000; 2000WO-US07532.

XX  
 PR 30-MAR-2000; 2000WO-US08439.

XX  
 PR 17-MAY-2000; 2000WO-US13705.

XX  
 PR 22-MAY-2000; 2000WO-US14042.

PA (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
 PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;  
 PI Wood WR;

XX WPI; 2001-025253/03.

DR N-PSDB; AAC91475.

XX Thirty three nucleic acids encoding PRO polypeptides which are useful  
 PT in the diagnosis and treatment of immune related disorders, e.g.  
 PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 PT thyroiditis and diabetes mellitus -

XX Claim 58; Fig 30; 218pp; English.

XX The present sequence is one of thirty three novel PRO polypeptides.

CC The PRO polypeptides, anti-PRO antibodies, agonists and  
 CC antagonists are useful for treating and diagnosing immune related  
 CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
 CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic  
 CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases  
 CC (such as infectious, autoimmune chronic active hepatitis, primary  
 CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
 CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
 CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
 CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
 CC food hypersensitivity and urticaria), immunological diseases of the  
 CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
 CC and hypersensitivity pneumonitis), transplantation associated diseases  
 CC including graft rejection and graft-versus-host diseases.

XX Sequence 99 AA;

Query Match 100.0%; Score 375; DB 22; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-41;  
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTIENYASRPEAFNTPTFLNIDKLSAFKADDFLWNLHAFESIKRKLPLNWDAPFKL 60  
 |||||

Db 29 EESTIENYASRPEAFNTPTFLNIDKLSAFKADDFLWNLHAFESIKRKLPLNWDAPFKL 88

QY 61 KGLRSATPDAQ 71  
 |||||

Db 89 KGLRSATPDAQ 99

RESULT 6  
 AAB53094

ID AAB53094 standard; Protein; 99 AA.

XX  
 AC AAB53094;

XX  
 DT 28-FEB-2001 (first entry)

XX  
 DE Human angiogenesis-associated protein PRO826, SEQ ID NO:158.

XX  
 KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
 KW gene therapy; transgenic animal.

XX  
 OS Homo sapiens.

XX WO200053753-A2.  
PN  
XX 14-SEP-2000.  
PD  
XX 05-JAN-2000; 2000WO-US00219.  
PF  
XX 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
XX  
DR WPI, 2001-090793/10.  
DR N-PSDB; AAC97491.  
XX  
PT New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
PT  
XX  
PS Claim 69; Fig 62; 293pp; English.  
XX  
CC The invention relates to novel human angiogenesis-associated proteins  
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
CC PRO proteins. The invention also relates to vectors and host cells  
CC comprising a PRO nucleic acid, the recombinant production of a PRO  
CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
CC compounds which inhibit the expression of a PRO gene. The invention  
CC additionally encompasses methods of identifying modulators of PRO  
CC expression or activity; diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
CC mutations in a PRO gene, or the expression level of a PRO gene within a  
CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
CC administration of a PRO protein, or an agonist or antagonist thereof.  
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
CC agonists and PRO antagonists may be used as therapeutic agents to treat  
CC cardiovascular, endothelial or angiogenic disorders, such as  
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
CC disease, or stroke. PRO nucleic acids are additionally useful in the  
CC recombinant production of PRO proteins, as hybridisation probes to  
CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
CC animals useful for the development and screening of potential  
CC therapeutic agents. The present sequence represents a PRO protein of the  
CC invention.  
XX  
SQ Sequence 99 AA;

Query Match 100.0%; Score 375; DB 22; Length 99;  
Best local similarity 100.0%; Pred. No. 5.1e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 EESTIENTYASRPEAFNTPFLNIDKLSAFAKADFLNMHALFESIKRKLPLNWDAPPKL 60  
Db 29 EESTIENTYASRPEAFNTPFLNIDKLSAFAKADFLNMHALFESIKRKLPLNWDAPPKL 88  
OY 61 KGLRSATPDQAQ 71  
Db 89 KGLRSATPDQAQ 99  
RESULT 7  
ID ABP69586 standard; Protein; 99 AA.  
XX  
AC ABP69586;  
XX  
DT 20-JAN-2003 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 1633.  
XX  
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;  
KW cell-proliferative disorder; neurodegenerative disease; bacterial;  
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;  
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;  
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;  
KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;  
KW antiarthritic.  
XX  
OS Homo sapiens.  
XX  
PN WO200270539-A2.  
XX  
PD 12-SEP-2002.  
XX  
PF 05-MAR-2002; 2002WO-US05095.  
XX  
PR 05-MAR-2001; 2001US-0799451.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;  
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
PI Wehrman T, Wang J, Wang D, Drmanac RT;  
XX  
DR WPI, 2002-759812/82.  
DR N-PSDB; ABZ11803.  
XX  
PT New polynucleotides comprising sequences assembled from expressed  
PT sequence tags (ESTs), useful for treating cell-proliferative,  
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or  
PT platelet or coagulation disorders -  
XX  
PS Claim 9; SEQ ID NO 1633; 1012pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated polynucleotide (I) comprising a  
CC nucleotide sequence selected from any of 948 sequences  
CC (ABZ1119-ABZ12066) or their mature protein coding portion, active domain  
CC coding protein or complementary sequences. The polynucleotides are useful  
CC for identifying expressed genes or for physical mapping of human genome.  
CC The encoded polypeptides (ABP68902-ABP69849) are useful as molecular  
CC weight markers, as a food supplement, for generating antibodies, in  
CC medical imaging, screening and diagnostic assays and for treating  
CC cell-proliferative disorders (cancer), neurodegenerative diseases  
CC (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple  
CC sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid  
CC disorders, platelet or coagulation disorders, wound, burns, incision,  
CC ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal,  
CC parasitic), arthritis, etc.  
CC  
Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 99 AA;

Query Match 100.0%; Score 375; DB 23; Length 99;  
Best Local Similarity 100.0%; Pred. No. 5.1e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBESTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPPKL 60  
|||  
Db 29 EBESTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPPKL 88

OY 61 KGLRSATPDAQ 71  
|||  
Db 89 KGLRSATPDAQ 99

## RESULT 8

ABB95488  
ID ABB95488 standard; Protein; 99 AA.

XX  
AC ABB95488;

XX  
DT 19-JUL-2002 (first entry)

XX  
DE Human angiogenesis related protein PRO826 SEQ ID NO: 132.

XX  
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
KW cardiant; cytosclastic; antiangiogenic; hypotensive; vulnerary;  
KW antiarteriosclerotic.

XX  
OS Homo sapiens.

XX  
PN WO200208284-A2.

XX  
PD 31-JAN-2002.

XX  
PF 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 02-AUG-2000; 2000US-222695P.  
PR 17-AUG-2000; 2000US-0643657.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 07-SEP-2000; 2000US-230978P.  
PR 15-SEP-2000; 2000US-000000P.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-0709238.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.

PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 28-JUN-2001; 2001WO-US00000.

XX  
PA (GETH ) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONTI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WJ, Ye W;  
XX  
XX WPI; 2002-171999/22.  
DR N-PSDB; ABL95626.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal -  
XX  
XX Claim 11; Fig 132; 567pp; English.

XX  
XX The present invention provides the protein and coding sequences of human  
CC PRO proteins. These are useful for treating or diagnosing a  
CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
CC hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The present sequence is a PRO protein of the invention.

XX  
SQ Sequence 99 AA;

Query Match 100.0%; Score 375; DB 23; Length 99;  
Best Local Similarity 100.0%; Pred. No. 5.1e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBESTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPPKL 60  
|||  
Db 29 EBESTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPPKL 88

OY 61 KGLRSATPDAQ 71  
|||  
Db 89 KGLRSATPDAQ 99

## RESULT 9

ABG34040  
ID ABG34040 standard; Protein; 99 AA.

XX  
AC ABG34040;

XX  
DT 15-JUL-2002 (first entry)

XX  
DE Human Pro peptide #11.

XX  
KW Human; PRO; secreted protein; transmembrane protein;  
KW genetic disorder; tumour; cancer.

OS Homo sapiens.  
XX  
PN WO200224888-A2.  
XX  
PD 28-MAR-2002.  
XX  
PF 29-AUG-2001; 2001WO-US27099.  
XX  
PR 01-SEP-2000; 2000US-229896P.  
PR 05-SEP-2000; 2000US-230621P.  
PR 22-SEP-2000; 2000US-235147P.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 12-JAN-2001; 2001US-261878P.  
PR 16-JAN-2001; 2001US-261910P.  
PR 16-JAN-2001; 2001US-261939P.  
PR 16-JAN-2001; 2001US-262150P.  
PR 25-JAN-2001; 2001US-264395P.  
PR 02-FEB-2001; 2001US-266421P.  
PR 09-FEB-2001; 2001US-267623P.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 09-MAR-2001; 2001US-274399P.  
PR 03-APR-2001; 2001US-280982P.  
PR 04-APR-2001; 2001US-282129P.  
PR 04-APR-2001; 2001US-282199P.  
PR 09-MAY-2001; 2001US-290589P.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
XX  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;  
XX  
DR WPI; 2002-362426/39.  
DR N-PSDB; ABK69971.  
XX  
PT New PRO polypeptides and polynucleotides encoding the polypeptides,  
PT useful in gene therapy, chromosome identification, tissue typing, or  
PT for genetic analysis of individuals with genetic disorders -  
XX  
PS Claim 11; Figure 22; 218pp; English.  
XX  
CC This invention relates to the cDNA and protein sequences of novel  
CC secreted and transmembrane polypeptides PRO polypeptides. The  
CC invention also comprises a method for producing the proteins of the  
CC invention by recombinant means and antibodies specific for the protein  
CC of the invention. The antibody may be used for detecting the PRO  
CC proteins of the invention and may be used to modify their activity.  
CC polynucleotides may be used as hybridisation probes for a cDNA library  
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, to  
CC construct hybridisation probes for mapping the gene which encodes that  
CC PRO and for genetic analysis of individuals with genetic disorders, in  
CC assays to identify other proteins or molecules involved in binding  
CC reaction, to generate transgenic animals or knock-out animals which in  
CC turn are useful in the development and screening of therapeutically  
CC useful reagents, for chromosome identification, and tissue typing. The  
CC PRO polypeptides are useful in gene therapy, and as molecular weight  
CC markers for protein electrophoresis purposes. The sequences may  
CC also be used to detect overexpression on PRO polypeptides in cancerous  
CC tumours and for screening for differentially expressed genes using  
CC microarray technology. The present sequence represents a human PRO  
CC protein of the invention.  
XX  
SQ Sequence 99 AA;

Query Match 100.0%; Score 375; DB 23; Length 99;  
Best Local Similarity 100.0%; Pred. No. 5,1e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEESTIENYASRPEAFNTPLNIDKLSAFKADFLNWTALLFESIKRKLPLFNWDAPPKL 60  
Db 29 EEESTIENYASRPEAFNTPLNIDKLSAFKADFLNWTALLFESIKRKLPLFNWDAPPKL 88  
Qy 61 KGLRSATPDAQ 71  
Db 89 KGLRSATPDAQ 99  
RESULT 10  
ABB84882  
ID ABB84882 standard; Protein; 99 AA.  
XX  
AC ABB84882;  
XX  
DT 16-MAY-2002 (first entry)  
XX  
DE Human PRO826 protein sequence SEQ ID NO:132.  
XX  
KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
KW vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
KW age-related macular degeneration; arterial restenosis; angina;  
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
KW wound healing; chromosome mapping; gene mapping.  
XX  
OS Homo sapiens.  
XX  
PN WO200200690-A2.  
XX  
PD 03-JAN-2002.  
XX  
PF 20-JUN-2001; 2001WO-US19692.  
XX  
PR 23-JUN-2000; 2000US-213637P.  
PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 02-AUG-2000; 2000US-222695P.  
PR 17-AUG-2000; 2000US-0643657.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 07-SEP-2000; 2000US-230978P.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-0709238.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
PA (GETH ) GENENTECH INC.



```
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2002-090516/12.
DR N-PSDB; ABL88137.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
PS Claim 11; Fig 132, 565pp; English.
XX
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC degeneration, atherosclerosis, hypertension, arterial restenosis,
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC carcinoma) and wound healing. The PRO polynucleotides have applications
CC in molecular biology, including use as hybridisation probes, and in
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC probes used in the exemplification of the present invention.
XX
SQ Sequence 99 AA;

Query Match 100.0%; Score 375; DB 23; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.1e-41;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTIENYASRPEAFNTPFLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPPKL 60
   |||||||
DB 29 EESTIENYASRPEAFNTPFLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPPKL 88
   |||||||

QY 61 KGLRSATPDAQ 71
   |||||||
DB 89 KGLRSATPDAQ 99

RESULT 11
AAU83664
ID AU83664 standard; Protein; 99 AA.
XX
AC AAU83664;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human PRO protein, Seq ID No 146.
XX
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha.
XX
OS Homo sapiens.
XX
PN WO200208288-A2.
XX
PD 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US21066.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220585P.
PR 25-JUL-2000; 2000US-220605P.
PR 25-JUL-2000; 2000US-220607P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220638P.
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PR 25-JUL-2000; 2000US-220664P.
PR 25-JUL-2000; 2000US-220666P.
PR 26-JUL-2000; 2000US-220893P.
PR 28-JUL-2000; 2000WO-US20710.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 15-SEP-2000; 2000US-000000P.
PR 10-NOV-2000; 2000WO-US30873.
PR 28-NOV-2000; 2000US-253646P.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001WO-US17092.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2002-172001/22.
DR N-PSDB; ABK33608.
XX
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumours
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT tumour or liver tumour -
XX
PS Claim 11; Figure 146; 359pp; English.
XX
CC The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC protein sequences of the invention.
XX
SQ Sequence 99 AA;

Query Match 100.0%; Score 375; DB 23; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.1e-41;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTIENYASRPEAFNTPFLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPPKL 60
   |||||||
DB 29 EESTIENYASRPEAFNTPFLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPPKL 88
   |||||||

QY 61 KGLRSATPDAQ 71
   |||||||
DB 89 KGLRSATPDAQ 99

RESULT 12
AAU81964
ID AU81964 standard; Protein; 99 AA.
XX
AC AAU81964;
XX
DT 09-APR-2002 (first entry)
XX
DE Human PRO826.
XX
```

KW Human; PRO; antiinflammatory; ophthalmological; vasotropic;  
KW retinal cell injury; ocular disease; retinitis pigmentosa;  
KW macular degeneration; retinal detachment; retinal tear; retinopathy;  
KW retinal degenerative disease; macular hole; degenerative myopia;  
KW acute retinal necrosis syndrome; traumatic chorioretinopathy;  
KW Putscher's retinopathy; oedema; ischaemic condition;  
KW retinal vision occlusion; collagen vascular disease;  
KW thrombocytopaenic purpura; uveitis; retinal vasculitis; Eales disease;  
KW systemic lupus erythematosus; environmental trauma.  
XX  
OS Homo sapiens.  
XX WO200109327-A2.  
XX  
PD 08-FEB-2001.  
XX  
PF 28-JUL-2000; 2000WO-US20710.  
XX  
PR 28-JUL-1999; 99US-146222P.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;  
PI Kljavin IJ, Lafleur M, Mark MR, Marsters SA, Pitti RM;  
PI Watanabe CK, Wood WI;  
XX  
DR WPI; 2002-130120/17.  
DR N-PSDB; ABK28600.  
XX  
PT Promoting survival of retinal cells, or delaying or preventing retinal  
PT cell injury or death, by contacting retinal cells with PRO175, 220,  
PT 216, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132  
PT polypeptide -  
XX  
PS Claim 44; Fig 25; 152pp; English.  
XX  
CC The invention relates to promoting the survival of retinal cells, or  
CC delaying or preventing retinal cell injury or death, by contacting the  
CC retinal cells with the polypeptide such as PRO175, PRO220, PRO216,  
CC PRO243, PRO306, PRO346, PRO322, PRO536, PRO943, PRO840, PRO828, PRO826,  
CC PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids  
CC encoding the PRO proteins, a vector comprising the nucleic acid, a host  
CC cell comprising the vector, and anti-PRO antibody. The PRO proteins are  
CC useful for promoting survival of retinal cells (retinal neurons such as  
CC retinal ganglion cells, displaced retinal ganglion cells, amacrine  
CC cells, displaced amacrine cells, horizontal neurons or bipolar neurons,  
CC rod photoreceptors, or supportive cells such as Muller cells or pigment  
CC epithelial cells), or delaying or preventing retinal cell injury or  
CC death caused by ocular disease (which is or is associated with  
CC retinitis pigmentosa, macular degenerative disease, macular hole,  
CC tear, retinopathy, retinal degenerative disease, traumatic  
CC degenerative myopia, acute retinal necrosis syndrome, traumatic  
CC chorioretinopathy or contusion, Putscher's retinopathy, oedema, an  
CC ischaemic condition, central or branch retinal vision occlusion,  
CC collagen vascular disease, thrombocytopaenic purpura, uveitis, retinal  
CC vasculitis, occlusion associated with Eales disease or systemic lupus  
CC erythematosus), retinal injury or environmental trauma. The retinal  
CC cell injury or death is delayed or prevented by substantially not

CC causing angiogenesis or mitogenesis. The present sequence represents  
CC a PRO protein.  
XX  
SQ Sequence 99 AA;  
Query Match 100.0%; Score 375; DB 23; Length 99;  
Best Local Similarity 100.0%; Pred. No. 5.1e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EESTIENYASRPEAFNTPFLNIDKLSAFKADEFINWHALFESIKRKLPLINWDAFPKL 60  
DB 29 EEBSTIENYASRPEAFNTPFLNIDKLSAFKADEFINWHALFESIKRKLPLINWDAFPKL 88  
QY 61 KGLRSATPDAQ 71  
DB 89 KGLRSATPDAQ 99  
RESULT 13  
ABU59097  
ID ABU59097 standard; Protein; 99 AA.  
XX  
AC ABU59097;  
XX  
DT 28-APR-2003 (first entry)  
XX  
DE Novel human secreted or transmembrane protein PRO826.  
XX  
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis.  
XX  
OS Homo sapiens.  
XX  
PN US2002132252-A1.  
XX  
PD 19-SEP-2002.  
XX  
PF 14-NOV-2001; 2001US-0990442.  
XX  
PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 06-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 02-MAR-2000; 2000WO-US05004.  
PR 10-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.

PR 30-MAR-2000; 200WO-US08439.  
PR 15-MAY-2000; 200WO-US13358.  
PR 17-MAY-2000; 200WO-US13705.  
PR 22-MAY-2000; 200WO-US14042.  
PR 30-MAY-2000; 200WO-US14941.  
PR 02-JUN-2000; 200WO-US15264.  
PR 28-JUL-2000; 200WO-US20710.  
PR 11-AUG-2000; 200WO-US22031.  
PR 23-AUG-2000; 200WO-US23522.  
PR 24-AUG-2000; 200WO-US23328.  
PR 08-NOV-2000; 200WO-US30952.  
PR 01-DEC-2000; 200WO-US32678.  
PR 28-FEB-2001; 200WO-US06520.  
PR 01-JUN-2001; 200WO-US17800.  
PR 20-JUN-2001; 200WO-US19692.  
PR 29-JUN-2001; 200WO-US21066.  
PR 09-JUL-2001; 200WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
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PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
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PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
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PR 17-JUN-1998; 98US-089599P.  
PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 28-AUG-2001; 2001US-0941992.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;

PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
DR WPI; 2003-247083/24.  
DR N-PSDB; ABX80254.  
XX  
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
PT are therapeutically useful for enhancing immune response and in cancer  
PT treatments -  
XX  
PS Claim 12; Fig 129; 648pp; English.  
XX  
CC The invention describes an isolated human PRO polypeptide. The PRO  
CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
CC in modulating at least one biological activity of a cell expressing a PRO  
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
CC useful for treating conditions or disorders where angiogenesis would be  
CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
CC useful for treating cancerous tumours. PRO812 inhibits vascular  
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
CC cells and is thus useful for inhibiting endothelial cell growth in  
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
CC rod photoreceptor cells) and therefore are useful for treating retinal  
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813  
CC and PRO1106 induce proliferation of mammalian kidney mesangial cells,  
CC and therefore are useful for treating kidney disorders associated with  
CC decreased mesangial cell function such as Berger disease or other  
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
CC proliferation and/or redifferentiation of chondrocytes in culture and  
CC are thus useful for treating sports injuries, and arthritis. This  
CC is the amino acid sequence of a novel human PRO protein.  
XX  
SQ Sequence 99 AA;  
  
Query Match 100.0%; Score 375; DB 24; Length 99;  
Best Local Similarity 100.0%; Pred. No. 5.1e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 29 EEESTIENYASRPEAFNTPEFLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPKTL 88  
QY 61 KGLRSATPDAQ 71  
Db 89 KGLRSATPDAQ 99  
  
RESULT 14  
ABUS9244  
ID ABUS9244 standard; Protein; 99 AA.  
XX  
XX AC ABUS9244;  
XX  
DT 22-APR-2003 (first entry)  
XX  
DE Human secreted/transmembrane protein, #78.  
XX  
KW Human; PRO; secreted; transmembrane; pharmaceutical;  
KW diagnostic; biosensor; bioreactor; tumour; therapeutic;  
KW gene therapy; tumour-associated antigenic target; TAT; ADEPT;  
KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.

OS Homo sapiens.  
XX  
PN US2003027162-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 15-NOV-2001; 2001US-0997428.  
XX  
PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
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PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
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PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
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PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
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PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
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PR 31-AUG-1998; 98US-098525P.  
PR 16-SEP-1998; 98US-100634P.  
PR 17-SEP-1998; 98US-100858P.  
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PR 12-MAR-1999; 99US-123957P.  
PR 23-JUN-1999; 99US-141037P.

Query Match 100.0%; Score 375; DB 24; Length 99;  
Best Local Similarity 100.0%; Pred. No. 5.1e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EESTIENYASRPEAFNTPLNIDKLSAFKAEFLNMWALFESIKRKLPLNWDAPPKL 60  
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OY 61 KGLRSATPDAQ 71  
DB 89 KGLRSATPDAQ 99

RESULT 15  
ABU59393  
ID ABU59393 standard; Protein; 99 AA.  
XX AC ABU59393;  
XX DT 22-APR-2003 (first entry)  
DE Novel human secreted or transmembrane protein PRO819.  
XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;

KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis.  
XX OS Homo sapiens.  
XX PN US2003027985-A1.  
XX PD 06-FEB-2003.  
XX PF 14-NOV-2001; 2001US-0990562.  
XX PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
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PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
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PR 01-DEC-1999; 99WO-US28634.  
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PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
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PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
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PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
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PR 25-FEB-1998; 98US-075945P.  
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## ALIGNMENTS

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Sequence 201, Application US/09989722  
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GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C63  
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; APPLICANT: Baker, Kevin P.
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; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 375; DB 9; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7.9e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 KGLRSATPDQAQ 71  
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DB 89 KGLRSATPDQAQ 99

RESULT 3  
US-09-989-279-201  
; Sequence 201, Application US/09989279  
; Patent No. US20020072496A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary B.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C56  
; CURRENT APPLICATION NUMBER: US/09/989, 279  
; PRIOR FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
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; PRIOR FILING DATE: 1997-11-24





; PRIOR APPLICATION NUMBER: 60/091519  
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 375; DB 9; Length 99;  
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QY 61 KGLRSATPDAQ 71  
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## RESULT 4

US-09-989-727-201  
; Sequence 201, Application US/09989727  
; Patent No. US20020072497A1

## GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
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; APPLICANT: Gurney, Austin L.  
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; APPLICANT: Napier, Mary A.  
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; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C65

; CURRENT APPLICATION NUMBER: US/09/989,727

; PRIOR APPLICATION NUMBER: 60/049787  
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; PRIOR FILING DATE: 1998-07-09

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Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEESTIENYASRPEAFNTPEFLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 60  
Db 29 EEESTIENYASRPEAFNTPEFLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 88

QY 61 KGLRSATPDAQ 71  
Db 89 KGLRSATPDAQ 99

#### RESULT 5 US-09-989-731-201

; Sequence 201, Application US/09989731  
; Patent No. US20020103125A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
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; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C70  
; CURRENT APPLICATION NUMBER: US/09/989,731  
; PRIOR FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/049787  
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; PRIOR FILING DATE: 1998-02-25  
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; PRIOR FILING DATE: 1998-03-20  
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31	PRIOR FILING DATE: 1998-06-24
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75	PRIOR FILING DATE: 1998-07-02

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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 375; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7.9e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEESTIENYASRPEAFNTPLNIDKLSAFKADDFLNWHALESIKRKLPLNWDAPPKL 60  
Db 29 EEESTIENYASRPEAFNTPLNIDKLSAFKADDFLNWHALESIKRKLPLNWDAPPKL 88

QY 61 KGLRSATPDQAQ 71  
Db 89 KGLRSATPDQAQ 99

## RESULT 6

US-09-989-732-201

; Sequence 201, Application US/09989732

; Patent No. US20020123463A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C57

; CURRENT APPLICATION NUMBER: US/09/989,732

; PRIOR FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

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; PRIOR FILING DATE: 1997-11-12

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; PRIOR FILING DATE: 1998-06-17



; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/089907  
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; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982

; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 375; DB 10; Length 99;  
Best local similarity 100.0%; Pred. No. 7.9e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEESTIENYASRPEAFNTPLNIDKLSAFKADDFLNWTHALFESIKRKLPLNWDAPPKL 60  
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Db 29 EEESTIENYASRPEAFNTPLNIDKLSAFKADDFLNWTHALFESIKRKLPLNWDAPPKL 88

Qy 61 KGLRSATPDAQ 71  
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Db 89 KGLRSATPDAQ 99

## RESULT 7

US-09-991-073-201

; Sequence 201, Application US/09991073  
; Patent No. US20020127576A1

## ; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavik, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C15  
; CURRENT APPLICATION NUMBER: US/09/991,073  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091626
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091633
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091788
PRIOR FILING DATE:	1998-07-07
PRIOR APPLICATION NUMBER:	60/091982
PRIOR FILING DATE:	1998-07-07
PRIOR APPLICATION NUMBER:	60/092182
PRIOR FILING DATE:	1998-07-09

Query Match 100.0%; Score 375; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7.9e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEESTIENYASRPEAFNTPTLNIDKLSAFKADFLNWHALFESIKRKLPLFNDAPFKL 60  
Db 29 EEESTIENYASRPEAFNTPTLNIDKLSAFKADFLNWHALFESIKRKLPLFNDAPFKL 88

QY 61 KGLRSATPDAQ 71  
Db 89 KGLRSATPDAQ 99

## RESULT 8

US-09-990-442-201

; Sequence 201, Application US/09990442

; Patent No. US20020132252A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

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; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

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; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730P1C8

; CURRENT APPLICATION NUMBER: US/09/990,442

; PRIOR APPLICATION NUMBER: 2001-11-14

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-10-17

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; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
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; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C17  
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; PRIOR APPLICATION NUMBER: 60/049787  
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## RESULT 10

US-09-993-604-201

; Sequence 201, Application US/09993604  
; Patent No. US20020137075A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
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; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same

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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 375; DB 10; length 99;  
Best Local Similarity 100.0%; Pred. No. 7.9e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEEESTIENYASRPEAFNTPLNIDKLSAFKADBFNLWHAJFESIKRKLPLNLWDAPFKL 60  
DB 29 EEEESTIENYASRPEAFNTPLNIDKLSAFKADBFNLWHAJFESIKRKLPLNLWDAPFKL 88

QY 61 KGLRSATPDQA 71  
DB 89 KGLRSATPDQA 99

## RESULT 11

US-09-990-456-201  
; Sequence 201, Application US/09990456  
; Patent No. US20020137890A1  
; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Geritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Grimaldi, J. Christopher  
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;; APPLICANT: Kjaevn, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.

;; APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

;; FILE REFERENCE: P2730P1C22

;; CURRENT APPLICATION NUMBER: US/09/990,456

;; PRIOR FILING DATE: 2001-11-14  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 375; DB 10; Length 99;  
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Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEESTIENTYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 60  
Db 29 EEESTIENTYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 88  
QY 61 KGLRSATPDAQ 71  
Db 89 KGLRSATPDAQ 99

## RESULT 12

US-09-989-721-201

; Sequence 201, Application US/09989721  
; Patent No. US20020142961A1

## ; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavir, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
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; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C55  
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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 375; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7.9e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEESTIENYASRPEAFNTPLNIDKLSAFKADFLNTHALFESIKRKLPLNWDAPFKL 60  
Db 29 EEESTIENYASRPEAFNTPLNIDKLSAFKADFLNTHALFESIKRKLPLNWDAPFKL 88

OY 61 KGLRSATPDAQ 71  
Db 89 KGLRSATPDAQ 99

RESULT 13

US-09-992-598-201  
; Sequence 201, Application US/09992598  
; Patent No. US20020160384A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan L.  
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; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zhenli  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C20  
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QY 61 KGLRSATPDQAQ 71  
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Sequence 142, Application US/09984245  
Patent No. US20020165374A1

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;; GENERAL INFORMATION:
;; APPLICANT: Young et al.
;; TITLE OF INVENTION: 87 Human Secreted Proteins
;; FILE REFERENCE: P2004P1
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;; CURRENT FILING DATE: 2001-10-29
;; PRIOR APPLICATION NUMBER: 09/154,707
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; Patent No. US20020177164A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gertltsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kijavlin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tamas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C66
;; CURRENT APPLICATION NUMBER: US/09/989,293A
;; CURRENT FILING DATE: 2001-11-20
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;; PRIOR FILING DATE: 1998-07-09

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Db 29 EEESTIENYASRPEAFNTPLNIDKLSAFKADDFLWHLFESIKRKLPLNWDAPKX 88  
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Sat Nov 29 17:52:41 2003

us-10-059-395-142\_copy\_29\_99.rapb

Page 23

Db 89 KGRSATPDAQ 99

Search completed: November 28, 2003, 13:42:18  
Job time : 43 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 13:43:49 ; Search time 217 Seconds

(without alignments)  
883.226 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Perfect score: 375

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Fgapop 6.0 , Fgapext 7.0  
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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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2	375	100.0	414	24 ABK28600	Human DNA57694-134
3	375	100.0	415	21 AAZ65018	Membrane-bound pro
4	375	100.0	415	22 AAF30059	Human cDNA encodin
5	375	100.0	415	22 AAF44164	Human PRO826 (UNQ4
6	375	100.0	415	22 AAC97491	Human anglogenesis
7	375	100.0	415	24 ABL95626	Human anglogenesis
8	375	100.0	415	24 ABK69971	cDNA encoding huma
9	375	100.0	415	24 ABL88137	Human PRO826 cDNA
10	375	100.0	415	24 ABK33608	cDNA encoding huma
11	375	100.0	415	25 ABX80255	Novel human secret
12	375	100.0	415	25 ABX80759	Human secreted/tra
13	375	100.0	415	25 ABX81142	Novel human secret
14	375	100.0	415	25 ABX90232	Human secreted/tra
15	375	100.0	415	25 ABX77843	Human PRO polynuc
16	375	100.0	415	25 ABX79439	Human secreted/tr
17	375	100.0	415	25 ABX64078	Human encoding huma
18	375	100.0	415	25 ABX17042	Human PRO polynuc
19	375	100.0	428	24 ABZ11803	Human polynucleoti
20	375	100.0	456	20 AAX00632	Human secreted pro
21	375	100.0	518	22 ABA09519	Human secreted pro
22	308	82.1	278	21 AAC68806	Human head/neck tu
23	286	76.3	386	24 ABZ11804	Human polynucleoti
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25	166	44.3	313	24 ABL35083	Murine cDNA isolat
26	143	38.1	305	24 ABZ11886	Human polynucleoti
27	82.5	22.0	530	21 AAC01489	Human secreted pro
28	78.5	20.9	437	24 ABV96116	Human pancreatic c
29	78.5	20.9	686	21 AAZ80280	Human colon cancer
30	78.5	20.9	700	22 AAH23810	Human transferrase
31	78	20.8	3525	23 ABL23024	Drosophila melanog
32	78	20.8	5397	23 ABL08196	Drosophila melanog
33	69	18.4	641	24 ABQ39286	Oligonucleotide fo
34	69	18.4	641	24 ABQ39287	Oligonucleotide fo
35	69	18.4	1152	24 ABN67526	Streptococcus poly
36	69	18.4	2155561	24 ABN71527	Streptococcus poly
37	67.5	18.0	1830121	17 AAT42063	Haemophilus influe
38	65.5	17.5	349	22 AAL00189	Human reproductive
39	65.5	17.5	914	20 AAZ42019	Human endometrium
40	65.5	17.5	1897	21 AAZ43803	Human adult skin c
41	65	17.3	398	25 ABX19934	Human GDP-mannose
42	65	17.3	349980	22 AAH41225	Pyrococcus abyssi
43	64.5	17.2	352	21 AAC01488	Human secreted pro
44	64.5	17.2	349980	24 ABQ81845	Bifidobacterium lo
45	64	17.1	447	23 ABV17783	Human prostate exp

ALIGNMENTS

RESULT 1	
ID AAC91475	standard; cDNA; 414 BP.
XX	
AC AAC91475;	
XX	
DT 21-MAR-2001	(first entry)
XX	
DE Human PRO826	cDNA.
XX	
KW Human; PRO;	antiinflammatory; dermatological; antiarthritic;
KW antirheumatic;	cardiant; antianaemic; immunosuppressive; antithyroid;
KW antidiabetic;	nootropic; neuroprotective; hepatotropic; virucide;
KW antiallergic;	antiasthmatic; immune related disorder;
KW hepatobiliary	disease; autoimmune disease; allergy; ss.
XX	
OS Homo sapiens.	



XX PN WO200073452-A2.  
XX PD 07-DEC-2000.  
XX PF 02-JUN-2000; 2000WO-US15264.  
XX PR 02-JUN-1999; 99WO-US12252.  
PR 20-JUL-1999; 99US-0144732.  
PR 20-JUL-1999; 99US-0144758.  
PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 29-OCT-1999; 99US-0162506.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28634.  
PR 09-DEC-1999; 99US-0170262.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
XX PA (GETH ) GENENTECH INC.  
XX PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;  
PI Wood WI;  
XX DR WPI; 2001-025253/03.  
DR P-PSDB; AAB50916.  
XX PT Thirty three nucleic acids encoding PRO polypeptides which are useful  
PT in the diagnosis and treatment of immune related disorders, e.g.  
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
PT thyroiditis and diabetes mellitus -  
XX PS Claim 48; Fig 29; 218pp; English.  
XX CC The present sequence is one of thirty three nucleic acids encoding PRO  
CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and  
CC antagonists are useful for treating and diagnosing immune related  
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
CC demyelinating polynuropathy or Guillain-Barre syndrome, and chronic  
CC inflammatory demyelinating polynuropathy), hepatobiliary diseases  
CC (such as infectious, autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
CC food hypersensitivity and urticaria), immunological diseases of the  
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
CC and hypersensitivity pneumonitis), transplantation associated diseases  
CC including graft rejection and graft-versus-host diseases.  
XX SQ Sequence 414 BP; 98 A; 126 C; 92 G; 98 T; 0 other;

Alignment Scores:  
Pred. No.: 7,86e-47 Length: 414  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0  
US-10-059-395-142\_copy\_29\_99 (1-71) x AAC91475 (1-414)  
QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 97 GAGGAAGAAGACACCATTTGAGATTATGCGTCACGACCGAGCGCTTTAACACCCGCTTC 156  
QY 21 LeuAsnIleAspIlyLeuArgSerAlaPheIlySA1AAspGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACAATTCGATCGATCTTAAAGCTGATGAGTTCCTGAAGTGCACGCC 216  
QY 41 LeuPheGluSerIleIlyBAArgIlyLeuProPheLeuAsnTrpAspAlaPheProIlyBleu 60  
Db 217 CTCCTTGAGTCTATCAAAAGGAACCTTCCTCCTCAACTGGAGTGCCTTCTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGACTGAGGAGCGCAACTCTGATGCCAG 309  
RESULT 2  
ABK28600  
ID ABK28600 standard; cDNA, 414 BP.  
XX AC ABK28600;  
XX DT 09-APR-2002 (first entry)  
XX DE Human DNA57694-1341 encoding PRO826.  
XX KW Human; ss; gene; PRO; antiinflammatory; ophthalmological; vasotropic;  
KW retinal cell injury; ocular disease; retinitis pigmentosa;  
KW macular degeneration; retinal detachment; retinal tear; retinopathy;  
KW retinal degenerative disease; macular hole; degenerative myopia;  
KW acute retinal necrosis syndrome; oedema; ischaemic condition;  
KW Puttcher's retinopathy; collagen vascular disease;  
KW retinal vision occlusion; uveitis; retinal vasculitis;Eales disease;  
KW thrombocytopenic purpura; uveitis; retinal vasculitis;  
KW systemic lupus erythematosus; environmental trauma.  
XX OS Homo sapiens.  
XX PN WO200109327-A2.  
XX PD 08-FEB-2001.  
XX PF 28-JUL-2000; 2000WO-US20710.  
XX PR 28-JUL-1999; 99US-146222P.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
XX PA (GETH ) GENENTECH INC.

XX PI Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;  
PI Kljavin LJ, Lafleur M, Mark MR, Marsters SA, Pitti RM;  
PI Watanabe CK, Wood WI;  
XX  
DR WPI; 2002-130120/17.  
DR P-PSDB; AAU81964.  
XX  
PT Promoting survival of retinal cells, or delaying or preventing retinal  
PT cell injury or death, by contacting retinal cells with PRO175, 220,  
PT 216, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132  
PT polypeptide -  
XX  
PS Claim 33; Fig 24; 152pp; English.  
XX  
CC The invention relates to promoting the survival of retinal cells, or  
CC delaying or preventing retinal cell injury or death, by contacting the  
CC retinal cells with the polypeptide such as PRO175, PRO220, PRO216,  
CC PRO243, PRO306, PRO346, PRO322, PRO536, PRO943, PRO840, PRO828, PRO826,  
CC PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids  
CC encoding the PRO proteins, a vector comprising the nucleic acid, a host  
CC cell comprising the vector, and anti-PRO antibody. The PRO proteins are  
CC useful for promoting survival of retinal cells (retinal neurons such as  
CC retinal ganglion cells, displaced retinal ganglion cells, amacrine  
CC cells, displaced amacrine cells, horizontal neurons or bipolar neurons,  
CC rod photoreceptors, or supportive cells such as Muller cells or pigment  
CC epithelial cells), or delaying or preventing retinal cell injury or  
CC death caused by ocular disease (which is or is associated with  
CC retinitis pigmentosa, macular degeneration, retinal detachment, retinal  
CC tear, retinopathy, retinal degenerative disease, macular hole,  
CC degenerative myopia, acute retinal necrosis syndrome, traumatic  
CC chorioretinopathy or contusion, Purtscher's retinopathy, oedema, an  
CC ischaemic condition, central or branch retinal vision occlusion,  
CC collagen vascular disease, thrombocytopaenic purpura, uveitis, retinal  
CC vasculitis, occlusion associated with Bales disease or systemic lupus  
CC erythematosus), retinal injury or environmental trauma. The retinal  
CC cell injury or death is delayed or prevented by substantially not  
CC causing angiogenesis or mitogenesis. The present sequence is a cDNA  
CC encoding a PRO protein.  
XX  
SQ Sequence 414 BP; 98 A; 126 C; 92 G; 98 T; 0 other;

Alignment Scores:  
Pred. No.: 7.86e-47 Length: 414  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x ABK28600 (1-414)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 97 GAGGAGAAAGCACCATTTGAGATTATGCGTCACGACCCGAGCGCTTTAACACCCCGTTC 156

QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACAATTGCGATTCGGTTTAAGGCTGATGAGTTCCTGAAGTGCACGCC 216

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 217 CTCTTTGAGTCTATCAAAAGAACTTCTTCTCAACTGGAGATGCTTCTTAAGCTG 276

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGGACTGAGGAGCGCACTCTGATGCCCAg 309

RESULT 3  
AAZ65018  
ID AAZ65018 standard; cDNA; 415 BP.  
XX  
AC AAZ65018;

XX DT 05-APR-2000 (first entry)  
XX  
XX Membrane-bound protein PRO826 encoding cDNA.  
DE  
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.  
KW  
XX Homo sapiens.  
OS  
XX WO963088-A2.  
PN  
XX 09-DEC-1999.  
PD  
XX 02-JUN-1999;  
PF 99WO-US12252.  
XX 02-JUN-1998;  
PR 98US-0087607.  
PR 02-JUN-1998;  
PR 98US-0087609.  
PR 02-JUN-1998;  
PR 98US-0087759.  
PR 03-JUN-1998;  
PR 98US-0087827.  
PR 04-JUN-1998;  
PR 98US-0088021.  
PR 04-JUN-1998;  
PR 98US-0088025.  
PR 04-JUN-1998;  
PR 98US-0088028.  
PR 04-JUN-1998;  
PR 98US-0088030.  
PR 04-JUN-1998;  
PR 98US-0088033.  
PR 04-JUN-1998;  
PR 98US-0088326.  
PR 05-JUN-1998;  
PR 98US-0088167.  
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PR 98US-0088202.  
PR 05-JUN-1998;  
PR 98US-0088212.  
PR 05-JUN-1998;  
PR 98US-0088217.  
PR 09-JUN-1998;  
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PR 98US-0088730.  
PR 10-JUN-1998;  
PR 98US-0088734.  
PR 10-JUN-1998;  
PR 98US-0088738.  
PR 10-JUN-1998;  
PR 98US-0088740.  
PR 10-JUN-1998;  
PR 98US-0088741.  
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PR 10-JUN-1998;  
PR 98US-0088810.  
PR 10-JUN-1998;  
PR 98US-0088811.  
PR 10-JUN-1998;  
PR 98US-0088824.  
PR 10-JUN-1998;  
PR 98US-0088825.  
PR 10-JUN-1998;  
PR 98US-0088826.  
PR 11-JUN-1998;  
PR 98US-0088858.  
PR 11-JUN-1998;  
PR 98US-0088861.  
PR 11-JUN-1998;  
PR 98US-0088863.  
PR 11-JUN-1998;  
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PR 12-JUN-1998;  
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PR 12-JUN-1998;  
PR 98US-0089105.  
PR 16-JUN-1998;  
PR 98US-0089440.  
PR 16-JUN-1998;  
PR 98US-0089512.  
PR 16-JUN-1998;  
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PR 17-JUN-1998;  
PR 98US-0089600.  
PR 17-JUN-1998;  
PR 98US-0089653.  
PR 18-JUN-1998;  
PR 98US-0089801.  
PR 18-JUN-1998;  
PR 98US-0089907.  
PR 18-JUN-1998;  
PR 98US-0089908.  
PR 19-JUN-1998;  
PR 98US-0089947.  
PR 19-JUN-1998;  
PR 98US-0089948.  
PR 19-JUN-1998;  
PR 98US-0089952.  
PR 22-JUN-1998;  
PR 98US-0090246.  
PR 22-JUN-1998;  
PR 98US-0090252.  
PR 22-JUN-1998;  
PR 98US-0090254.  
PR 23-JUN-1998;  
PR 98US-0090349.  
PR 23-JUN-1998;  
PR 98US-0090355.  
PR 24-JUN-1998;  
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PR 24-JUN-1998;  
PR 98US-0090431.  
PR 24-JUN-1998;  
PR 98US-0090435.

PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090445.  
PR 24-JUN-1998; 98US-0090461.  
PR 24-JUN-1998; 98US-0090472.  
PR 24-JUN-1998; 98US-0090535.  
PR 24-JUN-1998; 98US-0090538.  
PR 24-JUN-1998; 98US-0090540.  
PR 24-JUN-1998; 98US-0090557.  
PR 25-JUN-1998; 98US-0090676.  
PR 25-JUN-1998; 98US-0090678.  
PR 25-JUN-1998; 98US-0090688.  
PR 25-JUN-1998; 98US-0090690.  
PR 25-JUN-1998; 98US-0090691.  
PR 25-JUN-1998; 98US-0090694.  
PR 25-JUN-1998; 98US-0090695.  
PR 25-JUN-1998; 98US-0090696.  
PR 26-JUN-1998; 98US-0090862.  
PR 26-JUN-1998; 98US-0090863.  
PR 01-JUL-1998; 98US-0091358.  
PR 01-JUL-1998; 98US-0091360.  
PR 01-JUL-1998; 98US-0091544.  
PR 02-JUL-1998; 98US-0091478.  
PR 02-JUL-1998; 98US-0091486.  
PR 02-JUL-1998; 98US-0091519.  
PR 02-JUL-1998; 98US-0091626.  
PR 02-JUL-1998; 98US-0091628.  
PR 02-JUL-1998; 98US-0091633.  
PR 02-JUL-1998; 98US-0091646.  
PR 02-JUL-1998; 98US-0091673.  
PR 07-JUL-1998; 98US-0091978.  
PR 07-JUL-1998; 98US-0091982.  
PR 09-JUL-1998; 98US-0092182.  
PR 10-JUL-1998; 98US-0092472.  
PR 20-JUL-1998; 98US-0093339.  
PR 30-JUL-1998; 98US-0094651.  
PR 04-AUG-1998; 98US-0095282.  
PR 04-AUG-1998; 98US-0095285.  
PR 04-AUG-1998; 98US-0095301.  
PR 04-AUG-1998; 98US-0095302.  
PR 04-AUG-1998; 98US-0095318.  
PR 04-AUG-1998; 98US-0095321.  
PR 04-AUG-1998; 98US-0095325.  
PR 10-AUG-1998; 98US-0095916.  
PR 10-AUG-1998; 98US-0095929.  
PR 10-AUG-1998; 98US-0096012.  
PR 11-AUG-1998; 98US-0096143.  
PR 11-AUG-1998; 98US-0096146.  
PR 12-AUG-1998; 98US-0096329.  
PR 17-AUG-1998; 98US-0096757.  
PR 17-AUG-1998; 98US-0096766.  
PR 17-AUG-1998; 98US-0096768.  
PR 17-AUG-1998; 98US-0096773.  
PR 17-AUG-1998; 98US-0096791.  
PR 17-AUG-1998; 98US-0096867.  
PR 17-AUG-1998; 98US-0096891.  
PR 17-AUG-1998; 98US-0096894.  
PR 17-AUG-1998; 98US-0096895.  
PR 17-AUG-1998; 98US-0096897.  
PR 18-AUG-1998; 98US-0096949.  
PR 18-AUG-1998; 98US-0096950.  
PR 18-AUG-1998; 98US-0096959.  
PR 18-AUG-1998; 98US-0096960.  
PR 18-AUG-1998; 98US-0097022.  
PR 19-AUG-1998; 98US-0097141.  
PR 20-AUG-1998; 98US-0097218.  
PR 24-AUG-1998; 98US-0097661.  
PR 26-AUG-1998; 98US-0097951.  
PR 26-AUG-1998; 98US-0097952.  
PR 26-AUG-1998; 98US-0097954.  
PR 26-AUG-1998; 98US-0097955.  
PR 26-AUG-1998; 98US-0097971.  
PR 26-AUG-1998; 98US-0097974.  
PR 26-AUG-1998; 98US-0097978.

PR 26-AUG-1998; 98US-0097979.  
PR 26-AUG-1998; 98US-0097986.  
PR 26-AUG-1998; 98US-0098014.  
PR 31-AUG-1998; 98US-0098525.  
PR 16-SEP-1998; 98US-0100634.  
PR 12-JAN-1999; 99US-0115565.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood WI, Yuan J;  
XX  
DR WPI, 2000-072883/06.  
DR P-PSDB; AAY66681.  
XX  
PT Membrane-bound proteins and related nucleotide sequences -  
XX  
PS Claim 2, Fig 128; 822pp; English.  
XX  
CC The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIE  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
CC will also be useful for the preparation of PRO polypeptides, especially  
CC by recombinant techniques.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
Alignment Scores:  
Pred. No.: 7.89e-47 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 21 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AAZ65018 (1-415)  
QY 1 GIUGLUGLuserThrIleGIuAsnTYrAlaSerArgProGLuAlaPheAsnThrProPhe 20  
Db 97 GAGGAGAAGAACCACTTGAGAAATTATGCGTACGACCCGAGGCTTTAACACCCCGCTTC 156  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrPheAla 40  
Db 157 CTGAACATCGACAATTCGATCTGCGTTAAGGCTGATGAGTTCCTGAACCTGGCACGCC 216  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 217 CTCTTTGAGTCTATCAAGAAACTTCCTTCTCAACTGGATGCCCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGACTGAGAGCGCACTCCTGATGCCAG 309  
RESULT 4  
AAF30059  
ID AAF30059 standard; cDNA; 415 BP.  
XX  
AC AAF30059;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Human cDNA encoding PRO826.  
XX  
KW PRO826; UNQ467; human; immune disease; autoimmune disease;

KW antirheumatic; antiarthritic; antiinflammatory; antianaemic;  
KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
KW hepatotropic; virucide; dermatological; antipsoriatic;  
KW antiasthmatic; antiallergic; immunostimulant; ss.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 13..312  
FT sig\_peptide /tag= a  
FT 13..78  
FT /tag= b  
FT mat\_peptide 79..309  
FT /tag= c  
XX  
PN WO200105972-A1.  
XX  
PD 25-JAN-2001.  
XX  
PF 15-MAR-2000; 2000WO-US06884.  
XX  
PR 20-JUL-1999; 99US-0144758.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;  
PI Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK;  
PI Wood WI;  
XX  
DR WPI; 2001-103149/11.  
DR P-PSDB; AAB20117.  
XX  
PT New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
PT diagnosing and treating immune-related disorders, such as multiple  
PT sclerosis, rheumatoid arthritis and diabetes -  
XX  
PS Claim 21; Fig 19; 127pp; English.  
XX  
CC The present sequence is that of cDNA clone DNA57694-1341 (ATCC 203017)  
CC encoding novel human immunomodulator protein PRO826 (UNQ467) (see  
CC AAB20117). The clone was isolated following a database search by  
CC applying a signal sequence algorithm. The predicted protein has a  
CC mol.wt. of 11 kDa and a pI of 7.47. The invention provides  
CC polynucleotides (see AAF30050-62) encoding novel human PRO proteins  
CC (see AAB20108-20) including PRO826. Claimed compositions  
CC comprising these proteins or their agonists are useful for increasing  
CC infiltration of inflammatory cells into a tissue of a mammal,  
CC stimulating or enhancing an immune response in a mammal, or  
CC increasing the proliferation of T-lymphocytes in a mammal in response  
CC to an antigen. Claimed compositions comprising the PRO polypeptide  
CC or its antagonist have the opposite effect. A claimed method for  
CC treating an immune related disorder, such as a T cell disorder,  
CC involves administering the PRO polypeptide, an agonist antibody or  
CC an antagonist antibody. The disorder is selected from systemic  
CC lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
CC juvenile chronic arthritis, spondyloarthropathy, systemic  
CC sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome,  
CC systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia,  
CC autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinated diseases (such as  
CC multiple sclerosis), autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
CC inflammatory bowel disease (ulcerative colitis and Crohn's disease),  
CC gluten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated  
CC skin diseases (such as bullous skin disease, erythema multiforme and  
CC psoriasis), allergic diseases (such as asthma, allergic rhinitis,  
CC atopic dermatitis, food hypersensitivity and urticaria), immunologic  
CC diseases of the lung and transplantation associated diseases (such  
CC as graft rejection and graft-versus-host disease) (all claimed).  
CC Claimed methods of diagnosing these disorders comprise detecting  
CC the level of expression of the PRO gene. Also claimed are a method  
CC of identifying a compound capable of inhibiting the expression or  
CC activity of the PRO polypeptide, vectors, host cells, antibodies

CC and a method of stimulating the proliferation of T-lymphocytes  
CC using PRO826.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
Alignment Scores:  
Pred. No.: 7.89e-47 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AAF30059 (1-415)  
QY 1 GIUGLIGLuserThrIleGIuAsnTYrAlaSerArgProGLuAlaPheAsnThrProPhe 20  
Db 97 GAGGAAGAAAGCACCATGAGAATTATGCGTCACGACCCGAGCCTTAACACCCCGTTC 156  
QY 21 LeuAsnIleAspIlyLeuArgSerAlaPheIlyAlaAspGIuPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACAATTCGATCTGCGTTTAAGGCTGATGAGTTCCTGAACCTGGACGCC 216  
QY 41 LeuPheGLuserIleIyAsnArgIlySleuProPheLeuAsnTrpAspAlaPheProIlySleu 60  
Db 217 CTCTTGAGTCTATCAAGAAACTTCCTTCTCACTGGAGATGCCCTTCTTAAGCTG 276  
QY 61 LysGIlyLeuArgSerAlaThrProAspAlaGIu 71  
Db 277 AAAGCACTGAGGAGCGCAACTCTGATGCCAG 309  
RESULT 5  
AAF44164  
ID AAF44164 standard; cDNA; 415 BP.  
XX  
AC AAF44164;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Human PRO826 (UNQ467) nucleotide sequence SEQ ID NO:200.  
XX  
KW Human; secreted and transmembrane protein; PRO; cytosstatic;  
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
XX  
OS Homo sapiens.  
XX  
PN WO200073454-A1.  
XX  
PD 07-DEC-2000.  
XX  
PF 30-MAR-2000; 2000WO-US08439.  
XX  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 07-JUL-1999; 99US-0143048.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146222.  
PR 17-AUG-1999; 99US-0149396.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 08-OCT-1999; 99US-0158663.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.

PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Deenoyers I, Eaton DL,  
PI Ferrara N, Fong S, Gerber H, Gerltsen MB, Goddard A, Godowski PJ,  
PI Grimaldi CJ, Gurney AL, Kijavin IJ, Napier MA, Pan J, Paoni NF,  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
PI Zhang Z;  
XX  
DR WPI; 2001-032160/04.  
DR P-PSDB; AAB65204.  
XX  
PT PRO polynucleotides used to produce polypeptides used to target  
PT bioactive molecules such as toxins, radiolabels or antibodies, to  
PT specific cells, to cause targeted cell death -  
XX  
PS Claim 2; Fig 128; 935pp; English.  
XX  
CC The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins  
CC can be used for targeted delivery of bioactive molecules, such as  
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridisation probes, in  
CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
CC and DNA. They may also be used to produce transgenic animals which are  
CC used to develop and screen therapeutically useful reagents. The PRO  
CC nucleotide and protein sequence can be used for tissue typing and in  
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
XX  
Alignment Scores:  
Pred. No.: 7.89e-47 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AAF44164 (1-415)  
QY 1 GIUGLUGLuserThrIIeGIuaSntYrAlaSerArgProGIuaIaIaphaSnThrProPhe 20  
Db 97 GAGGAAGAAAGCACCATTGAGATTAATGCGTCACGACCCGAGCCTTAACACCCCGTTC 156  
QY 21 LeuAsnIleAspIysLeuArgSerAlaIaphelysAlaAspGIuPheLeuAsnTrpIsla 40  
Db 157 CTGAACATCGACAATTCGATCTGCGTTTAAGGCTGATGAGTTCTGAACTGGCAGCC 216  
QY 41 LeuPheGluSerIleIysArgIysLeuProPheLeuAsnTrpAspAlaPheProIysLeu 60  
Db 217 CTCCTTGAGTCTATCAAAAGAACTTCCTTCTCAACTGGATGCTTCTTAAGCTG 276  
QY 61 LysGIyLeuArgSerAlaIaphProAspAlaGln 71  
Db 277 AAGGACTGAGAGCGCAACTCCTGATGCCAG 309  
RESULT 6  
AAC97491  
ID AAC97491 standard; cDNA; 415 BP.  
XX  
AC AAC97491;  
XX  
DT 28-FEB-2001 (first entry)  
XX

DE Human angiogenesis-associated protein PRO826 cDNA, SEQ ID NO:157.  
XX  
KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
KW gene therapy; transgenic animal; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200053753-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 05-JAN-2000; 2000WO-US00219.  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A,  
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA,  
PI Paoni NF, Plitt RM, Watanabe CK, Williams PM, Wood WI;  
XX  
DR WPI; 2001-090793/10.  
DR P-PSDB; AAB53094.  
XX  
PT New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
XX  
PS Claim 58; Fig 61; 293pp; English.  
XX  
CC The invention relates to novel human angiogenesis-associated proteins  
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
CC PRO proteins. The invention also relates to vectors and host cells  
CC comprising a PRO nucleic acid, the recombinant production of a PRO  
CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
CC compounds which inhibit the expression of a PRO gene. The invention  
CC additionally encompasses methods of identifying modulators of PRO  
CC expression or activity; diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
CC mutations in a PRO gene, or the expression level of a PRO gene within a  
CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
CC administration of a PRO protein, or an agonist or antagonist thereof.  
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
CC agonists and PRO antagonists may be used as therapeutic agents to treat  
CC cardiovascular, endothelial or angiogenic disorders, such as  
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's



CC disease, or stroke. PRO nucleic acids are additionally useful in the  
CC recombinant production of PRO proteins, as hybridisation probes to  
CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
CC animals useful for the development and screening of potential  
CC therapeutic agents. The present sequence represents a cDNA encoding a PRO  
CC protein of the invention.

XX SQ Sequence 415 BP, 99 A, 126 C, 92 G, 98 T, 0 other;

Alignment Scores:

Pred. No.:	7.89e-47	Length:	415
Score:	375.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AAC97491 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAAGAAGACCACTTGAGAAATTATGCTCAGACCCGAGGGCTTTAACAACCCCGTTC 156  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
DB 157 CTGAACATGCACAAATTGCGATCTGCTTAAGGCTGATGAGTTCCTGAACCTGGACAGCC 216  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
DB 217 CTCTTGAGTCTATCAAAAGAACTCTTCTCAACTGGAGTGCCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGGACTGAGAGCGCAACTCCTGATGCCAG 309

RESULT 7

ABL95626  
ID ABL95626 standard; cDNA, 415 BP.

XX ABL95626;

XX 19-JUL-2002 (first entry)

DE Human angiogenesis related cDNA PRO826 SEQ ID NO: 131.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;

KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;

KW cardiant; cytosclastic; antiangiogenic; hypotensive; vulnary;

KW antiarteriosclerotic; gene; ss.

XX Homo sapiens.

XX WO200208284-A2.

XX 31-JAN-2002.

PF 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.

PR 25-JUL-2000; 2000US-220624P.

PR 25-JUL-2000; 2000US-220664P.

PR 28-JUL-2000; 2000WO-US20710.

PR 02-AUG-2000; 2000US-222695P.

PR 17-AUG-2000; 2000US-0643657.

PR 23-AUG-2000; 2000WO-US23522.

PR 24-AUG-2000; 2000WO-US23328.

PR 07-SEP-2000; 2000US-230978P.

PR 15-SEP-2000; 2000US-000000P.

PR 18-SEP-2000; 2000US-0664610.

PR 18-SEP-2000; 2000US-0665350.

PR 24-OCT-2000; 2000US-242922P.

PR 08-NOV-2000; 2000US-0709238.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 28-JUN-2001; 2001WO-US00000.

XX (GETH ) GENENTECH INC.  
PA (BAKE ) BAKER K P.  
PA (FER ) FERRARA N.  
PA (GERB ) GERBER H.  
PA (GERR ) GERRITSEN M E.  
PA (GODD ) GODDARD A.  
PA (GODO ) GODOWSKI P J.  
PA (GURN ) GURNEY A L.  
PA (HILL ) HILLAN K J.  
PA (MARS ) MARSTERS S A.  
PA (PANJ ) PAN J.  
PA (PAON ) PAONI N F.  
PA (STEP ) STEPHAN J F.  
PA (WATA ) WATANABE C K.  
PA (WILL ) WILLIAMS P M.  
PA (WOOD ) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX WPI; 2002-171999/22.  
DR P-PSDB; ABB95488.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal -  
XX Claim 1, Fig 131, 567pp; English.

XX The present invention provides the protein and coding sequences of human  
CC PRO proteins. These are useful for treating or diagnosing a  
CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
CC hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The present sequence is a coding sequence of the invention.

XX SQ Sequence 415 BP, 99 A, 126 C, 92 G, 98 T, 0 other;

Alignment Scores:

Pred. No.:	7.89e-47	Length:	415
Score:	375.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x ABL95626 (1-415)

QY 1 GIUGLUGLuserThrileGluAsnTYrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAAGAAAGCACCATTTGAGATTATGCGTCACGACCGAGCCCTTTAACACCCCGCTTC 156  
QY 21 LeuAsnIleAspIlyLeuArgSerAlaPheIlysAlaAspGluPheLeuAsnTrpHisAla 40  
DB 157 CTGAACATCGACAATTTGCGATCTGCGTTTAAGGCTGATGATGCTTCTGAAGTGGACGCC 216  
QY 41 LeuPheGluSerIleIlysArgIlyLeuProPheLeuAsnTrpAspAlaPheProIlysLeu 60  
DB 217 CTCTTTGAGTCTATCAAAAGAACTTCTTCTCACTGGATGCGCTTCTCTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGGAGCGCAACTCTGATGCCAG 309  
RESULT 8  
ABK69971  
ID ABK69971 standard; DNA; 415 BP.  
XX AC ABK69971;  
XX DT 15-JUL-2002 (first entry)  
XX DE cDNA encoding human Pro peptide #11.  
KW Human; ss; gene; PRO; secreted protein; transmembrane protein;  
KW genetic disorder; tumour; cancer.  
OS Homo sapiens.  
XX PN WO200224888-A2.  
XX PD 28-MAR-2002.  
XX PF 29-AUG-2001; 2001WO-US27099.  
XX PR 01-SEP-2000; 2000US-229896P.  
PR 05-SEP-2000; 2000US-230621P.  
PR 22-SEP-2000; 2000US-235147P.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 12-JAN-2001; 2001US-261878P.  
PR 16-JAN-2001; 2001US-261910P.  
PR 16-JAN-2001; 2001US-261939P.  
PR 16-JAN-2001; 2001US-262150P.  
PR 25-JAN-2001; 2001US-264395P.  
PR 02-FEB-2001; 2001US-266421P.  
PR 09-FEB-2001; 2001US-267623P.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 09-MAR-2001; 2001US-274399P.  
PR 03-APR-2001; 2001US-280982P.  
PR 04-APR-2001; 2001US-282129P.  
PR 04-APR-2001; 2001US-282199P.  
PR 09-MAY-2001; 2001US-290589P.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
XX PA (GETH ) GENENTECH INC.  
XX PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;  
XX WPI; 2002-362426/39.  
DR P-PSDB; ABG34040.  
XX PT New PRO polypeptides and polynucleotides encoding the polypeptides,

PT useful in gene therapy, chromosome identification, tissue typing, or  
PT for genetic analysis of individuals with genetic disorders -

XX Claim 2; Figure 21; 218bp; English.

XX This invention relates to the cDNA and protein sequences of novel  
CC secreted and transmembrane polypeptides PRO polypeptides. The  
CC invention also comprises a method for producing the proteins of the  
CC invention by recombinant means and antibodies specific for the protein  
CC of the invention. The antibody may be used for detecting the PRO  
CC proteins of the invention and may be used to modify their activity.  
CC polynucleotides may be used as hybridisation probes for a cDNA library  
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, to  
CC construct hybridisation probes for mapping the gene which encodes that  
CC PRO and for genetic analysis of individuals with genetic disorders, in  
CC assays to identify other proteins or molecules involved in binding  
CC reaction, to generate transgenic animals or knock-out animals which in  
CC turn are useful in the development and screening of therapeutically  
CC useful reagents, for chromosome identification, and tissue typing. The  
CC PRO polypeptides are useful in gene therapy, and as molecular weight  
CC markers for protein electrophoresis purposes. The sequences may  
CC also be used to detect overexpression on PRO polypeptides in cancerous  
CC tumours and for screening for differentially expressed genes using  
CC microarray technology. The present sequence represents a cDNA encoding  
CC a human PRO protein of the invention.

XX Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

SO Alignment Scores:

Pred. No.: 7,89e-47 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x ABK69971 (1-415)

QY 1 GIUGLUGLuserThrileGluAsnTYrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAAGAAAGCACCATTTGAGATTATGCGTCACGACCGAGCCCTTTAACACCCCGCTTC 156  
QY 21 LeuAsnIleAspIlyLeuArgSerAlaPheIlysAlaAspGluPheLeuAsnTrpHisAla 40  
DB 157 CTGAACATCGACAATTTGCGATCTGCGTTTAAGGCTGATGATGCTTCTGAAGTGGACGCC 216  
QY 41 LeuPheGluSerIleIlysArgIlyLeuProPheLeuAsnTrpAspAlaPheProIlysLeu 60  
DB 217 CTCTTTGAGTCTATCAAAAGAACTTCTTCTCACTGGATGCGCTTCTCTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGGAGCGCAACTCTGATGCCAG 309  
RESULT 9  
ABL88137  
ID ABL88137 standard; cDNA; 415 BP.  
XX AC ABL88137;  
XX DT 16-MAY-2002 (first entry)  
XX DE Human PRO826 cDNA sequence SEQ ID NO:131.  
XX KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
KW vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
KW age-related macular degeneration; arterial restenosis; angina;  
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
KW wound healing; chromosome mapping; gene mapping; gene; ss.  
XX

OS Homo sapiens.  
XX  
PN WO200200690-A2.  
XX  
PD 03-JAN-2002.  
XX  
PF 20-JUN-2001; 2001WO-US19692.  
XX  
PR 23-JUN-2000; 2000US-213637P.  
PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 02-AUG-2000; 2000US-222695P.  
PR 17-AUG-2000; 2000US-0643657.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 07-SEP-2000; 2000US-230978P.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-0709238.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX  
DR WPI; 2002-090516/12.  
DR P-PSDB; ABB84882.  
XX  
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal -  
XX  
PS Claim.2; Fig 131; 565pp; English.  
XX  
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
CC antiangiogenic, hypotensive, vulnery and antiarteriosclerotic  
CC activities, and can be used in gene therapy. The PRO polynucleotides,  
CC proteins, agonists and antagonists are useful for treating or diagnosing  
CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
CC carcinoma) and wound healing. The PRO polynucleotides have applications  
CC in molecular biology, including use as hybridisation probes, and in  
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
CC probes used in the exemplification of the present invention.

XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
Alignment Scores:  
Pred. No.: 7.89e-47 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x ABL88137 (1-415)  
QY 1 GUGUGUGUSeThrIleGluasnTYrAlaSerArgProGluAlaPheasnThrProphe 20  
Db 97 GAGGAAGAAAGCACCAATTGAGAATTATGCGTCACGACCCGAGCCTTTAACACCCCGTTC 156  
QY 21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnThrPHisAla 40  
Db 157 CTGAACATCGACAATTCGCATCTCGCTTAAGGCTGATGAGTTCCTGAACCTGCACGCC 216  
QY 41 LeuPheGluSerIleIysArgIysLeuProPheLeuAsnTrpAspAlaPheProIysLeu 60  
Db 217 CTCTTGAGTCTATCAAAAGAAACTTCCTTCCCTCAACTGGGATGCCCTTCTTAAGCTG 276  
QY 61 IysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGACTGAGAGCGCACTCCTGATGCCAG 309  
RESULT 10  
ABK33608  
ID ABK33608 standard; cDNA; 415 BP.  
XX  
AC ABK33608;  
XX  
DT 08-MAY-2002 (first entry)  
XX  
DE cDNA encoding human PRO protein, Seq ID No 145.  
XX  
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
KW pericyte cell proliferation; chondrocyte cell proliferation;  
KW tumour necrosis factor-alpha; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200208288-A2.  
XX  
PD 31-JAN-2002.  
XX  
PF 29-JUN-2001; 2001WO-US21066.  
XX  
PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220585P.  
PR 25-JUL-2000; 2000US-220605P.  
PR 25-JUL-2000; 2000US-220607P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220638P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 25-JUL-2000; 2000US-220666P.  
PR 26-JUL-2000; 2000US-220893P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 15-SEP-2000; 2000US-000000P.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 28-NOV-2000; 2000US-253646P.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001WO-US17092.

XX (GETH ) GENENTECH INC.  
PA  
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,  
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
XX WPI, 2002-172001/22.  
DR P-PSDB; AAU83664.  
XX  
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,  
PT useful for treating a PRO related disorder and for diagnosing tumours  
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal  
PT tumour or liver tumour -  
XX  
XX  
PS Claim 2; Figure 145; 359pp; English.  
XX  
CC The invention relates to one hundred and twenty two nucleic acids  
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
CC agonists and antagonists are useful for treating a PRO related disorder.  
CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
CC liver tumour. The PRO polypeptides are useful for stimulating the  
CC proliferation of, or gene expression, in pericyte cells, for stimulating  
CC the proliferation or differentiation of chondrocyte cells, for  
CC stimulating the release of tumour necrosis factor-alpha from human blood,  
CC for stimulating or inhibiting the proliferation of normal human dermal  
CC fibroblast cells. The PRO polypeptide may also be used as molecular  
CC weight markers and for tissue typing. The PRO nucleic acids have  
CC applications in molecular biology, including use as hybridisation probes,  
CC and in chromosome and gene mapping. ABK3536-ABK3657 represent human  
CC PRO protein coding sequences of the invention.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 7.89e-47 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0  
  
US-10-059-395-142\_COPY\_29\_99 (1-71) x ABK3608 (1-415)  
  
QY 1 GIUGLUGLuserThrllegluasntYrAlaSerArxProgluAlaPheAsnthrProphe 20  
Db 97 GAGGAAGAAAGCACCATTGAGATATGCGTCACGACCGAGCCTTAAACACCCGCTTC 156  
QY 21 LeuAsnIleAsplysIleuArGserAlaPheIysAlaAspGluPheIeuAsnthrHisAla 40  
Db 157 CTGAACATCGACAATTGCGATCTGCGTTAAGCGCTGATGAGTTCTCGAAGTGGACGCC 216  
QY 41 LeuPheGluSerIleIysArGlyIleuProPheIeuAsnthrPaspAlaPheProIysIeu 60  
Db 217 CTCTTTGAGTCTATCAAAAGAACTTCCTTCTCACTGGGATGCCCTTCTTAAGCTG 276  
QY 61 LySGlyIeuArGserAlaThrProAspAlaGln 71  
Db 277 AAAGGACTGAGGAGCGCACTCCTGATGCCAG 309  
  
RESULT 11  
ABX80255  
ID ABX80255 standard; DNA; 415 BP.  
XX  
AC ABX80255;  
XX  
DT 28-APR-2003 (first entry)  
XX  
DE Novel human secreted or transmembrane protein PRO819 DNA.  
XX  
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;

KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN US2002132252-A1.  
XX  
PD 19-SEP-2002.  
XX  
PF 14-NOV-2001; 2001US-0990442.  
XX  
PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 06-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.

PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089599P.  
PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 28-AUG-2001; 2001US-0941992.

(GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Thomas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
DR WPI; 2003-247083/24.  
DR P-PSDB; ABUS9098.

PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
PT are therapeutically useful for enhancing immune response and in cancer  
PT treatments -

XX Claim 2; Fig 130; 648pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO  
CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
CC in modulating at least one biological activity of a cell expressing a PRO  
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
CC useful for treating conditions or disorders where angiogenesis would be  
CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
CC useful for treating cancerous tumours. PRO812 inhibits vascular  
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
CC cells and is thus useful for inhibiting endothelial cell growth in  
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
CC stimulated T-lymphocytes and are therapeutically useful for enhancing

CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
CC rod photoreceptor cells) and therefore are useful for treating retinal  
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813  
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
CC and therefore are useful for treating kidney disorders associated with  
CC decreased mesangial cell function such as Berger disease or other  
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
CC proliferation and/or redifferentiation of chondrocytes in culture and  
CC are thus useful for treating sports injuries, and arthritis. This  
CC sequence represents a novel human PRO protein polynucleotide.

XX SQ Sequence 415 BP, 99 A, 126 C, 92 G, 98 T, 0 other;

Alignment Scores:

Pred. No.:	7,89e-47	Length:	415
Score:	375.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	25	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x ABX80255 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 97 GAGGAAGAACGACCATTTGAGATTATGCTCAAGACCGAGGCGCTTTAACACCCCGTTG 156

QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACAAATTGCGATCTGCGTTTAAAGCTGATGATGCTTCAACTGGACGCC 216

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 217 CTCTTGAATCTATCAAAAGAAACTCTTCTCAACTGGAGTGCCTTCTTAAGCTG 276

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGACTGAGGAGCGCAACTCCTGATGCCAG 309

RESULT 12  
ABX80759  
ID ABX80759 standard; cDNA; 415 BP.

XX AC ABX80759;

DT 22-APR-2003 (first entry)

DE Human secreted/transmembrane protein cDNA, #78.

XX Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;  
KW diagnostic; biosensor; bioreactor; tumour; therapeutic;  
KW gene therapy; tumour-associated antigenic target; TAT; ADEPT;  
KW antibody-dependent enzyme mediated prodrgug therapy; cytostatic.

XX Homo sapiens.

PN US2003027162-A1.

PD 06-FEB-2003.

PF 15-NOV-2001; 2001US-0997428.

XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.



PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089599P.  
PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 19-JUN-1998; 98US-089947P.  
PR 19-JUN-1998; 98US-089948P.  
PR 19-JUN-1998; 98US-089952P.  
PR 22-JUN-1998; 98US-090246P.  
PR 22-JUN-1998; 98US-090252P.  
PR 22-JUN-1998; 98US-090254P.  
PR 23-JUN-1998; 98US-090349P.  
PR 23-JUN-1998; 98US-090355P.  
PR 24-JUN-1998; 98US-090429P.  
PR 24-JUN-1998; 98US-090431P.  
PR 24-JUN-1998; 98US-090435P.  
PR 24-JUN-1998; 98US-090444P.  
PR 24-JUN-1998; 98US-090445P.  
PR 24-JUN-1998; 98US-090472P.  
PR 24-JUN-1998; 98US-090535P.  
PR 24-JUN-1998; 98US-090540P.  
PR 24-JUN-1998; 98US-090542P.  
PR 24-JUN-1998; 98US-090557P.  
PR 25-JUN-1998; 98US-090676P.  
PR 25-JUN-1998; 98US-090678P.  
PR 25-JUN-1998; 98US-090690P.  
PR 25-JUN-1998; 98US-090694P.  
PR 25-JUN-1998; 98US-090695P.  
PR 25-JUN-1998; 98US-090696P.  
PR 26-JUN-1998; 98US-090862P.  
PR 26-JUN-1998; 98US-090863P.  
PR 01-JUL-1998; 98US-091360P.  
PR 01-JUL-1998; 98US-091544P.  
PR 02-JUL-1998; 98US-091478P.  
PR 02-JUL-1998; 98US-091519P.  
PR 02-JUL-1998; 98US-091626P.  
PR 02-JUL-1998; 98US-091628P.  
PR 02-JUL-1998; 98US-091633P.  
PR 02-JUL-1998; 98US-091646P.  
PR 02-JUL-1998; 98US-091673P.  
PR 07-JUL-1998; 98US-091978P.  
PR 07-JUL-1998; 98US-091982P.  
PR 09-JUL-1998; 98US-092182P.  
PR 10-JUL-1998; 98US-092472P.  
PR 20-JUL-1998; 98US-093339P.  
PR 30-JUL-1998; 98US-094651P.  
PR 04-AUG-1998; 98US-095282P.  
PR 04-AUG-1998; 98US-095285P.  
PR 04-AUG-1998; 98US-095301P.  
PR 04-AUG-1998; 98US-095302P.  
PR 04-AUG-1998; 98US-095318P.  
PR 04-AUG-1998; 98US-095321P.  
PR 04-AUG-1998; 98US-095325P.  
PR 10-AUG-1998; 98US-095916P.  
PR 10-AUG-1998; 98US-095929P.  
PR 10-AUG-1998; 98US-096012P.  
PR 11-AUG-1998; 98US-096143P.  
PR 11-AUG-1998; 98US-096146P.  
PR 12-AUG-1998; 98US-096329P.  
PR 17-AUG-1998; 98US-096757P.  
PR 17-AUG-1998; 98US-096766P.  
PR 17-AUG-1998; 98US-096768P.  
PR 17-AUG-1998; 98US-096773P.  
PR 17-AUG-1998; 98US-096791P.  
PR 17-AUG-1998; 98US-096867P.  
PR 17-AUG-1998; 98US-096891P.  
PR 17-AUG-1998; 98US-096894P.  
PR 17-AUG-1998; 98US-096895P.

PR 17-AUG-1998; 98US-096897P.  
PR 18-AUG-1998; 98US-096949P.  
PR 18-AUG-1998; 98US-096950P.  
PR 18-AUG-1998; 98US-096959P.  
PR 18-AUG-1998; 98US-096960P.  
PR 18-AUG-1998; 98US-097022P.  
PR 19-AUG-1998; 98US-097141P.  
PR 20-AUG-1998; 98US-097218P.  
PR 24-AUG-1998; 98US-097661P.  
PR 26-AUG-1998; 98US-097952P.  
PR 26-AUG-1998; 98US-097954P.  
PR 26-AUG-1998; 98US-097955P.  
PR 26-AUG-1998; 98US-097971P.  
PR 26-AUG-1998; 98US-097974P.  
PR 26-AUG-1998; 98US-097978P.  
PR 26-AUG-1998; 98US-097979P.  
PR 26-AUG-1998; 98US-097986P.  
PR 26-AUG-1998; 98US-098014P.  
PR 31-AUG-1998; 98US-098525P.  
PR 16-SEP-1998; 98US-100634P.  
PR 17-SEP-1998; 98US-100858P.  
PR 22-DEC-1998; 98US-113296P.  
PR 12-MAR-1999; 99US-123957P.  
PR 23-JUN-1999; 99US-141037P.

## Alignment Scores:

Pred. No.:	7,898-47	Length:	415
Score:	375.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	25	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x ABX80759 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAAGAAGCAACATTGAGATTATGCTGACGACCGAGGCTTTAAACACCCCGTTC 156  
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrPheIleAla 40  
DB 157 CTGAACATCGACAATTGCGATCTGCTTAAAGCTGATGAGTTCCTGAACCTGGCAGCC 216  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTyrAspAlaPheProLysLeu 60  
DB 217 CTCTTGAGTCTATCAAGAAGAACTCTTCTCACTGGGATGCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGGACTGAGGAGCGCACTCCTGATGCCAG 309

## RESULT 13

ABX81142  
ID ABX81142 standard; DNA; 415 BP.

XX AC ABX81142;

DT 22-APR-2003 (first entry)

DE Novel human secreted or transmembrane protein PRO819 DNA.

XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney; mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
XX OS Homo sapiens.

XX PN US2003027985-A1.  
XX PD 06-FEB-2003.  
XX PF 14-NOV-2001; 2001US-0990562.  
XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
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PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
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PR 30-MAR-2000; 2000WO-US08439.  
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PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
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PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
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PR 23-JUN-1998; 98US-090349P.  
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PR 17-AUG-1998; 98US-096867P.  
PR 17-AUG-1998; 98US-096891P.  
PR 17-AUG-1998; 98US-096894P.  
PR 17-AUG-1998; 98US-096895P.  
PR 17-AUG-1998; 98US-096897P.  
PR 18-AUG-1998; 98US-096949P.  
PR 18-AUG-1998; 98US-096950P.  
PR 18-AUG-1998; 98US-096959P.  
PR 18-AUG-1998; 98US-096960P.  
PR 18-AUG-1998; 98US-097022P.  
PR 19-AUG-1998; 98US-097141P.  
PR 20-AUG-1998; 98US-097218P.  
PR 24-AUG-1998; 98US-097661P.  
PR 26-AUG-1998; 98US-097952P.  
PR 26-AUG-1998; 98US-097954P.  
PR 26-AUG-1998; 98US-097955P.  
PR 26-AUG-1998; 98US-097971P.  
PR 26-AUG-1998; 98US-097974P.  
PR 26-AUG-1998; 98US-097978P.  
PR 26-AUG-1998; 98US-097979P.  
PR 26-AUG-1998; 98US-097986P.  
PR 26-AUG-1998; 98US-098014P.

## Alignment Scores:

Pred. No.:	7.89e-47	Length:	415
Score:	375.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	25	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x ABX81142 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAAGAAAGCACCATTTGAGATTATGCGTCACGACCGAGCCCTTAACACCCCGTTC 156  
QY 21 LeuAsnIleAspIleuArgSerAlaPheIleuAlaAspGluPheLeuAsnThrIleAla 40  
DB 157 CTGAACATCGACAATTCGATCTGCGTTAAGGCTGATGAGTTCCTGAACGGCAGGCC 216  
QY 41 LeuPheGluSerIleIleuArgIleuProPheLeuAsnTyrPaspAlaPheProIleu 60  
DB 217 CTCCTTGAGTCTATCAAAAGAACTTCCTTCTCACTGGGATGCCCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGGACTGAGGAGCGCACTCTGATGCCAG 309

## RESULT 14

ABX90232 ABX90232 standard; cDNA; 415 BP.

XX AC ABX90232;

XX DT 01-MAY-2003 (first entry)

DE Human secreted/transmembrane protein cDNA, #78.

KW Human; gene; ss; PRO; secreted; transmembrane; signal peptide; pharmaceutical; diagnostic; therapeutic; gene therapy.



Query Match: 100.00% Indels: 0  
DB: 25 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x ABX90232 (1-415)  
QY 1 Glu[GluserThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 97 GAGGAGAAAGCACCATTTGAGAATTATGCGTCACGACCCGAGGCTTTAAACCCCGTTC 156  
QY 21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACAAATTGCGATCTGCGTTAAGGCTGATGAGTTCCTGAAGTGGACGCGC 216  
QY 41 LeupheGluSerIleIysArgIysLeuProPheLeuAsnTrpAspAlaPheProIysLeu 60  
Db 217 CTCTTGAGTCTATCAAAAGAACTTCCTTCTCACTGGATGCGCTTCTTAAGCTG 276  
QY 61 LysGIysLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGACTGAGGAGCGCAACTCCTGATGCCAG 309  
RESULT 15  
ABX77843 ID ABX77843 standard; cDNA; 415 BP.  
XX AC ABX77843;  
XX DT 14-APR-2003 (first entry)  
XX DE Human PRO polynucleotide #51.  
XX KM Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;  
XX KW liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;  
XX KW antibody-dependent enzyme mediated prodrug therapy.  
OS Homo sapiens.  
XX PN US2003027163-A1.  
XX PD 06-FEB-2003.  
XX PF 15-NOV-2001; 2001US-0997666.  
XX XX  
PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.

PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
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PR 31-AUG-1998; 98US-098525P.  
PR 16-SEP-1998; 98US-100634P.  
PR 17-SEP-1998; 98US-100858P.

PR 22-DEC-1998; 98US-113296P.  
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Job time : 221 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 13:45:19 ; Search time 252 Seconds  
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928.266 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a  
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## ALIGNMENTS

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; Patent No. US20020072067A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
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; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zhen  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
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; PRIOR FILING DATE: 1998-07-09
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Petrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Goddard, Audrey
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
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; PRIOR FILING DATE: 1998-07-09

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; Patent No. US20020072496A1  
; GENERAL INFORMATION:



APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
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APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
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; PRIOR FILING DATE: 1998-07-09

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QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
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## RESULT 4

US-09-989-727-200

; Sequence 200, Application US/09989727  
; Patent No. US20020072497A1

## GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
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; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zhen  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
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; APPLICANT: Gerber, Hanspeter  
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; APPLICANT: Godowski, Paul J.  
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; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
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; APPLICANT: Baker, Kevin P.  
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; APPLICANT: Desnoyers, Luc  
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; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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## GENERAL INFORMATION:

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: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
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: TITLE OF INVENTION: Acids Encoding the Same
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#### RESULT 8

US-09-990-442-200

; Sequence 200, Application US/09990442

; Patent No. US20020132252A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
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; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.

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APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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## RESULT 9

US-09-991-163-200  
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; Patent No. US20020132253A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Kljavin, Ivar J.  
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; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David

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APPLICANT: Zhang, Zemin  
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; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

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Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

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DB 157 CTGAACATCGACAAATGCGATCTGCGTTTAAGGCTGATGAGTTCTCTGAACGCGCC 216  
OY 41 leuPheGluSerIleIysArgIlyleuProPheleuAsnTrpAspAlaPheProIysleu 60  
DB 217 CTCTTTGAGTCTATCAAAAGAAACTTCTTCTCAACTGGGATGCTTCTTAAGCTG 276  
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; Patent No. US20020137890A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
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; APPLICANT: Gerritsen, Mary B.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: KJaviin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
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; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: p2730P1C22  
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; PRIOR FILING DATE: 1998-07-09

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Db 157 CTGACATCGACCAATGCGATCTGCGTTTAAGCGTGAATGATTCCTGAAGTGGACGCC 216  
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; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
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; APPLICANT: Williams, P. Mickey  
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; TITLE OF INVENTION: Acids Encoding the Same  
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PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
Pred. No.: 6.08e-48  
Score: 375.00  
Percent Similarity: 100.00%

Length: 415  
Matches: 71  
Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-989-721-200 (1-415)

QY 1 GIUGLUGLUSERTHRILEGUASNTYRLASERARGPROGLUALAPHEASNTHRPROPHE 20  
DB 97 GAGGAAGAAAGCACCAATTGAGAAATTATGCGTCACGACCCGAGCCCTTAACCCCGTTC 156  
QY 21 LEUASNILEASPLYLEUARGSERALAPHELYSALAASPGLUPEHELEUASNTGPHISALA 40  
DB 157 CTGAACATGACAAATTGCGATCTGCGTTAAGGTGATGAGTTCCTGAACCTGCAAGCC 216  
QY 41 LEUPHEGLUSERILEYSAAGLYSLEUPROPHLEUASNTTPASPALAPHEPROLYSLEU 60  
DB 217 CTCTTGAGTCTATCAAGAAACTTCCTTCTCAACTGGATGCCCTTCTTAAGCTG 276  
QY 61 LYSGLYLEUARGSERALATHRPROASPALAGLN 71  
DB 277 AAAGACTGAGAGCGCACTCCTGATGCCAG 309

## RESULT 13

US-09-992-598-200

Sequence 200, Application US/09992598

Patent No. US20020160384A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey J.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C20  
CURRENT APPLICATION NUMBER: US/09/992,598  
PRIOR APPLICATION NUMBER: 2001-11-14  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600

[illegible]

;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.:	6,08e-48	Length:	415
Score:	375.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-992-598-200 (1-415)

Qy 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
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Db 97 GAGGAAGAAAGCACCATTGAGATTATGCGTCACGACCCGAGCGCTTTAACACCCCGTTC 156  
  
Qy 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
|||  
Db 157 CTGAACATCGACAAATTGCGATCTGCGTTTAAGGCTGATGAGTTCCTGAACCTGGCACGCC 216  
  
Qy 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
|||  
Db 217 CTCCTTGAGTCTATCAAAAGGAACCTTCCTTCTCAACTGGATGCGCTTCTTAAGCTG 276  
  
Qy 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
|||  
Db 277 AAAGACTGAGAGCGCAACTCCTGATGCCAG 309

## RESULT 14

US-09-989-293A-200  
; Sequence 200, Application US/09989293A  
; Patent No. US20020177164A1

## GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerlitsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Goddard, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kljavin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC66  
; CURRENT APPLICATION NUMBER: US/09/989,293A  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311

;; PRIOR FILING DATE: 1997-11-13  
;; PRIOR APPLICATION NUMBER: 60/066770  
;; PRIOR FILING DATE: 1997-11-24  
;; PRIOR APPLICATION NUMBER: 60/075945  
;; PRIOR FILING DATE: 1998-02-25  
;; PRIOR APPLICATION NUMBER: 60/078910  
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;; PRIOR FILING DATE: 1998-05-07  
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;; PRIOR APPLICATION NUMBER: 60/089514  
;; PRIOR FILING DATE: 1998-06-16

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;; PRIOR FILING DATE: 1998-06-19  
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;; PRIOR FILING DATE: 1998-06-22  
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;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478

;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.:	6.08e-48	Length:	415
Score:	375.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-989-293A-200 (1-415)

QY 1 GUGUGUGUSeRThrIleGluAsnTYrAlaSeRArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAGAAAGCACCATTGAGATTATGCGTCACGACCCGAGGCTTTAAACACCCCGCTC 156

QY 21 LeuAsnIleAspIlySeuArgSerAlaPheIlySAlaAspGluPheLeuAsnTrpHisAla 40  
DB 157 CTGAACATCGACAATTCGATTCGCTTAAAGGCTGATGAGTTCGAACTGGCAGCC 216

QY 41 LeupheGluSerIleIlySArgIlySeuProPheLeuAsnTrpAspAlaPheProIlySeu 60  
DB 217 CTCTTGAGCTATCAAAAGAACTTCCTTCTCAACTGGGATGCTTCTTAAGCTG 276

QY 61 IyegIlyeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGAGCGCACTCTGATGCCAG 309

## RESULT 15

US-09-989-735-200

; Sequence 200, Application US/09989735

; Publication No. US20020193299A1

; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary B.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kjaevlin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; TITLE OF INVENTION: Acids Encoding the Same





; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: 60/090696  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: 60/090862  
; PRIOR FILING DATE: 1998-06-26  
; PRIOR APPLICATION NUMBER: 60/090863  
; PRIOR FILING DATE: 1998-06-26  
; PRIOR APPLICATION NUMBER: 60/091360  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091478  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091544  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091519  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091626  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091633  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.:	6.08e-48	Length:	415
Score:	375.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-989-735-200 (1-415)

QY	1	GlUGlUGlUSeRThrIlEgLUaenTYrAlaSeRArgProGluAlaPheAsnThrProPhe	20
Db	97	GAGGAAGAAAGCACCATTTGAGAAATTATGCGTCAAGACCCGAGGCTTTAAACACCCCGTTTC	156
QY	21	LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla	40
Db	157	CTGAACATCGACAATTCGATTCGCTTTAAGGCTGATGAGTTCTGAACTGGCACGCC	216
QY	41	LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu	60
Db	217	CTCTTGAGTCTATCAAAAGAACTTCCTTCTCAACTGGAGTGCCCTTCTTAAGCTG	276
QY	61	LysGlyLeuArgSerAlaThrProAspAlaGln	71
Db	277	AAAGGACTGAGGAGCGCACTCCTGATGCCAG	309

Search completed: November 28, 2003, 15:05:24  
Job time : 258 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 13:44:14 ; Search time 1605 Seconds

(without alignments)  
1075.151 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99  
Perfect score: 375

Sequence: 1 EESTIENTYASRPEAFNTFF.....LNMDFPKLKGLRSATPDAQ 71

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Deiop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO\_spool/US10059395/runat\_25112003\_141913\_11706/app\_query.fasta\_1.263  
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10059395 @CGN 1 1 2810 @runat\_25112003\_141913\_11706 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DEIOP=6 -DELEXT=7

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vr1:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	375	100.0	318 9	AA586846	AA586846 nm67e11.s
C 2	375	100.0	334 9	AA297512	AA297512 EST113061
C 3	375	100.0	339 9	AA778414	AA778414 zt39e05.s
C 4	375	100.0	348 9	AW238758	AW238758 xp03e08.x
C 5	375	100.0	359 10	BE466728	BE466728 h224g06.x
C 6	375	100.0	362 9	AI140605	AI140605 qe05f03.x
C 7	375	100.0	373 9	AA722694	AA722694 z982b06.s
C 8	375	100.0	381 14	W69108	W69108 zd44c04.s1
C 9	375	100.0	394 14	W60320	W60320 zd29g01.s1
C 10	375	100.0	412 14	W60268	W60268 zd29g01.r1
C 11	375	100.0	424 14	W69083	W69083 zd44b06.s1
C 12	375	100.0	432 13	BX112106	BX112106 BX112106
C 13	375	100.0	432 14	W69233	W69233 zd44c04.r1
C 14	369	98.4	359 10	BG150312	BG150312 7j98g03.x
C 15	364	97.1	378 9	AI184682	AI184682 qd68b02.x
C 16	362	96.5	413 9	AA393296	AA393296 zc74f05.r
C 17	362	96.5	431 14	W69227	W69227 zd44b06.r1
C 18	352	93.9	358 9	AW003825	AW003825 wg33f12.x
C 19	343	91.5	345 9	AI217565	AI217565 qd43d02.x
C 20	341	90.9	377 9	AA582988	AA582988 nm72h02.s
C 21	328	87.5	334 9	AI217587	AI217587 qd43f04.x
C 22	323.5	86.3	326 9	AA297513	AA297513 EST113062
C 23	300	80.0	241 9	AA595989	AA595989 nm64g08.s
C 24	286	76.3	345 9	AA583942	AA583942 nm64f07.s
C 25	286	76.3	376 14	W95920	W95920 ze08d01.r1
C 26	280	74.7	330 14	W95883	W95883 ze08d01.s1
C 27	276.5	73.7	421 9	AV618771	AV618771 AV618771
C 28	258	68.8	339 14	W52030	W52030 zd13b01.s1
C 29	252	67.2	436 9	AV597545	AV597545 AV597545
C 30	225	60.0	368 9	AW260965	AW260965 EQUK0243
C 31	222.5	59.3	444 12	BI286103	BI286103 UI-R-DDO-
C 32	219.5	58.5	394 12	BI281142	BI281142 UI-R-DDO-
C 33	219.5	58.5	446 12	BI283220	BI283220 UI-R-DDO-
C 34	219.5	58.5	448 12	BI282568	BI282568 UI-R-DDO-
C 35	219.5	58.5	452 12	BI277693	BI277693 UI-R-CZO-
C 36	219.5	58.5	454 12	BI282573	BI282573 UI-R-DDO-
C 37	219.5	58.5	461 12	BI285632	BI285632 UI-R-DDO-
C 38	219.5	58.5	466 12	BI277761	BI277761 UI-R-CZO-
C 39	218	58.1	239 9	AA595930	AA595930 nm66a07.s
C 40	214	57.1	344 9	AA619595	AA619595 v154a08.r
C 41	214	57.1	346 13	BY137356	BY137356 BY137356
C 42	214	57.1	382 9	AA727573	AA727573 vu97a02.r
C 43	214	57.1	386 9	AA169065	AA169065 me21b01.r
C 44	214	57.1	409 9	AA572239	AA572239 v151g12.r
C 45	214	57.1	427 9	AA726579	AA726579 vu93a07.r

#### ALIGNMENTS

RESULT 1  
AA586846/c 318 bp mRNA EST 26-SEP-1997  
LOCUS nm67e11.s1 NCI\_CGAP\_lar1 Homo sapiens cDNA clone IMAGE:1088972 3',  
DEFINITION mRNA sequence.  
ACCESSION AA586846  
VERSION AA586846.1 GI:2397660  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 318)

**AUTHORS** NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
**JOURNAL** Unpublished  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.  
 Bmmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Stratagene, Inc.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/BLNL at:  
[www-bio.lnl.gov/bbrp/image/image.html](http://www-bio.lnl.gov/bbrp/image/image.html)  
 Insert length: 465 Std Error: 0.00  
 Seq primer: -40ml3 fwd. ET from Amersham.

**FEATURES**  
 source location/Qualifiers

1..318  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1088972"  
 /tissue\_type="larynx"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /clone\_lib="NCI CGAP lary" /  
 /note="Organ: larynx; Vector: Bluescript SK-; Site\_1:  
 EcoRI; Site\_2: XhoI; Cloned unidirectionally. Primer:  
 Oligo dT. larynx. 5' adaptor sequence: 5' GAATTCGGCAGCAG  
 3' 3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'  
 Average insert size: 0.9 kb."  
 BASE COUNT 76 a 67 c 90 g 85 t  
 ORIGIN

**Alignment Scores:**  
 Pred. No.: 4.66e-44 Length: 318  
 Score: 375.00 Matches: 71  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AA586846 (1-318)

QY 1 GtuglgluserThrllgluasntYrAlaserArpProgluaAlapheAsnThrProphe 20  
 |||||  
 DB 316 GAGGAAGAAAGCAACCATGTGAGATTTGCGTCACGACCCGAGGCTTTAACCCTTC 257  
 QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
 |||||  
 DB 256 CTGAACATCGACAATTTGCGATTCGCTTTAAGGCTGATGATTCCTGAACCTGGACAGCC 197  
 QY 41 LeuphegluserIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
 |||||  
 DB 196 CTCCTTGAGTCTATCAAAAGAAACTTCCTTCTCAACTGGATGCTTCTTAAGCTG 137

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
 |||||  
 DB 136 AAAGGACTGAGAGCGCAACTCTGATGCCAG 104

**RESULT 2**  
 AA297512 334 bp mRNA linear EST 18-APR-1997  
 LOCUS EST113061 Fetal skin Homo sapiens cDNA 5' end, mRNA sequence.  
 DEFINITION  
 AA297512  
 ACCESSION  
 VERSION AA297512.1 GI:1949866  
 KEYWORDS  
 EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
 1 (bases 1 to 334)  
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult  
 ,C.J., Lee,N.H., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D., White

,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,  
 Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald  
 ,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodex,A.,  
 Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,  
 Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,  
 Moreno-Palanges,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,  
 Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R.,  
 Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,  
 Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,  
 Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.,  
 Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,  
 Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L.,  
 Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon  
 ,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and  
 Venter,J.C.  
 Initial assessment of human gene diversity and expression patterns  
 based upon 83 million nucleotides of cDNA sequence  
 Nature 377 (6547 Suppl), 3-174 (1995)  
 96026280  
 MEDLINE 7566098  
 PUBMED  
 COMMENT Other\_ESTs: THCI51622  
 Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: [arkerlav@tigr.org](mailto:arkerlav@tigr.org)  
 For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/cdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse.

**FEATURES**  
 source location/Qualifiers

1..334  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="ATCC (lnhost):141532"  
 /db\_xref="taxon:9606"  
 /tissue\_type="epithelium"  
 /cell\_type="epithelial cell"  
 /dev\_stage="fetus"  
 /clone\_lib="Fetal skin"  
 /note="Organ: skin; Vector: pBluescript SK-; Site\_1: EcoRI  
 ; Site\_2: XhoI"  
 BASE COUNT 77 a 100 c 78 g 78 t 1 others  
 ORIGIN

**Alignment Scores:**  
 Pred. No.: 4.99e-44 Length: 334  
 Score: 375.00 Matches: 71  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AA297512 (1-334)

QY 1 GtuglgluserThrllgluasntYrAlaserArpProgluaAlapheAsnThrProphe 20  
 |||||  
 DB 98 GAGGAAGAAAGCAACCATGTGAGATTTGCGTCACGACCCGAGGCTTTAACCCTTC 157

QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
 |||||  
 DB 158 CTGAACATCGACAATTTGCGATTCGCTTTAAGGCTGATGATTCCTGAACCTGGACAGCC 217

QY 41 LeuphegluserIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
 |||||  
 DB 218 CTCCTTGAGTCTATCAAAAGAAACTTCCTTCTCAACTGGATGCTTCTTAAGCTG 277

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
 |||||  
 DB 278 AAAGGACTNAGAGCGCAACTCTGATGCCAG 310

```

RESULT 3
AA778414/c 339 bp mRNA linear EST 05-FEB-1998
LOCUS AA778414
DEFINITION 2f39e05.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
IMAGE:379328 3', mRNA sequence.
ACCESSION AA778414
VERSION AA778414.1 GI:2837745
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 339)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin,
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
TITLE Unpublished
JOURNAL
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham.

FEATURES
Source
1..339
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1287584"
/db_xref="taxon:9606"
/clone="IMAGE:379328"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NbHH19W"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHH19W."

BASE COUNT 79 a 77 c 96 g 87 t
ORIGIN
Alignment Scores:
Pred. No.: 5.1e-44 Length: 339
Score: 375.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 9

US-10-059-395-142_COPY_29_99 (1-71) x AA778414 (1-339)
QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20
Db 316 GAGGAAGAAAGCACCATTTGAGAAATTATGCTACAGACCCGAGGCTTTTAAACACCCGCTTC 257
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40
Db 256 CTGAACATCGACCAATTGGATCTGCTTTAAAGGCTGATGAGTCTCTGAACCTGGCAGCC 197
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60

```

```

Db 196 CTCTTTGAGTCTATCAAGAACTTCCTTCTCACTGGATGCTTCTTAAGCTG 137
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71
Db 136 AAAGACTGAGGAGCGCACTCTGATGCCAG 104

RESULT 4
AW238758 348 bp mRNA linear EST 13-DEC-1999
LOCUS AW238758
DEFINITION xp03e08.x1 NCI_CGAP_HN8 Homo sapiens cDNA clone IMAGE:2739302 3',
mRNA sequence.
ACCESSION AW238758
VERSION AW238758.1 GI:6571147
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 348)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Edward Shillitoe Ph.D., Silvio Gutkind Ph.D.,
Chidchanok Leethanakul D.D.S., Michael Emmert-Buck M.D. Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bbrp/image/image.html

FEATURES
Source
Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 331.
Location/Qualifiers
1..348
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2739302"
/tissue_type="well-differentiated invasive carcinoma,
floor of mouth"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_HN8"
/note="Vector: pAMP10; cDNA made by oligo-dT priming.
Non-directionally cloned into the UDG sites of pAMP10.
Size-selected on agarose gel, average insert size 500 bp.
Primary library; non-amplified. cDNA library
Preparation: David B. Krizman, Ph.D (NCI). Reference:
Krizman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT 82 a 104 c 84 g 78 t
ORIGIN
Alignment Scores:
Pred. No.: 5.3e-44 Length: 348
Score: 375.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 9

US-10-059-395-142_COPY_29_99 (1-71) x AW238758 (1-348)
QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20
Db 81 GAGGAAGAAAGCACCATTTGAGAAATTATGATCAAGACCCGAGGCTTTAAACACCCGCTTC 140
QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40

```

Db 141 CTGACATCGACAATTGCGATCTGCTTTAAGGCTGATGAGTCTCTGAAGTGGACGCC 200

Qy 41 LeuphegluserilelysarglysleuProphleuAsnTrpAspAlaPheProlylsleu 60  
|||||  
Db 201 CTCCTTGAGTCTATCAAAAGGAACTTCCTTCTCAACTGGATGCGCTTCTTAAGCTG 260

Qy 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
|||||  
Db 261 AAAGGACTGAGGAGCGCACTCCTGATGCCAG 293

RESULT 5  
BE466728/c 359 bp mRNA linear EST 27-JUL-2000  
LOCUS h224g06.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:3208954 3',  
DEFINITION mRNA sequence.  
ACCESSION BE466728 GI:9512503  
VERSION BE466728.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 359)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL, send email to: [info@image.lnl.gov](mailto:info@image.lnl.gov)  
Seq primer: -40UP from Gibco.  
FEATURES  
Source location/Qualifiers  
1..359  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3208954"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_GC6"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA from the normalized library NCI\_CGAP GC4 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 77 a 80 c 96 g 106 t  
ORIGIN

Alignment Scores: 5.54e-44 Length: 359  
Pred. No.: 375.00 Matches: 71  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
DB: 10

US-10-059-395-142\_COPY\_29\_99 (1-71) x BE466728 (1-359)

Qy 1 GluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
|||||  
Db 332 GAGGAAGAAAGCACCATGTGGAATATATGCGTCAGACCGAGGCTTTAAACACCCGTTTC 273

Qy 21 LeuAsnIleAspIleuArgSerAlaPheIleAlaAspGluPheLeuAsnTrpHisAla 40  
|||||  
Db 272 CTGACATCGACAATTGCGATCTGCGTTTAAAGCTGATGAGTCTCTGAAGTGGACGCC 213

Qy 41 LeuphegluserilelysarglysleuProphleuAsnTrpAspAlaPheProlylsleu 60  
|||||  
Db 212 CTCCTTGAGTCTATCAAAAGGAACTTCCTTCTCAACTGGATGCGCTTCTTAAGCTG 153

Qy 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
|||||  
Db 152 AAAGGACTGAGGAGCGCACTCCTGATGCCAG 120

RESULT 6  
A1140605/c 362 bp mRNA linear EST 29-OCT-1998  
LOCUS ge05f03.x1 Soares testis\_NHT Homo sapiens cDNA clone IMAGE:1738109  
DEFINITION 3', mRNA sequence.  
ACCESSION A1140605  
VERSION A1140605.1 GI:3648062  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 362)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: [www.bio.lnl.gov/bbrp/image/image.html](http://www.bio.lnl.gov/bbrp/image/image.html)  
Insert length: 425 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham.  
FEATURES  
Source location/Qualifiers  
1..362  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1738109"  
/sex="male"  
/lab\_host="DH10B"  
/clone\_lib="Soares testis\_NHT"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTTCTTTTCTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 77 a 81 c 99 g 105 t  
ORIGIN

Alignment Scores: 5.6e-44 Length: 362  
Pred. No.: 375.00 Matches: 71  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
DB: 9

US-10-059-395-142\_COPY\_29\_99 (1-71) x A1140605 (1-362)



Qy	1	Glut1glut1serThr1leu1asnTyr1alaSer1argPro1gual1aphe1asnThr1Pro1phe	20
Db	331	GAGGAAGAAAGCACCATTTGAGAAATTATGCGTCACGACCGAGGCTTTAAACACCCCGTTC	272
Qy	21	Leu1asn1leu1asp1lys1leu1arg1Ser1ala1Phe1lys1ala1asp1Glu1phe1Leu1asn1Trp1his1ala	40
Db	271	CTGAACATCGACAATTTGCGATTCTGCGTTTAAAGGCTGATGAGTTCTCGAACTGGCACGCTC	212
Qy	41	Leu1Phe1Glu1Ser1le1lys1arg1lys1leu1Pro1Phe1Leu1asn1Trp1Asp1ala1Phe1Pro1lys1leu	60
Db	211	CTCTTTGAGTCTATCAAAAGGAACTTCCTTCCTCACTGGGATGCGCTTTCCTAAGCTG	152
Qy	61	Lys1Gly1Leu1Arg1Ser1ala1Thr1Pro1Asp1ala1Gln	71
Db	151	AAAGGACTGAGAGCGCACTCCTGATGCCAG	119
RESULT 7			
AA722694/c			
LOCUS	AA722694	373 bp	mRNA
DEFINITION	z982b06.s1 Soares fetal heart NbHL19W	linear	EST 02-JAN-1998
ACCESSION	AA722694		
VERSION	AA722694.1	GI:2740401	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Scheilenberg, K., Steptoe, M., Tan, F., Thelshing, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.		
TITLE	WashU-NCI human EST Project		
JOURNAL	Unpublished		
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LIND; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Seq primer: -40m13 fwd. ET from Amerham.		
FEATURES	source		
	1..373		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="GDB:1307650"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:399827"		
	/sex="unknown"		
	/dev_stage="19 weeks"		
	/lab_host="DH10B (ampicillin resistant)"		
	/clone_lib="Soares_fetal_heart_NbHL19W"		
	/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' GTTACCAATCTGAAGTGGAGCGCGCCGCACTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."		
BASE COUNT	89 a	81 c	113 g 90 t
ORIGIN			
Alignment Scores:			
Pred. No.:	5.85e-44	length:	373
Score:	375.00	Matches:	71

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0
US-10-059-395-142_COPY_29_99 (1-71) x AA722694 (1-373)			
QY	1	GLUGLUGLuserThrIleGLUasntYrAlaSerArgProGLUAlaPheAsnthrProphe	20
Db	319	GAGGAGAAAGCACCATTGAGATATTATGCGTCACGACCCGAGGCCCTTTAACACCCCGTTC	260
QY	21	LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla	40
Db	259	CTGAACATCGACAAATTGCGATCTGCGTTTAAAGCTGATGAGTTCCTGAATGCGACGCC	200
QY	41	LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu	60
Db	199	CTCTTGAGTCTATCAAAAGAACTTCCTTCTCAACTGGATGCCCTTCTTAAGCTG	140
QY	61	LysGLYLeuArgSerAlaThrProAspAlaGln	71
Db	139	AAAGGACTGAGAGCGCAACTCCTGATGCCAG	107
RESULT 8			
W69108/c LOCUS 381 bp mRNA linear EST 16-OCT-1996			
DEFINITION zd44c04.s1 Soares fetal_heart_NBHH19W Homo sapiens cDNA clone			
IMAGE:343494 3', mRNA sequence.			
W69108			
W69108.1 GI:1378389			
EST.			
Homo sapiens (human)			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
1 (bases 1 to 381)			
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman			
, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maira, M., Parsons, J.,			
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston			
, R., Williamson, A., Wohlmann, P. and Wilson, R.			
The WashU-Merck EST Project			
Unpublished			
Contact: Wilson RK			
Washington University School of Medicine			
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108			
Tel: 314 286 1800			
Fax: 314 286 1810			
Email: est@watson.wustl.edu			
This clone is available royalty-free through LNL; contact the			
IMAGE Consortium (info@image.lnl.gov) for further information.			
Insert Length: 442 Std Error: 0.00			
Seq primer: mob.REGA+BT			
High quality sequence stop: 347.			
Location/Qualifiers			
1..381			
/organism="Homo sapiens"			
/mol_type="mRNA"			
/db_xref="GDB:1268869"			
/db_xref="taxon:9606"			
/clone="IMAGE:343494"			
/sex="unknown"			
/dev_stage="19 weeks"			
/lab_host="DH10B (ampicillin resistant)"			
/clone_lib="Soares_fetal_heart_NBHH19W"			
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a			
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st			
strand cDNA was primed with a Not I - oligo(dT) primer [5'			
TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3']			
double-stranded cDNA was size selected, ligated to Eco RI			
adapters (Pharmacia), digested with Not I and cloned into			
the Not I and Eco RI sites of a modified pT7T3 vector			
(Pharmacia). Library went through one round of			
normalization to a Cot = 5. Library constructed by			



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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1267471"
/db_xref="taxon:9606"
/clone="IMAGE:342096"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_1lb="Soares fetal heart NbHL19W"
/note="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGGCATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHL19W."
```

```
BASE COUNT      96 a      88 g      98 t      3 others
ORIGIN
Alignment Scores:
Pred. No.:      6.74e-44      Length:      412
Score:          375.00      Matches:      71
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              14      Gaps:      0
```

US-10-059-395-142\_COPY\_29\_99 (1-71) x W60268 (1-412)

```
QY      1 GUGUGUGUSeRThrIleGluAnTYrAlaSeRgProGluAlaPheAsnThrProPhe 20
      |||||
Db      97 GAGGAAGAAAGCACCATTGAGAAATTATGCGTCACGACCCGAGCCTTTAACACCCCGTTC 156
QY      21 LeuAsnIleAspLySLeuArgSerAlaPheLySAlaAspGluPheLeuAsnTrpHisAla 40
      |||||
Db      157 CTGAACATCGACAATTCGATTCGCTTAAAGGCTGATGAGTTCCTGAAGTGGCAGGCC 216
QY      41 LeuPheGluSerIleLySArgLySLeuProPheLeuAsnTrpAspAlaPheProLySLeu 60
      |||||
Db      217 CTCTTGAGTCTATCAAAAGAACTTCCTTCTCAACTGGAGTGCCTTCTTAAGCTG 276
QY      61 LySGLyLeuArgSerAlaThrProAspAlaGln 71
      |||||
Db      277 AAAGGACTGAGGAGCGCAACTCCTGATGCCAG 309
```

```
RESULT 11
W69083/c      424 bp      mRNA      linear      EST 16-OCT-1996
LOCUS      zd44b06.s1 Soares fetal heart NbHL19W Homo sapiens cDNA clone
DEFINITION      IMAGE:343475 3', mRNA sequence.
```

ACCESSION W69083  
VERSION W69083.1 GI:1378383  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 424)  
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE The Washu-Merck EST Project  
JOURNAL Unpublished  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800

Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Insert length: 466 Std Error: 0.00  
Seq primer: mob.REGA+ET  
High quality sequence stop: 339.  
Location/Qualifiers

#### FEATURES

Source

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1. 424
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1268850"
/db_xref="taxon:9606"
/clone="IMAGE:343475"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_1lb="Soares fetal heart NbHL19W"
/note="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGGCATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHL19W."
```

```
BASE COUNT      98 a      100 c      129 g      97 t
ORIGIN
```

```
Alignment Scores:
Pred. No.:      7.02e-44      Length:      424
Score:          375.00      Matches:      71
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              14      Gaps:      0
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US-10-059-395-142\_COPY\_29\_99 (1-71) x W69083 (1-424)

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QY      1 GUGUGUGUSeRThrIleGluAnTYrAlaSeRgProGluAlaPheAsnThrProPhe 20
      |||||
Db      317 GAGGAAGAAAGCACCATTGAGAAATTATGCGTCACGACCCGAGCCTTTAACACCCCGTTC 258
QY      21 LeuAsnIleAspLySLeuArgSerAlaPheLySAlaAspGluPheLeuAsnTrpHisAla 40
      |||||
Db      257 CTGAACATCGACAATTCGATTCGCTTAAAGGCTGATGAGTTCCTGAAGTGGCAGGCC 198
QY      41 LeuPheGluSerIleLySArgLySLeuProPheLeuAsnTrpAspAlaPheProLySLeu 60
      |||||
Db      197 CTCTTGAGTCTATCAAAAGAACTTCCTTCTCAACTGGAGTGCCTTCTTAAGCTG 138
QY      61 LySGLyLeuArgSerAlaThrProAspAlaGln 71
      |||||
Db      137 AAAGGACTGAGGAGCGCAACTCCTGATGCCAG 105
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RESULT 12
BX112106      432 bp      mRNA      linear      EST 07-FEB-2003
LOCUS      BX112106 Soares fetal heart NbHL19W Homo sapiens cDNA clone
DEFINITION      IMAGE:342096, mRNA sequence.
```

ACCESSION BX112106  
VERSION BX112106.1 GI:27878783  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 432)  
AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,

TITLE  
Human Unigeneset - RZPD3  
JOURNAL  
Unpublished  
COMMENT  
Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; IMAGP98D01781.  
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No.972)  
http://www.rzpd.de/Cloncards/cgi-bin/showlib.pl.cgi?response?libNo=972  
Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de

This clone is available royalty-free from RZPD;  
contact RZPD (clone@rzpd.de) for further information. Seq primer:  
M13r, Primer sequence: TTTCACACAGGAACAGCTATGAC.

## FEATURES

source

1.432  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGP98D01781 ; IMAGE:342096"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal heart NBH19W"  
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dt) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Facima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBH19W."

BASE COUNT 113 a 129 c 92 g 98 t  
ORIGIN

## Alignment Scores:

Pred. No.: 7.21e-44 Length: 432  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x BX112106 (1-432)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 99 GAGGAAGAAAGCACCATTGAGATATGCGTCACGACCCGAGGCTTTAAACACCCCGTTC 158  
QY 21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnTyrPheAla 40  
DB 159 CTGAACATCGACAAATTGCGATCTGCGTTTAAAGGCTGATGAGTTCTTGAAGTGGCAGGCC 218  
QY 41 LeuPheGluSerIleLeuArgIysLeuProPheLeuAsnTyrAspAlaPheProIysLeu 60  
DB 219 CTCTTTGAGTCTATCAAAAGAACTTCTTCTCTCAACTGGGATGCCCTTCTTAAGCTG 278  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 279 AAAGAGCTGAGGAGCGCAACTCTGATGCCAG 311

RESULT 13  
W69233 432 bp mRNA linear EST 16-OCT-1996  
LOCUS

DEFINITION zd44c04.r1 Soares fetal\_heart\_NBH19W Homo sapiens cDNA clone  
IMAGE:343494 5', mRNA sequence.  
ACCESSION W69233  
VERSION W69233.1 GI:1378493  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 432)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maira, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.  
The WashU-Merck EST Project

TITLE  
JOURNAL  
COMMENT

Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Insert Length: 442 Std Error: 0.00  
Seq primer: mob.REGA+ET  
High quality sequence stop: 341.

## FEATURES

source

1.432  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:1268869"  
/db\_xref="taxon:9606"  
/clone="IMAGE:343494"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal heart NBH19W"  
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dt) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Facima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBH19W."

BASE COUNT 106 a 127 c 94 g 102 t 3 others  
ORIGIN

## Alignment Scores:

Pred. No.: 7.21e-44 Length: 432  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x W69233 (1-432)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 96 GAGGAAGAAAGCACCATTGAGATATGCGTCACGACCCGAGGCTTTAAACACCCCGTTC 155  
QY 21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnTyrPheAla 40  
DB 156 CTGAACATCGACAAATTGCGATCTGCGTTTAAAGGCTGATGAGTTCTTGAAGTGGCAGGCC 215  
QY 41 LeuPheGluSerIleLeuArgIysLeuProPheLeuAsnTyrAspAlaPheProIysLeu 60



Db 216 CTCTTGAGTCTATCAAAAGAACTTCCTTCTCACTGGATGCTTCTTAAGCTG 275

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
|||||  
Db 276 AAAGAGCTGAGAGCGCACTCTGATGCCCAA 308

RESULT 14  
-BG150312/c 359 bp mRNA linear EST 05-FEB-2001  
LOCUS 739803.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:3443116 3',  
DEFINITION mRNA sequence.  
ACCESSION BG150312  
VERSION BG150312.1 GI:12662342  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 359)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
info@image.llnl.gov  
Seq primer: -40UP from Gibco.  
FEATURES  
source  
1..359  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3443116"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP GC6"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA  
from the normalized library NCI\_CGAP\_GC4 was prepared, and  
as circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (cloneids  
1257096-1258631, 1469064-1470983, and 1475592-1476743).  
Subtraction by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 78 a 80 c 96 g 105 t  
ORIGIN  
Alignment Scores: 4.08e-43 Length: 359  
Pred. No.: 369.00 Matches: 70  
Score: 98.59% Conservative: 0  
Percent Similarity: 98.59% Mismatches: 1  
Best Local Similarity: 98.40% Indels: 0  
Query Match: 98.40% Gaps: 0  
DB: 10  
US-10-059-395-142\_COPY\_29\_99 (1-71) x BG150312 (1-359)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
|||||  
Db 332 GAGGAAGAAAGCACCATTTGAGAAATATGCTCAGACCCGAGGCTTTAAACCCCGCTTC 273

QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrPheIleAla 40  
|||||  
Db 272 TTGAACATGACAAATGCGATCTGCGTTTAAAGGCTGATGATTCCTGAAGCTGGACGCC 213

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTyrAspAlaPheProLysLeu 60  
|||||  
Db 212 CTCTTGAGTCTATCAAAAGAACTTCCTTCTCACTGGATGCTTCTTAAGCTG 153

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
|||||  
Db 152 AAAGAGCTGAGAGCGCACTCTGATGCCCAG 120

RESULT 15  
A1184682 378 bp mRNA linear EST 28-OCT-1998  
LOCUS qd68b02.x1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1734603  
DEFINITION 3', mRNA sequence.  
ACCESSION A1184682  
VERSION A1184682.1 GI:3735320  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 378)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert Length: 419 Std Error: 0.00  
Seq primer: -40UP from Gibco.  
FEATURES  
source  
1..378  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1734603"  
/sex="male"  
/lab\_host="DH10B"  
/clone\_lib="Soares testis NHT"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech Laboratories  
, Inc., and primed with a Not I - oligo(dt) primer [5',  
TGTTACCAATCTGAAGTGGAGCGCGCCCAATTCTTTTCTTTT 3'].  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. Library  
went through one round of normalization to Cots, and was  
constructed by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 80 a 89 c 105 g 104 t  
ORIGIN  
Alignment Scores: 2.32e-42 Length: 378  
Pred. No.: 364.00 Matches: 69  
Score: 97.18% Conservative: 0  
Percent Similarity: 97.18% Mismatches: 2  
Best Local Similarity: 97.07% Indels: 0  
Query Match: 97.07% Gaps: 0  
DB: 9  
US-10-059-395-142\_COPY\_29\_99 (1-71) x A1184682 (1-378)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
|||||  
Db 327 GAGGAAGAAAGCACCATTTGAGAAATATGCTCAGACCCGAGGCTTTAAACCCCGCTTC 268



```
QY      21 LeuAsnIleAspIleuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40
Db      267 CTGAACATCGACAAATTGCGATGTGCGTTTAAGGCTGATGATTCCTGAACGCGACGCC 208
QY      41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60
Db      207 CTCTTGAGTCTATCAAAAGAACTTCCTTCTCAAGTGGGATGCTTCTCTAAGCTG 148
QY      61 LysGlyLeuArgSerAlaThrProAspAlaGln 71
Db      147 AAAGGACTGAGGAGCGCACTCCTGATGCCAG 115
```

Search completed: November 28, 2003, 15:00:00  
Job time : 1608 secs